		ataatatacc	toocacacga	tctacacgcc	ccggagttat	60
caaagagaaa	aggegegeag	atggtatget	testatoco	gatetettee	accatatett	120
tcgcttctga	gatcgtcgag	tacttcgtcg	tactigitee	*****	accatatett	180
+	c++cattttc	ctacggtctt	cteetagcga	LLCLLEGGLLL	Cataatagee	
**********	ctatecttac	tttgtcggct	gtactgttga	tgtcttcaac	gaagugagua	240
Liccaccacg	- + 0 = 5 0 0 0 0 0 0	+ 22002000	tagcccnaat	agcaaggccc	actacagacc	300
cgctttcacg	attagtgaaa	Laagcagcag	toctcct	tacttattaa	atoctttgaa	360
gagagaaaac	tttccttgtg	agctcataaa	aaatttttt	tacccaccaa	atgctttgaa	406
tcaattttgt	cagaaaacca	attcacncga	atatgaatcg	tttcgt		400

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 664 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...664
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:311

agcagattat	gccatcacgg	cctctcactc	ggagggtttc	ggtctgaata	tctggaggct	60
agcagaccac	geeneenegg	totagccact	gatttgcccc	attcagagaa	atctgcggca	120
actgerige	gaaaacccgc	ttattttt	tgtaggaaac	caaaaagaat	tggaggattg	180
caggetttea	ggacaacgaa	teacttone	cctcaaaaag	totocgatat	caggcatcat	240
catactaaaa	agectigica	stangereate	agaactatta	tacogageta	tcagtccact	300
ttctcgcgga	aacaatgttt	gracaatacc	agaactatta	actcaatcat	actttataaa	360
aaaatgaatt	caatgaagag	tgcatgtttt	gattattact	ctctgatacg	otaactaaga	420
agcaaaccgg	atattattcg	ggatgtcatt	actccttttt	catatactac	8808808880	480
agaagcttat	cctcatagac	atteteegae	tgacagicii	cgcgccccc	aagaagaaag	540
accggaggat	ttcaggtatt	tctttaataa	ccgcaatata	ggatteggat	cagctcacat	600
atcggtatta	gagaggcagc	tcgcttcaat	ccttcttatc	attaatteta	atcctgatgt	660
gcagtttggc	cctgaagtgg	tgccgacatt	ggcttcaaca	tggaccgaga	atcctgatat	664
agga					•	004

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 969 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...969
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312

```
gggtaacgac agcattette aceggatega teatttggge aatageetgt tgaatgette
                                                                        60
cagaggaacc tgaggagcaa aagcattcac cgtctgattt ccacctcaat acccgggata
                                                                       120
tagccgccat cggtgaagta ggtggagatt cattggcata agcattgttc ttacgcttgt
                                                                       180
ctctttcgtt gtattgttct cgtatcgctt gagcacattc gngccgtgca cgatccgtat
                                                                       240
togocttggt gaataccgaa ctgacggagg ctttctatct ctgccaccaa tgcgtcatcg
                                                                       300
ctttctccgc ttcaccctca cgaaccgagg caacaaaatt gaagcgtcct tagtctgggt
                                                                       360
gatgtacatg aagttagaga agaaagctcc tgactgagga aaggagcgtt aggcttgtga
                                                                       420
gtaatctcgg acagacgctc atcacggctg tagtgatcac ctgtttcata tagtcttcca
                                                                       480
caagtccgaa atcgatcctc gcacttcttg aggagtgggg tcgctcttga agctgatggg
                                                                       540
agctgcgtgg tagtagcctc agcatcggta gcaatggcta cgataggcca tcgttgtcct
                                                                       600
ctaccggcgt atagatacgc tctgctggat tcacggggca ggaacgtcct tgaagagttc
                                                                       660
tttgatcttg ttctccacat agtccaatcg atatctccca cgatcaccag accttgcagg
                                                                       720
tcgggacgat accattctta taatagttgc gcagctcatc atgcttgaag ttgagcacga
                                                                       780
cgtcatcaga ccgatgggca tgcgttctgc atatttatta cccggcatag cctggcaagt
                                                                       840
atagcetega acatacgaag gttggcateg egacgagcae gcaetettee tggateacae
                                                                       900
egegeteete gtegatetea tgeeegtega ggtaatattg ttacteeaat catgeaggat
                                                                       960
aagcaagcg
                                                                       969
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 613 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...613
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313

tggttcgctg	ccccaagtcg	ttgtacgatc	gtcttcgcga	agaggatagg	cgcgtttccg	60
		ccgatgagga				120
		tcaggatgct				180
tgaagaaagt	cttcactccc	tccgcttcca	tatagatttg	ggcacctacc	acttcgccat	240
		gcagccggaa				300
tcggccgaat	acaggatttc	gccgaggagc	atagacccga	agatggaagc	gtttggtgcg	360
		ccggcgacaa				420
catatcgaga	aaggaaagat	cggctgaggt	tcgtgccgga	agggcagctt	ctttggccgt	480
cgccggaggt	ggagcaaccc	gaacgggacg	aaagcaaata	cgcccaagac	aaacggttcc	540
ggcagaagcc	ttcctgagcg	tacatgagct	gatgcccatg	atgtctatac	ttcctgctga	600
gagaaaagta	ttt					613

١

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1630
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314

```
gcatcagtag tatgagcgaa aggtattgat ttcagtgttt ttcaggttgt agctccgtcg
                                                                        60
ggaatcgaac ccgaatctat ggtttaggaa accactatct atccattgaa ctacagagcc
                                                                       120
gaaagaacaa gaccgacctt gatcggtttg tctcttttta tttcggggac aaagataggg
                                                                       180
aataaaccaa cttaatttgt tccttttctt tcttgagcaa gcgttcggcc gcttcagatg
                                                                       240
                                                                       300
ttgcttctgt cgatagtatt cctgactata accggggaaa tcaggcatgg cactaaaccg
                                                                       360
tatccatttg tcttgaatcg gccactctcc tctttcttgc gatgccatcc atgtacttta
                                                                       420
ccatcagata ttccccaaga cgcttccaac ggcagttgct ttctctgcct cttcgttgct
                                                                       480
gtaattigte aggaatgeta egetttggee ggateeagag egtatagete tigtgettge
ttgtcgatag cggaagtatg cggtcacaag ctccttcgag ttcacgctgt acagggcgat
                                                                       540
                                                                       600
atcggctatc atctgatcat agcggtgata tgccatatta gccacccatt gtggatccag
                                                                       660
aaagccgaag tccaagaaaa gtgcatcata tcgccatacc ctgacggaag cactccggca
                                                                       720
cacgcgttgt ggaacaatag atcggatcat aacggccata tcggcatcgt ccacgccaaa
ccaattaaca ccgccatggc atcggggagc caattacgca actgggctac gaaaacaaat
                                                                       780
ccggttgctg agtggcaatg gcacgttcat taacgtactc cttgccatcc actcgaagct
                                                                       840
catcggacgc caacggtagg gtactttata agggccggca ccggatcgtt cgtcatacat
                                                                       900
agggaagtac cttcgtagtg atcacgcatc aatcgcgaac atcagcgaca gagagcttgc
                                                                       960
                                                                      1020
gatccggaac aatatagaga gcattttatc cttgctctga ttccgtataa aagcttcata
                                                                      1080
cttacccatt gcgaattgaa cttattgaag aaagcccata cacgagcttc acaaccacaa
gaccaccttc ggtataaggg ttatatgctt cttggaagct aaaatcctgt ctgttccttg
                                                                      1140
                                                                      1200
gaagaatccc atctcacggg caaatgaaac gacatcggag aatagagata atctttactc
ttgaaatcga tctgctggat gcgagttgat tggcatgtgc actaatagca ttgtccggaa
                                                                      1260
tgcgcacagc tgccacacag cacctttgcg ccccttaccc ttgccgatca tctccagaat
                                                                      1320
                                                                      1380
ccaacttcgt tcttatcggc aacactaaaa ctttcgccac tgctatggta gcgtattcct
                                                                      1440
ttaccagatt ggttatgacg tctatagcct cacgagctgt ctagaacgct ggagagccac
atagatcagg ctgccatagt ccatgatacc tcactttcgg ccaattcggg acgtccgccc
                                                                      1500
catgtcgtct cggcaatagc acttggtgtt cgttcacatt accgatgaca ttgtaggtat
                                                                      1560
gcgtatgtcg ggaatgaatc caagtggttt gttcgtgtcc cattcgataa ttgggcgatt
                                                                      1620
                                                                      1630
gttccttcag
```

- (2) INFORMATION FOR SEQ ID NO:315
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...459
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:315

cactgttttt ggcattgcgg atgggatcat ggatgtcgat aggttcgtgc agatattgta	a 60
gtcaccgcac aggatcaagt tagggcgact cttgcggatt cattgacata agattggaag	
tgctccagcc aaaccatctt gaaggccgac gctcatcgcc actcgtcccg gatggatgat	
aaacgcttac gatagaagat cgccgaaatc ggcacggata aaacgacctt ccgcatcgta	a 240
ttcttcatac ccatgccata ttctatatga tcaggctgat gctttgtgat gataccacac	
cgctatatcc tttcttttga gcccgaaaaa aagatacgag ccgtagccca gtgcttcaaa	a 360
toottoattt ttogaattgg toattotgca totagtttoo tgcaggcaca agcacatcag	g 420
gattetette tegaageeaa egateagate ttttettea	459

- (2) INFORMATION FOR SEQ ID NO:316
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1400
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:316

tcgaaattta		tatatagga	aogaaaatat	atggcacctg	aaatggcccc	960
tcgaaattta	tcacatgctt	LECCEESE	agtaattete	gtaaagcagt	tgaggaaaat	1020
tcacttccga	cacataacca	ttttgtaggt	ggcaactctc	geaaageage	aaagacatct	1080
agagccgact	cattccggta	ttcttttatg	aagtgccatc	aargarrege	aaagacatct	1140
	atemorates	ttcagctttC	aatgcctgat	gagaatgita	CCECAECCE	1200
agagtatett	groattatag	caaaccggca	gcagaagcgc	tcatttagtt	ataggggaaa	
	nataccatat	otacaggcga	caactigati	Cacacacce	4666	1260
Caaccgcca	gangetacce	tatctattct	cttgcaaagc	ccaaaatcgg	agaagtagaa	1320
catcgtgatg	gcagccaccc	caccacactta	ttoaaoatoo	teccacacte	cactcggtat	1380
gaactatcgg	gcgtaattgt	gccgagccca	ccgaagacgg	08	00	1400
cggcgcgatt	cctgatgcag					_

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 628 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...628
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:317

```
gtgaatagac tcacgattgt cctcggcata agcatagcca gagcaaaacg agaaagctga
                                                                        60
ccagtagatt gacgccacaa ctgtagcgat aggccgactc acccgtcccg gatttttagc
                                                                       120
cccgtagttg aaacctacga tcggctgatc ccctgagcca caccgatgat aatcatgaaa
                                                                       180
aagagcatgg catagcattg ataatcccga atgctccgat ggccaagtcg gtagcatctg
                                                                       240
ctgtccgccg taggatacga aagaacgatt catgatgata ttgaccagac tgccgtaagg
                                                                       300
tgcatggcga agggtgctac ccctatagcc gttatgccgc cgacaccggc agggacaggc
                                                                       360
ggaaagccga gcggtggaaa cgtacgatac tgccttacgg aaaaagtgcg aaaggacgta
                                                                       420
gaccgaacat actatcatgg aacgacagtc gctatggcgg ctccgcttat ccccatcccc
                                                                       480
aacggataga gaagatgtag tocagcacca cgttcgtcat agccccgatg atcatcgtat
                                                                       540
catggctttg cgcggatagc ccgaaagctc tcatgatagc attgtagcga agcttcagag
                                                                       600
                                                                       628
ctgagaaaat attggcagga ccacgtat
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1372
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:318

```
60
tgcttcttcg agacagtccg aatgagtccg atccacaccg aaatcattgt gaatatgagc
                                                                       120
gtattcttcg tgatgtcgtc cacgctcgtt cgttcgtgtc gctggtagga gtggcgaaag
caccettete gregogatag acaggeagee tregatatre aartegeeae greegatree
                                                                       180
gacaaaaggt tcgtctcata tcccacgccg aatacaatgt cggagcctac cttatcacgg
                                                                       240
                                                                       300
tcgaaacccc gatagagtac cctgtacgaa gagataaaag gttgcctatg tccacaaagc
attgatataa taaagcccca atccgcgtac tacacgtcgg gacactgctc ggcagacggc
                                                                       360
ctgtagcggt taggatcctt gccggtacgt tttagcagct gcgtgtggct gctatggcag
                                                                       420
ggatttettt gatggeeggg agtegeaagt etgtateage egateaagee teteegttea
                                                                       480
totoatotat agagtggatg gcgaccggco tgotgcaact ttggccgtac cactootacc
                                                                       540
gaaaagccgg acaatgatgc agaataggta cgtcaaagct gatcccgggc atcgtctcct
                                                                       600
tegtategta ttegatetee aaateaaaat caatgteteg agacettett cateetegte
                                                                       660
                                                                       720
gtcttctatc gatgccggaa caaatctcct cctcatccca tgtaagactg gtcaaatcaa
gagettggeg tactagetgt ceggetegtg aagggtetee ttgetgagtt etttecacaa
                                                                       780
gtatctttag ctcttccagt ccctgttgtg ccacggcaga aatgaaaact acgggcaagc
                                                                       840
ctgtcggcag ctcctcccga agcatctcgc acagctcttt cgcgatgagg tcgcacttgg
                                                                       900
ttatggccag cactttgcgc ttttgtgcca atcttcgttg tatgccacca gctcccgact
                                                                       960
gagtatctcg tattccttgg aatgttgtcc gtatcggccg gaatcatgaa gaggagcaaa
                                                                      1020
gcgttccttc gatgtgccgc aggaaacgca gtcccagtcc tttccccgat gaagcccctc
                                                                      1080
gatgatgccc gggatgtccg ccattacaaa ggatcgcttg tctcgatggc tacgataccg
                                                                      1140
agattaggtt ccagcgtagt gaacggatag ttggcgtctt cggctttgca gcagtgagca
                                                                      1200
ctgatagcag tgtcgatttg ccggcttggg aaatccgacc agaccgacat cggccagcat
                                                                      1260
cttgagctgc atgacaccat acgctcctgt gccggctcgc cgggctgagc atatcggggg
                                                                      1320
gccgattggt agcggtcttg aagaacgtat tgccgtgtcc gcctcggcct cc
                                                                      1372
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...480
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:319

ttgcagtgat	gggtccgagc	ggagctgtag	aagtaatttt	tgccaaagag	tggcagcagc	60
cgagaatcct	caacaagcag	cattggaaaa	ggaagaagat	atcgtcaggc	ttttgccaat	120
ccgtacaatg	cagcctctta	cggctactgg	atgatgtgat	cgagcctcgc	aatactcgtt	180
tccgcattat	tcgtgccttg	aacagcttcg	tacgaaaaag	caaactattc	cggctaagaa	240
acacgcaatg	tgcctcttta	ataagaggag	tttagtgcat	cgaccatgaa	tattgcaggt	300
ttagccatat	ccttctgact	ttgtttgtca	tagcctccgg	acactctttg	cccagcaggc	360

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...444
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320

	++++00+000	caaaataaca	attcttttga	tacatacaga	gtggcttcaa	60
ctggaattgg	LLLLacigag	gattagataga	atttatator	taaaatactt	ttatcatgtc	120
aatgtcaaaa	ggaggtaaag	gccccggccg	actuacecc	acataatttt	acatttggtc	180
tcaattgaaa	gtatcttcta	tgaagaggca	aatataaaca	acgtagette	acatttggtc	240
	gataatgaaa	atgagcaaat	tgtagatatt	gaateegaet	Cigaccigua	300
t acactacan	ttttacatct	ttcttccatt	aagtcttttg	atttagataa	agggilgaag	
+++++accas	assactcoto	papcotttac	ttgtattctt	tgtcctggag	gggaatatac	360
Lialigeed	accettagg	aagagaatgg	ctcaattcaa	tagtattgaa	taactatatt	420
tccaaagatt	acgattaaag	aagagaacaa	• • • • • • • • • • • • • • • • • • • •	0 0		444
ggagacaatt	ctgatattca	aaaa			•	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...456
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:321

acaccactaa	cctgtcgaaa	agagogtgac	aactactcaa	attgaacgta	agcataatca	120
tteeetee	tgcccgactg	atagactagt	atagatgag	ttataatcat	ccaaaagatc	180
rrcgggrgcg	tgcccgactg	acagaccggc	acagaccaac	ccacaaccac	aggacacact	240
aggacgctcg	tgtgtgtaac	atcgggaaaa	ccaaagctaa	agegeageee	ggggcacaat	
ttgaaaaagg	caggtaaaaa	tcgcatccga	gaccgatctg	caccccgtaa	tcgtcgcttt	300
ggtataaatc	tccaacccct	tctttcgccc	cagctccata	gtcagtaagg	cccgccgatg	360
aggtattgga	cgcataattg	gttcaagcgc	cggaaccata	ttttcaataa	ttagcggaaa	420
	ttggatccga					456

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...474
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:322

ggcttgcgtg	tggatgagtt	cgggactgaa	ccacatacgg	ctctctttt	cgtggacagt	60
gtgcggtgtt	caaggaaatg	cagaaaggca	ggtatttctc	cttcaccctt	tgcaggaaat	120
ccgtgtcgtc	cctctctatc	ctccctattt	tcttacccaa	tagcgcgtct	cccctgcgtc	180
	ggcagggttc					240
	cttatcctcc					300
	tcctccctgc					360
	agttgaactg					420
	tttgaggaaa					474

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323

			ctcaacacct	gcagctttta	ctcatttaaa	60
ggctgcgaat	agcttgtaaa	tacgattgat	Cicaacaccc	tantacctat	otcaatcgga	120
		~++~++aaar	OCALLYPLAR	LEGICALLA	P	180
-		++02+22+00	acorocaval.	acactractr		240
			rrracryaca	Laketatek	66000000	300
		0001201001	araaatutat	allaggaala	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	
			CFFGATCALL	LLALEACTIC	CCCEMCACA	360
agatttcaat	LgLaacgacc	coccatatant	tratraagto	tttcaagagt	gcttttagtg	420
tggttggcag	cgttaccttc	Cadalacage	tttttgtaga	attacaatta	taataa	476
aaatttcgga	caaaatgctt	atgatgaatc	LLLLIGLAGA	56-64		

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1506
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324

```
aaggatoggo agooggttog aoggtagott actgtttggg natooggatt ogatoogato
                                                                        60
aagtaccatt tgcttttcga gcgttttctc aatccggacg tatctccatg cccgatatag
                                                                       120
acgtcgactt cgatgatgac gggcgtgcga aatactccgc tgggtgacgg aaaaatacgg
                                                                       180
caaggagaga gtggccacat catcacctac ggtacgatgg ccacaaagag ttctattaag
                                                                       240
gatgtgctcg cgtacagagg ctgcccttac tcgaaagcaa tcgtttagcc aagccgacca
                                                                       300
gacaaaattc ccggagagaa gaaagtcaat ctgaagaaag caacgaattt gttccagagc
                                                                       360
tgaagcaagc atcgctaagc tccgataagg tatgcgcgat accctgaaat acgcccaaat
                                                                       420
gctggagggg aatgtgcgca aacaggtgtg catgcctgcg gtatcatcat tgggaaaacg
                                                                       480
                                                                       540
gatatcagcg tgtcgttccg gtcagtacgg ctcccgacaa agacacgaag gaggagctgt
                                                                       600
ggtcacacaa tacgaagget etgtcatega acagaeggga etgatcaaat ggaetteete
gggctgaaaa cgctctcgat catcaaagaa gctttggcaa cataaagcgg cgccatggca
                                                                       660
ttgacttgaa tatagacacg atcccttcga cgatcctctt acatataagc tatacagcga
                                                                       720
tggacgtacc ataggacttt ccaattcgaa tccggtggga tgcaaaagta tcttagggag
                                                                       780
ctacgccctc tgctttcgag gacttgatag cgatgaatgc tctctatcgt cccgtccgat
                                                                       840
ggactatate cettettta tegeacgeaa geatgggegt gacetatega ttacgacetg
                                                                       900
cctgagatgg aagaatatct caaagaaact ttggtgtgac ggtgtatcag gagcaagtca
                                                                       960
tgcttctgag tcgcaagctt ccggttttac ccgaggccag agcgatgagc ttcgtaaggc
                                                                      1020
tatgggcaaa aactcatcga aaagatgaat gttctgaagg tgaagtttct cgagggggga
                                                                      1080
ataagaatgg acatccggaa gaagttctgg aaaagatctg gacagacggg agaagttcgc
                                                                      1140
cagctatgct ttcaacaaga gtcatgccac ctgctaagtt gggtagccta ccaaacggct
                                                                       1200
tacctgaaag caaacttatc ctgctaatat atggcaggag cattgagccg aaacctgaat
                                                                       1260
aacatcacgg aaataccaag ctcatggatg agtgcaagtc catgaagatc ggcgtattgg
                                                                       1320
tacggatgtg aacgagtccg aaatgaaatt ctcagtaaat gccaatgggg atttcggttc
                                                                       1380
ggtctcagcg ctgtaaaggg tgtaggatcg ggagccgtgg acagatcatt gccgaacgcg
                                                                       1440
aagccaacgg gctatataag gacatcttcg ctttgtggag cggatcaatc tctctgcctg
                                                                       1500
                                                                       1506
caatcg
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...588
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326

ggcgtaaaaa	tcgttataga	accacttacc	acttcaatga	caatacggaa	aggcatcccg	60
cctgatacga	tcatatacgg	tggaacatgg	catggctttt	ttgacctctc	tgcggctatg	120
gggggagagg	ctgaaacccg	acaatggtgc	gtagcgggct	gatgcatacc	gatcatatac	180
attatacggt	gggtggtata	cccgtcatgg	aggactggtg	gccgatgcct	tactcggctc	240
tattgccgtg	gcaaaatgga	taggagcgac	cagtccaaac	tctaaaataa	aagaagtcca	300
agatcgtgca	ctttttcgat	tcgatggata	tatcccgcct	gtggatatat	tacagtatga	360
tgcttctgcc	cccatgattt	tttcgagtgg	gagttcttca	tcctctttct	tttgttcctt	420
ccgctataca	tcctgctacg	cggcaaaccg	gactgcgtat	tgtatacgta	tctctcttt	480
ctctttattt	tactataaga	gcagcggtct	tttcgtcctg	cttcttttgg	ctgctgctag	540
agcgacttcc	tcatcggtcg	gctttttgtc	ccgtcagcag	atccaagt		588

- (2) INFORMATION FOR SEQ ID NO:327
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1014 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1014
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:327

gcgctctcga cggttcttcg atggcccgct caatggctcg	cacagtgtct	atcgcctcgt	gaagataacg	agtttctgct	60 120
ctggattacg ctccagactg					180
gggatcgtcg gagtagtgct	ccactgctca	tctagctggt	cgatgagggc	tagatcctga	240
cggagagatc aatgtattct	ggagcaaagt	cctcacgtcg	atactctcta	tttccccttt	300
ctcattcgat ccagaggagt					3.60

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...588
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326

	toattataga	accacttacc	acttcaatga	caatacggaa	aggcatcccg	60
ggcgcaaaaa	tcatatacoo	topaacateg	catggctttt	ttgacctctc	tgcggctatg	120
cctgatacga	ctatatacgg	acaatootoc	gtagcgggct	gatgcatacc	gatcatatac	180
gggggagagg	ccgaaacccg	cccatcatoo	aggactggtg	gccgatgcct	tactcggctc	240
attatacggt	gggtggtata	tadagedae	cagtccaaac	tctaaaataa	aagaagtcca	300
tattgccgtg	gcaaaacgga	tonatonata	tatcccgcct	gtggatatat	tacagtatga	360
agatcgtgca	citticgat	tttccagtgg	gagttcttca	tectettet	tttgttcctt	420
tgcttctgcc	cccatgattt	CCCCGGGCGG	gactgcgtat	totataceta	tctctcttt	480
ccgctataca	teetgetacg	cggcaaaccg	tttcatccta	cttcttttgg	ctgctgctag	540
ctctttattt	tactataaga	gcagcggccc	ccatcagcag	atccaagt		588
agcgacttcc	tcatcggtcg	getttttgte	ccgtcagcag	acceaage		

- (2) INFORMATION FOR SEQ ID NO:327
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1014 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1014
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:327

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...408
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329

ggtcgaagct	cgtagccact	gctacatgct	tggcctgatt	caaatcgcta	acggcacttc	60
ttccggaata	accaacacag	gtaccttgct	cgaatctata	cttcggctgc	aacgcttccg	120
atcagatccg	aatccttgcg	cgatttgctc	gcgtccccat	cacgatcatt	acgggtctgt	180
gtcgcttgca	gtaactagga	ttacatcttc	cggagcaccg	tccaaaagga	cagaggagaa	240
agatattcgg	gaagttcctc	tcgcgttatc	ctttcacgca	gctctttctt	gagctgttca	300
tcagacgttg	tacacgctgg	tattctttgc	gcaggctgac	ttcttgctga	gctggaacac	360
aagccgtatc	gcccaccgta	agaaggtgtg	gaaaaaatgg	actgatat		408

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 507 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...507
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:330

atattggatg	tgcccgtgaa	agatgagaaa	gctgcctgct	ggcatgtctt	tccatcatca	60
				atctccatcc		120
				atcggtgggt		180
attcgctccc	gtcgcaggac	gaggtggccg	aaagaggatt	ggctgctcac	tggaagtaca	240
aaggttcaag	agcgagagcg	gattggatga	gttcctcact	tccgtacgcg	agaccttgag	300
gcacgcgatc	actcctcgga	cgattcggcg	gagacggtga	aaacttcaag	atgaacctct	360
tcaccgatga	gatctatgct	ttcactccca	cggagaactg	atcaagttgc	ctcagggagc	420
ccagtgtgct	ggacttttgc	ttttgcccat	ccattngcgc	atcggctgtc	aggccgtcgg	480
agcttaatgt	aatggaaaga	atgtgcc				507

(2) INFORMATION FOR SEQ ID NO:331

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 966 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

1

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...408
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329

ggtcgaagct	cgtagccact	gctacatgct	tggcctgatt	caaatcgcta	acggcacttc	60
ttccggaata	accaacacag	gtaccttgct	cgaatctata	cttcggctgc	aacgcttccg	120
atcagatccg	aatccttgcg	cgatttgctc	gcgtccccat	cacgatcatt	acgggtctgt	180
gtcgcttgca	gtaactagga	ttacatcttc	cggagcaccg	tccaaaagga	cagaggagaa	240
agatattcgg	gaagttcctc	tcgcgttatc	ctttcacgca	gctctttctt	gagctgttca	300
tcagacgttg	tacacectee	tattctttgc	gcaggctgac	ttcttgctga	gctggaacac	360
aagccgtatc	gcccaccgta	agaaggtgtg	gaaaaaatgg	actgatat		408

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 507 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...507
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:330

atattegate	tgcccgtgaa	agatgagaaa	gctgcctgct	ggcatgtctt	tccatcatca	60
copacatota	tcagcccaat	ccacagcgaa	tgaaggacgg	atctccatcc	ccaaaagcaa	120
cagttataaa	togotocacg	ttacggtatg	ggaccgcaga	atcggtgggt	ggaggtgcag	180
attractor	ptcpcappac	gaggtggccg	aaagaggatt	ggctgctcac	tggaagtaca	240
accepticase	Pece and and a	gattggatga	gttcctcact	tccgtacgcg	agaccttgag	300
acacacaatc	actectegga	ceattceece	gagacggtga	aaacttcaag	atgaacctct	360
tcaccastas	gatctatgct	ttcactccca	copapaacte	atcaagttgc	ctcagggagc	420
ccaccgacga	gacctatec	ttttgcccat	ccattngcgc	atceectetc	aggccgtcgg	480
	aatggaaaga		courtings		- 88 0 00	507
aguitaatgi	aatggaaaga	acguguu				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 966 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2375
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333

```
60
tgctcgcaaa caaaaccaac tctattcgac actggagcag aaaggattca ccgccctcc
actacgatgt ggacttatga cgatcatatc cgcgacgaat gaacaaagcc atgagcctac
                                                                     120
tgcgcgaaaa agactacgac tccttcctgc agcatacaaa gagatggcta tcgttctgcg
                                                                     180
tgacctgatg gaaaaaaaga gcttatcctt tatccaacct ctctgaagct catttccgac
                                                                     240
aaagattcga agaaatgaaa catggcgatc gggaaatagg cttcttcctt atcgcatgcc
                                                                     300
ggaattagat gcaccggcca agcaatcaaa agaagcccac ggcaatcatt tatggcagaa
                                                                     360
ctgggagcct tacttgccaa acatggtatg ggacaggcgg acaagacgac aaggcgatac
                                                                     420
                                                                     480
tggatgtagc cgaaggaaag cgactttgga gcagatcaat ctgcttttcc gtcatctccc
                                                                     540
tgtggatatt cgttcgtgga cgaaaacgag ctggtttgtt tctatacgga cacaaagcaa
                                                                     600
gagtattccc cagaagcaag ggggtgatcg gccgagaagt acgcaactcc atccgcccaa
gagogttoat atagtagagg agataatoga taagttogao gtggogaaca ggatogoga
                                                                     660
gaattotgga toaataagoo oggagtttoa totacattgt otatgtggoo atcagagaog
                                                                     720
                                                                     780
ccgacgggcg tttcccggtg tgatggaaat gatgcaagac tgcacacgga tccgtagtct
                                                                     840
tgaagctcgc gtacacttct tacttgggac gaagagcaaa gtccggcaca aggtcgaaag
                                                                     900
aaagcgaatc cgatactgcc ggagaagacg gcattcggcc ggcacgaagc tgaagagtct
cttgcagcgg tatccgcaac tgatggatga ttgccaacga tcagttccaa gttcaccctc
                                                                     960
                                                                    1020
cttcgttctc cgatggccaa gtaattcttc ctgttgccac cattaaaatg atgagcgaac
                                                                    1080
gcgccgacat ccgtcggata tgctcatcgg caaactggaa tcgctcatcg cttcgtacat
                                                                    1140
aaaccggatc gatcggaaga gaaatagcat gaagaaggag gtgtgtcata atcatggcgc
                                                                    1200
acctccttgc attaatatgg gacggtcggg tacaccctat tccgagactc ctaaggagtc
cctaccgaga cccctaagga gtctcaccaa gacccctaag gagtctccac cgagatccct
                                                                    1260
                                                                    1320
aaggagteee taccagacee ctaaggggte ccaacagaga etecttaggg gtteetcaat
                                                                    1380
gcttacttca ggaggggttc gtgcggtctt ataatccatt cgaatggaga cacgggagca
                                                                    1440
gtgaccggcg aaaggaagcc gaagcttagc gaatcttacc gcgaacagat tgatgatgcg
                                                                    1500
gccggcacta cgtgcatcgt gctcggagtg gtcaccatga cgatggttgc accttcgcga
                                                                    1560
ttgagacctc tgagcagttc atgacatcgg ctccgttttt ggagtcgagg ttacccgtgg
                                                                    1620
gttcatcgcg aggatgagct tcggattggc caccacggcn cgggcgatag ccacgcgtgc
                                                                    1680
tgttgtcctc cggagagctg attggggaag tggccggccc ggtggcgatg ctcatcttgc
                                                                    1740
gcagtgcctc ctccactcgc tctttccgct cggagccttc acacccagat agacgagcgg
                                                                    1800
caactccacg ttctcgctta ccgtatctct tcgatgaggt tgaagctctg gaatacgaag
                                                                    1860
ccgatattgc cctacggacg gcagtcctgt ctttttcccg gaggttgccc acttctgccc
                                                                    1920
cacgagettg tagatacegg aagtgggatt gtegagaagg cegaggatat tageagagtg
gacttaccgc atcccgaagg ccccattatg gcgataaatt gcctttgtcc actttgagcg
                                                                    1980
                                                                    2040
2100
gatttcaatc attgttttct tgtttttatg aggtgaaagg aagagcgaca agccggacaa
                                                                    2160
tgcctggcta tgaatccgcc gtttgccgga ttgtcgccgt atttattcgt atcggattca
                                                                    22:20
ttgacagggt tgcggcgagc tatgcgccgg aggttgatga caacgccaat gcaataatca
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2375
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333

```
tgctcgcaaa caaaaccaac tctattcgac actggagcag aaaggattca ccgccctcc
                                                                      60
actacgatgt ggacttatga cgatcatatc cgcgacgaat gaacaaagcc atgagcctac
                                                                     120
tgcgcgaaaa agactacgac tccttcctgc agcatacaaa gagatggcta tcgttctgcg
                                                                     180
tgacctgatg gaaaaaaaga gcttatcctt tatccaacct ctctgaagct catttccgac
                                                                     240
aaagattcga agaaatgaaa catggcgatc gggaaatagg cttcttcctt atcgcatgcc
                                                                     300
ggaattagat gcaccggcca agcaatcaaa agaagcccac ggcaatcatt tatggcagaa
                                                                     360
ctgggagcct tacttgccaa acatggtatg ggacaggcgg acaagacgac aaggcgatac
                                                                     420
tggatgtagc cgaaggaaag cgactttgga gcagatcaat ctgcttttcc gtcatctccc
                                                                     480
tgtggatatt cgttcgtgga cgaaaacgag ctggtttgtt tctatacgga cacaaagcaa
                                                                     540
gagtattece cagaagcaag ggggtgateg geegagaagt aegeaactee ateegeecaa
                                                                      600
gagogttoat atagtagagg agataatoga taagttogac gtggogaaca ggatogogca
                                                                     660
gaattotgga toaataagoo oggagtttoa totacattgt otatgtggoo atcagagaog
                                                                      720
ccgacgggcg tttcccggtg tgatggaaat gatgcaagac tgcacacgga tccgtagtct
                                                                      780
tgaagctcgc gtacacttct tacttgggac gaagagcaaa gtccggcaca aggtcgaaag
                                                                      840
aaagcgaatc cgatactgcc ggagaagacg gcattcggcc ggcacgaagc tgaagagtct
                                                                      900
cttgcagcgg tatccgcaac tgatggatga ttgccaacga tcagttccaa gttcaccctc
                                                                      960
                                                                     1020
cttcgttctc cgatggccaa gtaattcttc ctgttgccac cattaaaatg atgagcgaac
gcgccgacat ccgtcggata tgctcatcgg caaactggaa tcgctcatcg cttcgtacat
                                                                     1080
aaaccggatc gatcggaaga gaaatagcat gaagaaggag gtgtgtcata atcatggcgc
                                                                     1140
acctecttge attaatatgg gaeggteggg tacaccetat teegagaete etaaggagte
                                                                     1200
cctaccgaga cccctaagga gtctcaccaa gacccctaag gagtctccac cgagatccct
                                                                     1260
aaggagteet taccagacee ctaaggggte ccaacagaga eteettaggg gtteetcaat
                                                                     1320
gcttacttca ggaggggttc gtgcggtctt ataatccatt cgaatggaga cacgggagca
                                                                     1380
gtgaccggcg aaaggaagcc gaagcttagc gaatcttacc gcgaacagat tgatgatgcg
                                                                     1440
 gccggcacta cgtgcatcgt gctcggagtg gtcaccatga cgatggttgc accttcgcga
                                                                     1500
 ttgagacete tgageagtte atgacategg etcegttttt ggagtegagg ttaccegtgg
                                                                     1560
 gttcatcgcg aggatgagct tcggattggc caccacggcn cgggcgatag ccacgcgtgc
                                                                     1620
 tgttgtcctc cggagagctg attgggggaag tggccggccc ggtggcgatg ctcatcttgc
                                                                     1680
 gcagtgcctc ctccactcgc tctttccgct cggagccttc acacccagat agacgagcgg
                                                                     1740
                                                                     1800
 caactccacg ttctcgctta ccgtatctct tcgatgaggt tgaagctctg gaatacgaag
 ccgatattgc cctacggacg gcagtcctgt ctttttcccg gaggttgccc acttctgccc
                                                                     1860
 cacgagettg tagatacegg aagtgggatt gtegagaagg eegaggatat tageagagtg
                                                                     1920
 gacttaccgc atcccgaagg ccccattatg gcgataaatt gcctttgtcc actttgagcg
                                                                     1980
 2040
 gatttcaatc attgttttct tgtttttatg aggtgaaagg aagagcgaca agccggacaa
                                                                      2100
 tgcctggcta tgaatccgcc gtttgccgga ttgtcgccgt atttattcgt atcggattca
                                                                      2160
 ttgacagggt tgcggcgagc tatgcgccgg aggttgatga clacgccaat gcaataatca
                                                                      2220
```

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...826
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335

actgcactga	aagactcgcc	atacagatct	cgtcccgatt	ctttgggcga	tacaatttcc	60
				ctcggccgac		120
				gacaggaagt		180
				ccggattgta		240
accggcccac	ggcataagaa	atacagcgca	tttgccctga	cggagtaccg	gtacggaggc	300
				ccctccacca		360
				tgttcgtccg		420
cactccactt	gcatcgacac	gatcttgacc	caatgtcccg	aagccattag	cgaacggtcg	480
				aagggcaagg		540
				gcttatttat		600
				gatagcaatg		660
				gtgaagaaac		720
				tgccctgctg	caccgtgcgt	780
nccgctatat	ccaatcgcag	gcccaattcc	tgcacaccgt	gcccgg		826

- (2) INFORMATION FOR SEQ ID NO:336
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 922 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...922
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:336

atatcatccc	gatacgcaac	ttatggtgaa	tgcggaacgg	aattgattcg	acacactcca	60
					aggtgagtcg	120
					gcttgttcga	180
					gtccggcaac	240

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...826
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335

actgcactga aa	agactcgcc	atacagatct	cgtcccgatt	ctttgggcga	tacaatttcc	60
tgttcatgga go	catcagete	atcgtagtag	tcgatcaagc	ctcggccgac	gcacctccac	120
ccgtatattg gg	gacatctgc	aaaggtgtcc	ggcagcatcc	gacaggaagt	agtagccatg	180
cgtactgtat g	tattcccgt	atgctccatg	gtggttttgg	ccggattgta	gaaccatgtc	240
accggcccac gg	gcataagaa	atacagcgca	tttgccctga	cggagtaccg	gtacggaggc	300
aaatcgtctg to	ceteatoce	gctcagatct	togggaagca	ccctccacca	taaccgaaca	360
cacctacctt g	pacggatcg	gagaagccat	tgcacggagc	tgttcgtccg	taaggcgata	420
cactccactt go	catogacac	gatcttgacc	caatgtcccg	aagccattag	cgaacggtcg	480
gccgtcttcc ca	atagctcgt	tgcgctttcg	caggcaaagc	aagggcaagg	aagagagaag	540
gaatgcgact at	ttogaagta	ttcgtttcat	ctgagaaata	gcttatttat	ggatatgtcg	600
agcagtttt g	ctcttcgag	ataggetteg	aggtgctccc	gatagcaatg	gggcctaccc	660
ctgccggagt c	cctotagag	ataagacccc	catacgaagt	gtgaagaaac	gactggcata	720
agcgatcaaa c	gatcacgga	aaagagcata	tcccgtgtat	tgccctgctg	caccgtgcgt	780
nccgctatat c	caatcocao	gcccaattcc	tecacaccet	5CCC55	2 0 0	826
HUCECLALAL C	caacegeag	600000000	-6	5 56		

- (2) INFORMATION FOR SEQ ID NO:336
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 922 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...922
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:336

atatcatccc gatacgcaac ttatggtgaa tgcggaacgg aattgattcg acac	actcca 60
ccatattagg atcttatccc aaaacgaaaa agcctccgct ctccctaaca aggt	gagtcg 120
gaggettttt agtateegtt agetaagett actteagegt acettgetgt gett	gttcga 180
tcatcttggc attcggaaga tataaacctc cacacggcgg ttggccgaac gtcc	ggcaac 240

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 749 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...749
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338

ggctcagtcc	ggacaggaga	aggccaaaga	gggaggggct	ttcgatcagc	cattgtcaaa	60
gggcgaaagg	ccatccacct	gcacagtatt	cgtaccaacc	ggagcgtaag	caaggttggc	120
agagcgatcc	caaagccgta	gctttccgaa	caaaagagaa	tacaaccgct	ttctgcacaa	180
teccteeate	ctcgtggcaa	atcgcagttc	tataatgccg	atttcctgca	ggcgcaggct	240
acatttctta	tatcgcacgc	ttatacagcg	acgaaccgat	aatccgcgat	gaagccgtct	300
ttggcaggta	cgctgctaca	gtgagatggg	gtggctgcat	gaagggagcg	tttgctcgag	360
cgcatcccta	aagatcttcc	gcatgtcgat	cgagagggtt	gtattctttg	gcagtggcag	420
agcgttcgat	cctgtcgggt	gcaagcgcgc	ggccatacct	tatctccaac	aggcagcaag	480
acaagagaaa	acaagcgaca	acgcgctcgt	atgtattatc	tgctcggaca	gcttttacag	540
aaaacaatcg	gccggaggag	gctcgcaagg	cctattccaa	agtgttgcgg	cttctccgcc	600
tttcgctttg	gactttgccg	cacggatcag	gaagatgagc	tggagggtga	acggaatccc	660
cgtacagtag	cccgctcgat	tggaacgatg	gccaacaaaa	ggcaagttcc	aaaggatgta	720
	atctttatgc					749

- (2) INFORMATION FOR SEQ ID NO:339
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 700 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...700
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339

pppcagatag	togttggacg	taccctcgcc	gcgtatggca	gctatgggcg	gaggtaatcg	60
cccaaagcat	tttccagttt	caggcctccg	catttgccag	aaagatcaca	gccttggggt	120
gtatagecea	gagcaagtcc	atgatggagc	cgcattggca	ctacccatgc	cgaagttgat	1.80

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 749 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION $1...7\overline{49}$ (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338 ggctcagtcc ggacaggaga aggccaaaga gggaggggct ttcgatcagc cattgtcaaa 60 gggcgaaagg ccatccacct gcacagtatt cgtaccaacc ggagcgtaag caaggttggc 120 agagogatoc caaagoogta gotttoogaa caaaagagaa tacaacogot ttotgoacaa 180 tgcctggatg ctcgtggcaa atcgcagttc tataatgccg atttcctgca ggcgcaggct 240 300 acatttetta tategeaege ttatacageg acgaacegat aateegegat gaageegtet ttggcaggta cgctgctaca gtgagatggg gtggctgcat gaagggagcg tttgctcgag 360 420 cgcatcccta aagatcttcc gcatgtcgat cgagagggtt gtattctttg gcagtggcag agcgttcgat cctgtcgggt gcaagcgcgc ggccatacct tatctccaac aggcagcaag 480 540 acaagagaaa acaagcgaca acgcgctcgt atgtattatc tgctcggaca gcttttacag 600 aaaacaatcg gccggaggag gctcgcaagg cctattccaa agtgttgcgg cttctccgcc 660 tttcgctttg gactttgccg cacggatcag gaagatgagc tggagggtga acggaatccc cgtacagtag cccgctcgat tggaacgatg gccaacaaaa ggcaagttcc aaaggatgta 720 749 ttgggatcag atctttatgc aagcaggca (2) INFORMATION FOR SEQ ID NO:339 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 700 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...700 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339

gggcagatag togttggacg taccotogco gogtatggca gotatgggog gaggtaatog cccaaagcat tttccagttt caggcctccg catttgccag aaagatcaca gccttggggt

gtatagccca gagcaagtcc atgatggagc cgcattggca ctacccatgc cgaagttgat

60

120

180

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...566
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341

cgtgtctt	tc	cattcagata	aaatcaaaga	ggcgaaagag	gatttggctg	cttcgagaaa	60
cgagtgga	ac	gggatgcaga	gggacttcca	atcaacaact	cacaattaag	ggtgtagaag	120
gaagtacg	gga	catcaaggtt	attgctgtcg	cttgcaggag	atcgaggaga	aagcacgcac	180
caagggtg	gaa	tacaataaat	cggtgagatt	tatggctttt	ccatcatggt	caagacggaa	240
aactctca	aaa	gagttgttcg	actgctcctc	caaccgcttt	tcgtgaaagg	gcanagagca	300
tctactat	ac	ctacaataac	gggaagttgg	cttctgatcc	caacttgctt	gtcagaactt	360
tatcaatg	gct	ctcgagcgta	ttccaaaggt	gatgaatcac	accgagaaag	ataaggaaaa	420
ggtttctg	gca	aacaaggagg	ttatatgacc	attgcgggtg	ggtcgtggaa	gaaagaggac	480
gagcttcg	gct	tctcaaagga	caggcagccc	gaactgggat	agaaaaattg	cactcacgcc	540
gcacctcc	cg	gaggaagaga	aagaaa				566

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1212
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:342

tcagaagaga	attttatcta	tctctatttg	caaaagaaaa	agccaacatt	atagaagaag	60
aaaatttgat	attttggact	aaaggatttg	ttgcaggcta	aataaagact	ttataagtgc	120
atctcatatc	ctaatgccat	atttagacat	gcgttgcgta	atattgctga	aatcaagaaa	180
ggaaacataa	ctacttagag	aaaaaacgac	aagaggctcc	ttctttaggt	gtaattttcc	240
ctatgttcaa	ggtgtaattg	aagaagaaat	actgtatgaa	atagaatcct	ttctaatcat	300
gggatagatg	tcaattttag	gaataattta	tctcatggac	ttcaacccct	tttgaaattg	360
aaaaatatgg	gatttatttg	tggtggatat	gctaaaacta	tattttgaag	aaaagaatat	420
gataaaaatc	gctccctaaa	ttataaaaga	gataaagaat	tactagcctt	acggcctctg	480
cgaggctttt	aaaaccagat	gaaagtgaat	aactttgcat	tttggcatca	aaattcttgt	5.40

- (C) STRANDEDNESS: double
 - (ii) MOLECULE TYPE: DNA (genomic)

(D) TOPOLOGY: circular

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...5\overline{66}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341

- (2) INFORMATION FOR SEQ ID NO:342
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{2}12$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:342

	a++++a+c+a	tetetattto	caaaagaaaa	agccaacatt	atagaagaag	60
tcagaagaga	attitation		ttacagacta	aataaagact	ttataagtgc	120
aaaatttgat	attttggact	aaaggatttg	tteseta	atattactas	aatcaagaaa	180
atctcatatc	ctaatgccat	atttagacat	gcgccgcgca	atattge ega	aatcaagaaa	240
ggaaacataa	ctacttagag	aaaaaacgac	aagaggctcc	ttctttaggt	gtaattttcc	300
	+-+	18880880ee	actotateaa	alagaalice	CCCCGGCCGG	360
	+000++++00	gaataattta	totoatggac	LLCAALLLLL	cccgaaaccg	
		taataaatat	octaaaacta	Lattickaas	44446444	420
	+	++ -+	oataaagaat	Lactageeee	4666666	480
gataaaaatc	getetetaaa	ccacaaaaga	anctttacat	+++opcatca	aaattcttgt	5.40
cgaggctttt	aaaaccagat	gaaagtgaat	aaccccgcac		` •	

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...544
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:344

gatogoagga	tcagattatc	cccgtgaagt	tgagtgattt	aagacggata	caaaagagtt	60
tatogoogg	cccacgaatc	gtgccgatct	tcccgagagg	aaaagcgcga	ggtagtaggg	120
cttagtacca	topaactegt	tacttctctt	atgctatttc	gatcaaaaat	cagatcgaga	180
cceggtatea	gatgtaatca	gtgtacaaaa	tgaactcatt	gctgcatata	acgaagtttg	240
ccagccatta	ctcaaaata	tttccacaaa	ccatacaagg	agcttactcc	ttccagcaga	300
ggacgattt	agaagaatat	ccgntgcaca	tttcagaaat	eccttetcta	atctcaagta	360
aggetgttt	agaagcatac	gaaagtttaa	taatccggcg	ggcgtgaaat	gcccgaactc	420
aagaataagg	aacaaaacgg	ctggtttttg	catteetet	ctttatcatg	ategtaacea	480
aatacctcgt	-t	nagtatoata	taataacctn	cctaaagcga	ctgaattgac	540
caattcgtga	gtgacgccca	aggtgtcgta	caacaaccen	cccaaagoga	0-8	544
aagc						•

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 851 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...851
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:345

	gcagagaaag	ttaggcccta	tetecatage	cactccggag	ctctcttgaa	60
gcaaaaaacc	atgctgagag	acaagataca	ctacttcaco	agcagacgca	atecaetete	120
tgcgcatgaa	atgutgagag	acaagacgca	Ctactcacb			180
ggtatttta	ttcatcgtgg	attcaagatg	cgggtaaggt	ettgeteetg	acggagaacg	
aaggtgacga	agaactctcg	cttatgctcg	ttcgttggct	cgcaacaatg	gcagtgtgct	240
cgatgactac	ccgagaccga	tggtttaccg	ccgactctat	ccatgggaga	aaacgactga	300
aaoccooatt	gccatcgaca	atcaatatca	gcagctacca	cttatgctcg	tcagctaccg	360
otattaatta	cgctttgccg	gtgagtgtcc	gatotoatco	agcacttgcc	ctctaccatc	420
CLALLEGILE	cgccccgccg	6-6-6-6-6	644646446	tocastasts	toacaataat	480
attatccatc	atcgaaatga	egetettega	Cattgaaagt	Lgcaacgaca	cgagaacaac	
cgaacaagat	cttggctgcg	cccatatgaa	tcagtaatag	aaagcagact	gaagtatgee	540
gcaaacgaga	gacggatttg	accggaggaa	gatccggagg	attgagcgct	tcgccaatgg	600
acatetetat	tacggtcttc	atcaggacgg	ggattcgggg	tgattcgtga	gttcgcgccc	660
acaccccac		astaggargg	************	acataaatta	ccacagtttc	720
gaagccacgg	ccgtatatet	galcgggaac	LLLEGEBELB	gcgcagaccg	ccacagtttc	780
ggtttgcgcc	tgtggtgaag	cgggttcatg	ggaattgcga	ctttcatgcc	gactgcttcc	
gcatgctctc	gctacaggct	cttcttcgaa	tggcccggtg	gcgaaggaga	gagataccgg	840
			00 00 0		• -	851
cttggtgcaa	C					

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...544
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:344

gatcgcagga	tcagattatc	cccgtgaagt	tgagtgattt	aagacggata	caaaagagtt	60
tatcgccaac	cccacgaatc	gtgccgatct	tcccgagagg	aaaagcgcga	ggtagtaggg	120
cttggtacca	tggaactggt	tacttctctt	atgctatttc	gatcaaaaat	cagatcgaga	180
ccagctatca	gatgtaatca	gtgtacaaaa	tgaactcatt	gctgcatata	acgaagtttg	240
ggacgatttg	ctcaaaagta	tttccacaaa	ccatacaagg	agcttactcc	ttccagcaga	300
aggctgtttt	agaagcatat	ccgntgcaca	tttcagaaat	gccttgtcta	atctcaagta	360
aagaataagg	aacaaaatgg	gaaagtttaa	taatccggcg	ggcgtgaaat	gcccgaactc	420
aatacctcgt	ctttgcctga	ctggtttttg	cgttcctctt	ctttatcatg	atggtaacga	480
caattcgtga	gtgacgccca	aggtgtcgta	taataacctn	cctaaagcga	ctgaattgac	540
aagc						544

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 851 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...851
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:345

gcaaaaaact	gcagagaaag	ttaggcccta	tctccatagc	cactccggag	ctctcttgaa	60
tgcgcatgaa	atgctgagag	acaagatgca	ctacttcacg	agcagacgca	atgcagtgtg	120
ggtatttta	ttcatcgtgg	attcaagatg	cgggtaaggt	cttgctcctg	atggägaatg	180
aaggtgacga	agaactctcg	cttatgctcg	ttcgttggct	cgcaacaatg	gcagtgtgct	240
cgatgactac	ccgagaccga	tggtttaccg	ccgactctat	ccatgggaga	aaacgactga	300
aagccggatt	gccatcgaca	atcaatatca	gcagctacca	cttatgctcg	tcagctaccg	360
ctattggttg	cgctttgccg	gtgagtgtcc	gatgtgatcg	agcacttgcc	ctctaccatc	420
attatccatc	atcgaaatga	cgctcttcga	cattgaaagc	tgcaatgata	tgagaataat	480
cgaacaagat	cttggctgcg	cccatatgaa	tcagtaatag	aaagcagact	gaagtatgcc	540
gcaaacgaga	gacggatttg	accggaggaa	gatccggagg	attgagcgct	tcgccaatgg	600
acatctctat	tacggtcttc	atcaggacgg	ggattcgggg	tgattcgtga	gttcgcgccc	660
gaagccacgg	ccgtatatct	gatcgggaac	tttcgcgctg	gcgtagattg	ccacagtttc	720
ggtttgcgcc	tgtggtgaag	cgggttcatg	ggaattgcga	ctttcatgcc	gactgcttcc	780
gcatgctctc	gctacaggct	cttcttcgaa	tggcccggtg	gcgaaggaga	gagataccgg	840
cttggtgcaa						851

			accettta	tetttetet	caccegtate	180
cggaaaggtg	ggctatcgtt	teggtateet	accelliga		caccggtatg	240
ctcttcggag	togatgatto	ggttttcagt	tttctaaatg	cccgatgtgg	gcacaagtcg	
CCCCCGGGG		attattetet	tracrootoo	tatggatacg	cggacagaaa	300
gtaggatcat	Cacterere	attattttt	000006086	tt-statatt	actascaact	360
ggtgcgtccg	gtcattgccc	agggacttac	gctgtctact	ttggtgtttt	gctgacagct	
	ggttctttat	cttttggctg	agggttcgga	ctttggccct	tacccgttcg	420
cttctatccg	ggtttttt	000006006	-666 00	acacactca	getteggtat	480
ctctttctac	ctctttgctg	cggctgccac	gatggctagt	acticgacteg	gcttcggtat	540
tercestect	cottcocaaa	agatgcagct	caaagagaat	ctggctcccg	acactggagt	540
LUBULALUUL	6666666	cooptagest	atatortoar	catogoacca	tcgatttcat	600
ggagagcggt	agtaacgacc	cccatggcgt	atatgetgae	caccacaca	8	608
Caccaccg						000

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...475
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:348

	togatacoot	catccagcgc	aacatcaaac	taagcgaggc	cccagccacg	60
gagetggtet	retretetac	gatgccgata	accacabaca	gtcaatcata	tgcagctggc	120
gtattccggc	attgetetae	acaaacaaaa	googoggeog	totoatatga	agcatacgaa	180
ggccgagctg	atcaaaaagc	acaacaaaa	ctccatacaa	aggtestagg	øtcttcttcc	240
gaaaacgctc	ggtcgtgcct	ggactetete	cccgacgcgg	tcaaccacac	gtcttcttcc	300
atcaggaagt	ggccatcagc	gatatatacc	ccaaccccga	atagattagt	acagreeate	360
ggaggagtcc	ctgaaagaac	tggccgcttc	geteegtteg	acagaccage	acageceate	420
acactactga	agaagtccgn	cggcgactat	atatcatctn	Cggagaacgc	cgcttggcgt	475
gcggcccgaa	tggccggtat	gccaccctgn	cggcatacat	caagacggaa	Rakka	4,5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 729 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

caassaata	ooctatogtt	tcggtatcct	acccttttga	tctttctctt	caccggtatg	180
ceeanages	togatgatto	pottttcagt	tttctaaatg	cccgatgtgg	gcacaagtcg	240
ctctccggag	cactetetee	attattctct	tcaccggtgg	tategatace	cggacagaaa	300
graggarcar	etenttacco	accaecttac	gctgtctact	tteetetctt	ecteacaect	360
ggtgcgtccg	gicaligue	aggacccac	agggttcgga	ctttggccct	tacccettce	420
cttctatccg	ggtttttat	cccctggccg	agggcccgga	achcaactca	acttcaatat	480
ctctttctac	ctctttgctg	eggergecae	gatggccagt	athegatees	acactagagt	540
tcgccatcct	cgttcgcaaa	agatgcagct	caaagagaat	etggeteetg	toactggagt	600
ggagagcggt	agtaacgacc	cccatggcgt	atatgctgac	catcgcacca	tcgatttcat	
caccaccg						608

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...475
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:348

pagetggtet	tcgatacggt	catccagcgc	aacatcaaac	taagcgaggc	cccagccacg	6.0
gtattccggc	actgctctac	gatgccgata	gccgcggacg	gtcaatcata	tgcagctggc	- 120
ppccgagctg	atcaaaaagc	acaaacaaaa	ggagcctgac	tctcatatga	agcatacgaa	180
paaaacgctc	ggtcgtgcct	ggactccctc	ctcgatgcgg	aggtcatagg	gtcttcttcc	240
atcaggaagt	ggccatcagc	gatatatacc	ccaatcccga	tcaaccgcgc	cggatttcga	300
ggaggagtcc	ctgaaagaac	tggccgcttc	gctccgttcg	atagattggt	acagcccatc	360
acactactga	agaagtccgn	cggcgactat	atatcatctn	cggagaacgc	cgcttggcgt	420
gcggcccgaa	tggccggtat	gccaccctgn	cggcatacat	caagacggaa	gagga	475
0 00 0		_				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 729 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...878
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351

gccgtgtaag	cgcaataggg	tcaagcgttt	ggtcagggag	gcttatcggt	caacaaacac	60
ctcctgaacg	atgtcctcca	agagagacag	atctatgcac	tattgcattt	atggtagtat	120
cggatgaact	tcctgacttt	cgtacaggga	gagagcgatg	caaaagagtc	tgatcagaat	180
tgccggaaat	gtacctcatc	ggctttgaaa	aacgagtaaa	tacgatgcga	ctgatcaagg	240
ctttttcgtg	caactcttac	tgctccccat	tttcttctac	aagcggttta	tatcccgctt	300
				atgcatcgaa		360
				attctccgct		420
				tcacttaatt		480
				atagcgagat		540
				ttgctccacg		600
				tccgtgaagg		660
				gtgcagtaca		720
				gagtttggca		780
				aaaacaggta		840
		ttcggagtag		•		878

- (2) INFORMATION FOR SEQ ID NO:352
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...500
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:352

gatttttctg	aaaccactag	tagatttttc	tgaaactaat	atcagattca	cgtactgaaa	60
				ctctactttt		120
				cgacggttca		180
				cggtgagcac		2.40

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...878
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351

			catcagggag	acttatoggt	caacaaacac	60
gccgtgtaag	cgcaataggg	tcaagcgttt	ggtcagggag	tettacattt	atootaotat	120
	atatactaca	agagagacag	atctatgcac	Latiguatur	4-666	180
	+octaacttt.	cotacappga	gagagugaug	Ladadgagee	66	
t	atacctcatc	ooctttgaaa	aacgagtaaa	Lacgargege	C C C C C C C C C C C C C C C C C C C	240
tgccggaaac	gcaccccac	tactecerat	+++cttctac	aagcggttta	tatcccgctt	300
ctttttcgtg	caactcttat	Lgccccat	tatteateet	atoratroaa	gccttacgta	360
acaccgcctt	catgccggtt	taccccctca	Lgittgitti	attotogen	gccttacgta	420
	0000000000	ctattgctga	gctcaagcgt	accece	64044-9-9	480
	aactatgacc	cottccottaa	gaagttttt	CCacccaacc		
	acattcatac	teattetgea	gctcgcaacg	acagegagae	caccob-b	540
ggtattttt	acacccacao	accatatete	coastacttt	ttgctccacg	gcattcatcc	600
ggaatctacg	accgaatgaa	accatatete	etteette	tccatasaga	attgaatcac	660
gtggagtgta	ccagagaatt	atagcggaga	guguude	cccgcgca66	attgaatcac	720
anagagatta	++actctggg	agaatggggc	tggataaggt	gigiagiaca	ccgcm-b	780
		atcaaattga	CCCEARCEAG	Kaki Leggia		
agcaacgaaa	taccaccato	ogatgatett	ttggcgatca	aaaacaggta	aagcttcaca	840
actgacatag	Lackageacg	ttoggagtag	tgaaaaac			878
gcccgtggat	cgttcatggt	ttcggagtag	cearage			

- (2) INFORMATION FOR SEQ ID NO:352
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...500
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:352

gattttctg aaaccactag aattaagtct tatcaaagca gcgattaacg caactcttct gactgactgc tgctcccggt	cacttggtac	ggctttgacg	cgacggttca	gttggtcgca	180
gactgactgc tgctcccggt	caaaggtgct	acgaattcct	Cagrageac	accaccaca	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354

ccgatgccgc	tacctccggt	tttggtcgta	tagaaaggaa	caaacatatg	tcgaacacct	60
				agtctgtgtt		120
				ccgtatcggc		180
				caattgccgg		240
ggacatcagc	tccacgggta	tttcttcaat	atccaccttt	atatcgttgg	aggaagaagc	300
tcttcttgca	ggcgcaatat	ccccgaaaga	aaagcatgta	aagaatgtcc	tccttctcgg	360
gaggaggaac	tgccgtaaac	ttacggtagt	ccgtacaaag	gataacagcc	ccactccggt	420
actacgaatg	gtatccaatc	cgtagacagc	atc			453

(2) INFORMATION FOR SEQ ID NO:355

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 988 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...988
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355

```
ggcggccttc taccaaatag cacaggcttt cagagggagc cgaagcctct agccattcct
                                                                        60
                                                                       120
tcttttgccg aatatgagga tgcttgtcgg atgtacgaca cgaagtctgc ttctatcctt
                                                                       180
ctaatgagga cataggcgag gctgattttc caatatggat ttctgctggc tttgtaaccc
gaacaatccc gatggcgact gctgcagcgg acagagatcc tgcgtctgct caacgatcat
                                                                       240
cctgaacgac attcgtcctc gaccagtcct atgtatcgtt tacgaccgag gaaggattcg
                                                                       300
tccggccgac atcaaaggac ggaaaaacct tgtcatggtc tatctttcag tcatgcctat
                                                                       360
gggataccgg ggcttcgcat cggctatatc gtgccaataa agattttatg aagcgtgtgg
                                                                       420
                                                                       480
cggctttcag tacgccgtgg gggtaaacgc actggctata gaggctgcca aattcatcct
                                                                       540
tatccatcct cacaattcac tctgccgatc cgcaagtggc aacgcaatac ggtagattta
                                                                       600
teacageest gaategeete gatggtgtag aagtacatee etcaggeaca egttetteet
                                                                       660
ccttcgcctc aagaaaggaa cagcggccga actgaaaaat atatgctgga ggaatataat
                                                                       720
atgctgattc gggatgcttc caatttcgtg gtctcgatga atcctacgtc cgaatcacca
cgcagcgacc tgctcgaacc agcttttcat caaagctctg gagacattcc tcgagaaata
                                                                       780
ctaaaatagc agatgctgca gatcagtctc tgtccttctc ctgtactcta tcctattaca
                                                                       840
                                                                       900
agacggagca agaagagtac acggtgttat cgtggatatc ttcgtgccgg taccaccatc
                                                                       960
acaacggcac tgatgaacgg tgccgtagca tatccgatgc accgttgaga gcggaaatct
                                                                       988
atgccgggaa cggttcttcg agagcgag
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 685 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354

ccastaccac	tacctccggt	tttegtcgta	tagaaaggaa	caaacatatg	tcgaacacct	60
ctgatgeege	aggagtacca	ttettetea	catgaagggt	agtctgtgtt	catccaacga	120
cttgaggaat	teeteracae	gaatacgaaa	agtogtttct	ccetatceec	aggatattcc	180
atcgagacgt	cattttgacac	agatttatca	gtaccgaagt	caatteccee	cggtcggccg	240
gcctcggcag	taccoggets	tttcttcaat	atccaccttt	atatogttgg	aggaagaagc	300
ggacatcagc	tccacgggta	coccean	acccactata	aadaatotcc	teettetegg	360
tcttcttgca	ggcgcaatat	CCCCgaaaga	aaagcacgca	antancacc	tccttctcgg	420
gaggaggaac	tgccgtaaac	ttacggtagt	Cuguadaaag	gataatagtt	ccactccggt	453
actacgaatg	gtatccaatc	cgtagacagc	atc			433

(2) INFORMATION FOR SEQ ID NO:355

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 988 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...988
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355

```
60
ggcggccttc taccaaatag cacaggcttt cagagggagc cgaagcctct agccattcct
                                                                       120
tcttttgccg aatatgagga tgcttgtcgg atgtacgaca cgaagtctgc ttctatcctt
                                                                       180
ctaatgagga cataggcgag gctgattttc caatatggat ttctgctggc tttgtaaccc
gaacaatccc gatggcgact gctgcagcgg acagagatcc tgcgtctgct caacgatcat
                                                                       240
                                                                       300
cctgaacgac attcgtcctc gaccagtcct atgtatcgtt tacgaccgag gaaggattcg
teeggeegae ateaaaggae ggaaaaaeet tgteatggte tatettteag teatgeetat
                                                                       360
                                                                       420
gggataccgg ggcttcgcat cggctatatc gtgccaataa agattttatg aagcgtgtgg
cggctttcag tacgccgtgg gggtaaacgc actggctata gaggctgcca aattcatcct
                                                                       480
                                                                       540
tatccatcct cacaattcac totgoogato ogcaagtggo aacgcaatac ggtagattta
                                                                       600
tcacagccct gaatcgcctc gatggtgtag aagtacatcc ctcaggcaca cgttcttcct
                                                                       660
ccttcgcctc aagaaaggaa cagcggccga actgaaaaat atatgctgga ggaatataat
                                                                       720
atgctgattc gggatgcttc caatttcgtg gtctcgatga atcctacgtc cgaatcacca
cgcagcgacc tgctcgaacc agcttttcat caaagctctg gagacattcc tcgagaaata
                                                                       780
                                                                       840
ctaaaatagc agatgctgca gatcagtctc tgtccttctc ctgtactcta tcctattaca
                                                                       900
agacggagca agaagagtac acggtgttat cgtggatatc ttcgtgccgg taccaccatc
                                                                       960
acaacggcac tgatgaacgg tgccgtagca tatccgatgc accgttgaga gcggaaatct
                                                                       988
atgccgggaa cggttcttcg agagcgag
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 685 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1812 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1812
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:358

```
ggaaaataat acaaagtact ctcatattgg taattcacaa tggcaaaaaa tatctaagca
                                                                        60
cactgaaagt atcggccgga ctattctccg ccatcttgtt gtcttattgg ccagcggact
                                                                       120
totggocaat goacagacag ttagcacgag acgaaagato aaggtotgoa gatgagooto
                                                                       180
ttgatctctt ctcctttaca gaagcggtat acactcgcta cggtcatgtc gcattcagga
                                                                       240
ttctcatccc gtacaaggga cggatattgc ttacaattat ggcatgttcg attaaacgaa
                                                                       300
cctaatttca tgcttcgatt tgtacgaggc gaaacggatt attccgttga agctctttat
                                                                       360
acatcctatt atgtggaaga ataccttcgg agggaagagg aatcgtggaa ttagtattga
                                                                       420
atctcacaca ggaagagatc gaaaagctga gaggtatttg gcatggaata ttcgccccga
                                                                       480
gaataaacga accgctataa tatcttttat gacaactgtg ctacccgcct tatcgagata
                                                                       540
taaaagaaac cacaggagct accttgcaaa tccctcatga gggtgaggga gaaagtggag
                                                                       600
acagctgatc gatgaatgct gtaccgatgc cccttggtca agttcggcat cgatctggct
                                                                       660
                                                                       720
ctcggggcga aaacagatac ctatgcaatc cggaggagca gttattcctg ccgaatagaa
                                                                       780
tgttggatct gctacacgta ccactctact ctatcccaat ggtcgatcaa cgccactcat
caggatacca aagagtggtt tccggctaag ccggccagta tggaacctgc ggagagggct
                                                                       840
ggcctacacc tttattggct tctatagctt tgctgatagt tttattgcag tagctgtttg
                                                                       900
ggatgttcgt cgcaaggata tatgctatgt aatgactcta tcttattagc cattatgggg
                                                                       960
ttatcgggat gtgttatttt attctgtcat ttttctcaga acatccgcat accaacccga
                                                                      1020
attacaatct ttcctgcttc atccccttca tctgcttatc gggttgcctc tgactgtgta
                                                                      1080
ccgctctttc accgagcagg ctttgtctat cattttatta actttgcgag ctaagtttga
                                                                      1140
teggtttgge aatatggttt ttgeegeaac aagtaggete eegetetatg tggeeggeat
                                                                      1200
tgctctatgg ttgctttccg ctcgcggata ttggtaaata gatggagaaa gaacgttcgg
                                                                      1260
 tgaaacgact tgtacgaccc ttttggccgt attgactata gggaatgtta cagtacaggg
                                                                       1320
 gcatcggttc atcccaagct ggtggtggta attaccattg accagttgag agtgatctcc
                                                                      1380
 tetegttttg eegeteacaa tatggeacag gtggatttaa tatetgetge aggatggact
                                                                       1440
 tgtttttagc aacgtagact tcggattcga ggggtagacg aagcatcggc tattgcaggt
                                                                       1500
 atatataccg gcacctatct aatcgtcaca gtattacagg cagtactgta ttcgacagag
                                                                       1560
 aaaagaacag toggtatoca ttttggaaga caaaaactto ttaggcaatt atacatogaa
                                                                       1620
 catctgtctc ctctcaagct cacttccggc actatcggcg atgaacacgg agtgcaacgg
                                                                       1680
 atggaaggag caaggtttat gcgatagcac cgaatccgta gcagcaatcg tagctgcagg
                                                                       1740
                                                                       1800
 tcagtctgga aatggtgcat tctgctcgaa gatcgtaagg ggatgtgggc tacgactacc
                                                                       1812
 tactacaaag at
```

(2) INFORMATION FOR SEQ ID NO:359

(i) SEQUENCE CHARACTERISTICS:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1812 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1812
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:358

```
ggaaaataat acaaagtact ctcatattgg taattcacaa tggcaaaaaa tatctaagca
                                                                        60
cactgaaagt atcggccgga ctattctccg ccatcttgtt gtcttattgg ccagcggact
                                                                       120
tctggccaat gcacagacag ttagcacgag acgaaagatc aaggtctgca gatgagcctc
                                                                       180
                                                                       240
ttgatctctt ctcctttaca gaagcggtat acactcgcta cggtcatgtc gcattcagga
ttctcatccc gtacaaggga cggatattgc ttacaattat ggcatgttcg attaaacgaa
                                                                       300
cctaatttca tgcttcgatt tgtacgaggc gaaacggatt attccgttga agctctttat
                                                                       360
acatcctatt atgtggaaga ataccttcgg agggaagagg aatcgtggaa ttagtattga
                                                                       420
                                                                       480
atctcacaca ggaagagatc gaaaagctga gaggtatttg gcatggaata ttcgccccga
                                                                       540
gaataaacga accgctataa tatcttttat gacaactgtg ctacccgcct tatcgagata
                                                                       600
taaaagaaac cacaggagct accttgcaaa tccctcatga gggtgaggga gaaagtggag
acagctgatc gatgaatgct gtaccgatgc cccttggtca agttcggcat cgatctggct
                                                                       660
                                                                       720
ctcggggcga aaacagatac ctatgcaatc cggaggagca gttattcctg ccgaatagaa
                                                                       780
tgttggatct gctacacgta ccactctact ctatcccaat ggtcgatcaa cgccactcat
                                                                       840
caggatacca aagagtggtt tccggctaag ccggccagta tggaacctgc ggagagggct
ggcctacacc tttattggct tctatagctt tgctgatagt tttattgcag tagctgtttg
                                                                       900
ggatgttcgt cgcaaggata tatgctatgt aatgactcta tcttattagc cattatgggg
                                                                       960
                                                                      1020
ttatcgggat gtgttatttt attctgtcat ttttctcaga acatccgcat accaacccga
                                                                      1080
attacaatct ttcctgcttc atccccttca tctgcttatc gggttgcctc tgactgtgta
                                                                      1140
ccgctctttc accgagcagg ctttgtctat cattttatta actttgcgag ctaagtttga
                                                                      1200
toggtttggo aatatggttt ttgoogcaac aagtaggoto cogototatg tggooggoat
                                                                      1260
tgctctatgg ttgctttccg ctcgcggata ttggtaaata gatggagaaa gaacgttcgg
                                                                      1320
tgaaacgact tgtacgaccc ttttggccgt attgactata gggaatgtta cagtacaggg
                                                                      1380
gcatcggttc atcccaagct ggtggtggta attaccattg accagttgag agtgatctcc
                                                                      1440
tctcgttttg ccgctcacaa tatggcacag gtggatttaa tatctgctgc aggatggact
                                                                      1500
tgtttttagc aacgtagact tcggattcga ggggtagacg aagcatcggc tattgcaggt
                                                                      1560
atatataccg gcacctatct aatcgtcaca gtattacagg cagtactgta ttcgacagag
aaaagaacag toggtatooa ttttggaaga caaaaactto ttaggcaatt atacatogaa
                                                                      1620
catctgtctc ctctcaagct cacttccggc actatcggcg atgaacacgg agtgcaacgg
                                                                      1680
                                                                      1740
atggaaggag caaggtttat gcgatagcac cgaatccgta gcagcaatcg tagctgcagg
                                                                      1800
tcagtctgga aatggtgcat tctgctcgaa gatcgtaagg ggatgtgggc tacgactacc
                                                                      1812
tactacaaag at
```

- (2) INFORMATION FOR SEQ ID NO:359
 - (i) SEQUENCE CHARACTERISTICS:

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...691
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:360

gccgtgctcg tccatttcg	a cctcgcacag	gccgaggtcc	ttcatctctt	ggccaaatga	60
cgcagcagca ccaattgct	t atroatroad	gggaaagtgt	agaggattcg	togotttgcg	120
cgcagcagca ccaattgct	- acceptedas	+++canttcc	atattettte	tttcgttgtt	180
tatcgaagcc tacatatcg	g agaaaccccc	cccagcccc	tagagaatga	taaacacata	240
atgetteatg tttetteet	c tgatgctgtc	gacgacgaag	Lagagaacga	anancatora	300
catgcgatgg ccaaccatt	c ggcgcctgcc	atggcgtgcc	attettggge	aaaacaccga	360
actocatota tttgaggat	c gcacttacca	cacccatcaa	agccctccgg	cgatgaattt	
ggaagggatg agggtaccg	c gttccttgcg	gatttattga	cagaagcgtc	cttcgagcgg	420
gtgctgacga accagctga	c ggtccgccga	tgaggagagg	tgtatttagt	tgtaacggga	480
taaacatacc agtgcaaaa	g gcagtgcggg	cacgcctata	ctcgtcagga	tcagagccat	540
atagetecta egecataga	g aatccaapgc	gtattaccgc	cttccatcgc	ggcttgatca	600
cggctgccat cgcattggc	e tacaasaccs	ccapaoctoa	togocogtaa	agccataggt	660
cggctgccat cgcattggc	.c cgcggagcca	2	0-3-0	0 00	691
cttgttcagg atcatcato	a caccgggggg	a			

- (2) INFORMATION FOR SEQ ID NO:361
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1057 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1057
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:361

				toattacaga	tcoooaaata	60
agattaataa	ttgctggtga	ttacttcagg	attattttgt	LUGLLECABA	CCBBBaaaca	120
ctacagcagg	cttgaacacn	tgggcttcct	ccatcgggat	ccaggcatat	gccatgatga	120
	cooperates	acgatgcggc	agetgeteca	ttgagacaga	ttacccccga	180
tgatgatgtc	gcccggacga	acgatgegge	ageegeeee		at concunt t	240
acctcttttg	cccggttggt	ataggtctcc	aagcgtgctc	cgttgttgtt	giccacgare	
tagacttctc	tropprostp	atgttggcag	catccatcag	atcttcatcg	atgggatgct	300
LEGACCICCE	000660606		aattnogong	tattttaga	ttttaatact	360
acccacatag	ttgaggttgg	cctccgtaat	ggctacgcgg	CECCCCEE		420
togacgtaca	tettetttc	caattctcta	tatttttacg	attgcaaagt	aacttaaaat	
cooteteet	ttcccatasa	acggcagttt	aacgcaattg	ggcttgatta	ttaaggacat	480
cgctgtaata	LLCGCataaa	acegouge .			gattattaca	540
acggcgcaaa	tgcagaaaat	ccgccacctg	ccacgaggca	gtaatatgtg	gattattgca	
cagaaaggtt	ttcaaatcgt	tacccgaaag	caaggtaatc	acctccgtaa	agaggagaaa	600
cagaaaggee		anattactat	tactctatac	tctatatttt	gcatagcagg	660
aacagcggtt	ttccgtgcat	CCGCCGC	cgccccacgc		gcatagcagg	720
gttaggctct	ttcatgttta	attttgaacc	aaaaagaaaa	gacaatggca	agaagcacat	
b	attatata	atooraoraa	орарааараа	ggtatcgtcc	ccatcatggg	780
tcaaggtgct	gilligiga	acgeougeau	66-66	-Angenerat	cccaaggagt	840
acggttacaa	tcaacggcac	ggtggctcag	ttcagttgca	agogoaccac	cccaaggagt	• • • • • • • • • • • • • • • • • • • •

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...691
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:360

gccgtgctcg	tccatttcga	cctcgcacag	gccgaggtcc	ttcatctctt	ggccaaatga	60
cgcagcagca	ccaattgctt	gtccgtcgag	gggaaagtgt	agaggattcg	tcgctttgcg	120
tatcgaagcc	tacatatcgg	agaaatcctc	tttcagttcc	atattctttg	tttcgttgtt	180
atgcttcatg	tttcttcctc	tgatgctgtc	gacgatgaag	tagagaatga	tgagcgcata	240
catgcgatgg	ccaaccattc	ggcgcctgcc	atggcgtgcc	attcttgggc	aaaacatcga	300
actccatgta	tttgaggatc	gcacttacca	cacccatcaa	agccctccgg	cgatgaatcc	360
ggaagcgatg	agcgtaccgc	gttccttgcg	gatttattga	cagaagcgtc	cttcgagcgg	420
gtgctgacga	accagctgac	ggtccgccga	tgaggagagg	tgtatttagt	tgtaacggga	480
taaacatacc	agtgcaaaag	gcagtgcggg	cacgcctata	ctcgtcagga	tcagagccat	540
atagctccta	cgccatagag	aatccaaggc	gtattaccgc	cttccatcgc	ggcttgatca	600
cggctgccat	cgcattggcc	tgcggagcca	ccagagctga	tcgcccgtaa	agccataggt	660
cttgttcagg	atcatcatca	caccgggggg	a		- 00	691

- (2) INFORMATION FOR SEQ ID NO:361
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1057 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1057
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:361

agattaataa	ttgctggtga	ttacttcagg	attatcttgt	tcgttgcaga	tcgggaaata	60
ctacagcagg	cttgaacacn	tgggcttcct	ccatcgggat	ccaggcatat	gccatgatga	120
tgatgatgtc	gcccggatga	acgatgcggc	agctgctcca	ttgagacaga	ttacccccga	180
acctcttttg	cccggttggt	ataggtctcc	aagcgtgctc	cgttgttgtt	gtccacgatt	240
tggacttctc	tccggcgatg	atgttggcag	catccatcag	atcttcatcg	atgggatgct	300
acccacatag	ttgaggttgg	cctccgtaat	ggttacgcgg	tgtttttgga	ttttaatact	360
tegaegtaca	tgttgttttc	caattctcta	tatttttacg	attgcaaagt	aacttaaaat	420
cgctgtaata	ttcgcataaa	acggcagttt	aacgcaattg	ggcttgatta	ttaaggacat	480
acggcgcaaa	tgcagaaaat	ccgccacctg	ccacgaggca	gtaatatgcg	gattattgca	540
cagaaaggtt	ttcaaatcgt	tacccgaaag	caaggtaatc	acctccgtaa	agaggagaaa	600
aacagcggtt	ttccgtgcat	ccgttgctgt	tgctctatgc	tctatatttt	gcatagcagg	660
gttaggctct	ttcatgttta	attttgaacc	aaaaagaaaa	gacaatggca	agaagcacat	720
tcaaggtgct	gttcttgtga	atggcagcaa	ggagaaagaa	ggtatcgtcc	ccatcatggg	780
acggttacaa	tcaacggcac	ggtggctcag	ttcagttgca	agcgcaccat	cccaaggagt	840

gcctttccac ttggctctgc aacccaattc	gtaagcctgt ggtcagatag gatccgaata	cggccgctat tccgaggttg tccgattgtc	tagcatcggg	gcctttcctg	gactaccgta caccacggat tcggcatgcg tcgtccaagc	300 360 420 480 500
tcttcatgct	ttcgggcgaa					500

- (2) INFORMATION FOR SEQ ID NO:353
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 570 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...570
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:353

agaagataaa gacttcggcc ccgtcagccg cgtatcatga gtggtcgcta ccggctatgc caccggaaga agccgccgtc tctggagccg gtcacaagac gtccggatat tctggtgaca tcaggccggt gtcgctgcca gtgcttgaga ttcttttgga ctgtatggcc ctcatatgat	tcgccaaaat cgactgcgat aagctgtgga gctgatccct gccggaggtg tcttcggccc aaataatctc tcctcgaaag	ggggcaggcg tcgacgtcga aaacgacgtc caggtaatag ttataccggc cgtaccccg tactctcgat ggagtcgtat	ggcatgaccg tatggggcct cacgtgatgg cagagctgga gcagattacg tggcctactc aaggagtatt	ctgttccaaa gcgtttcctc gaagtcggcc acttcctcta ggcagccaaa tcagcattct	60 120 180 240 300 360 420 480 540
ctgtatggcc ctcatatgat agtcattagt gtcctaaaag	tcctcgaaag tttcttcttg	ggagtcgtat	gagugguuu	cccacgccca	570

- (2) INFORMATION FOR SEQ ID NO:354
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...4\overline{53}$

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...659
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:363

ggcttggaga	gccgtttcga	agagatttcc	acgcttatca	cggatccggc	gtaatcgcgg	60
acatgaagcg	tttcacgaag	ttgagcaagg	agtatcgcat	ctggaaaaga	tecatacage	120
cgggcgcgac	tategeaate	tgctcgcaac	atcgaggaag	caaagcatac	Categorgaa	180
gagagegaeg	aggagtgcgc	gagatggctc	gcgagatgct	ggccgaggct	aacgaacget	240
rgccctttg	gaggaggaga	tcaagatgct	actcattccg	gccaatccgg	Aggagacaag	300
aatgccatcg	tggaaattcg	cggaggaacg	gggggcgatg	aggtgcactt	tttaccaaca	360
acciciaccg	catgtacgtc	aagtattgcg	aggcaaaggc	teecagetee	aggtracrea	420
cccgagcgaa	ggagctacgg	gggttacaaa	gagatcgtct	tctcggtcaa	ррррряяоря	480
grgrarggra	cctgaaatat	gagagcggtg	tgcaccgtgt	ccagcgcgta	CCtgcgacca	540
gacacagggg	egcatacata	cctcggcagc	taccgtggct	gtcttgccga	арссраярая	600
gtggacgtgg	agatcaatcc	ggcagacatc	gagatgctga	cgttccgttc	aggcggtgc	659

- (2) INFORMATION FOR SEQ ID NO:364
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1298
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:364

cgaagcaaac tacaagcgag gttctcttt acgaaagagg agatctgtat catgcaccat cttttggaat gggagaaaac ggtctctgtt tcggactgcg ggactgggcg tacaacgctc	gccattcgca tgctgaggac tacgatgttt gcgtcaaagt gacgggcaat ttgggaaagg taagtttttc agatcttacc tccgcgaggg cacccacaag gcaataccgg	aggagtgaaa gattactgga tcttccgcca cgtcatgcag agtcctgctc ggaatggtct attgccggac gattcgaaga tgattatatg gattggcat ccagcgcatt	atatccagat cgcatgcacc tcgatcgacc tgaggagaag ctatatgctc ttgcaactgg atcacgctag aagacgactg gacggatgcc ccacgcttgc aggagacttc atacagctcc atacagctcc	tactatctgg atctggtatt gaaaaatgca ctgaaacgtg cattgttcac tcagtggagc agaaggatga ctccgacatc tatggtgcgt cggcaccgtc ggtgcactnc tgcccatcaa atcggtcatc	cccaaacca cccgaccaga aagcccgtgc attacctcca cgttgggaaa ctatttggcc atcccctat gccgtatggt cgacaccact	60 120 180 240 300 360 420 480 540 600 660 720 780
cacaacgccc	Ctategegae	tcctatccat cgctaccacg	ataatatagt	atoggtoato	protocator	780 840 900 '

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1812 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1812
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:358

```
60
aataat acaaagtact ctcatattgg taattcacaa tggcaaaaaa tatctaagca
gaaagt atcggccgga ctattctccg ccatcttgtt gtcttattgg ccagcggact
                                                                   120
gccaat gcacagacag ttagcacgag acgaaagatc aaggtctgca gatgagcctc
                                                                   180
tctctt ctcctttaca gaagcggtat acactcgcta cggtcatgtc gcattcagga
                                                                   240
catccc gtacaaggga cggatattgc ttacaattat ggcatgttcg attaaacgaa
                                                                   300
                                                                   360
atttca tgcttcgatt tgtacgaggc gaaacggatt attccgttga agctctttat
                                                                   420
cctatt atgtggaaga ataccttcgg agggaagagg aatcgtggaa ttagtattga
cacaca ggaagagatc gaaaagctga gaggtatttg gcatggaata ttcgccccga
                                                                   480
aaacga accgctataa tatcttttat gacaactgtg ctacccgcct tatcgagata
                                                                   540
agaaac cacaggagct accttgcaaa tccctcatga gggtgaggga gaaagtggag
                                                                   600
ctgatc gatgaatgct gtaccgatgc cccttggtca agttcggcat cgatctggct
                                                                   660
gggcga aaacagatac ctatgcaatc cggaggagca gttattcctg ccgaatagaa
                                                                   720
ggatct gctacacgta ccactctact ctatcccaat ggtcgatcaa cgccactcat
                                                                   780
atacca aagagtggtt tccggctaag ccggccagta tggaacctgc ggagagggct
                                                                   840
tacacc tttattggct tctatagctt tgctgatagt tttattgcag tagctgtttg
                                                                   900
gttcgt cgcaaggata tatgctatgt aatgactcta tcttattagc cattatgggg
                                                                   960
cgggat gtgttatttt attctgtcat ttttctcaga acatccgcat accaacccga
                                                                  1020
caatct ttcctgcttc atccccttca tctgcttatc gggttgcctc tgactgtgta
                                                                  1080
tctttc accgagcagg ctttgtctat cattttatta actttgcgag ctaagtttga
                                                                  1140
                                                                  1200
tttggc aatatggttt ttgccgcaac aagtaggctc ccgctctatg tggccggcat
ctatgg ttgctttccg ctcgcggata ttggtaaata gatggagaaa gaacgttcgg
                                                                  1260
acgact tgtacgaccc ttttggccgt attgactata gggaatgtta cagtacaggg
                                                                  1320
                                                                  1380
cggttc atcccaagct ggtggtggta attaccattg accagttgag agtgatctcc
                                                                  1440
gttttg ccgctcacaa tatggcacag gtggatttaa tatctgctgc aggatggact
                                                                  1500
tttagc aacgtagact tcggattcga ggggtagacg aagcatcggc tattgcaggt
                                                                  1560
ataccg gcacctatct aatcgtcaca gtattacagg cagtactgta ttcgacagag
                                                                  1620
gaacag teggtateca ttttggaaga caaaaactte ttaggeaatt atacategaa
                                                                  1680
tgtctc ctctcaagct cacttccggc actatcggcg atgaacacgg agtgcaacgg
                                                                  1740
aaggag caaggtttat gcgatagcac cgaatccgta gcagcaatcg tagctgcagg
                                                                  1800
tctgga aatggtgcat tctgctcgaa gatcgtaagg ggatgtgggc tacgactacc
                                                                   1812
acaaag at
```

INFORMATION FOR SEQ ID NO:359

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...354
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:366

gagttgatct	cctttggacg	agacgtctcg	gatttcctgc	cggaggggtt	gtcctcgatt	60
age egater	222228222	ccttgcagtt	cagacttcgc	aaggcttttt	tgtgtccaaa	120
aagaaaacca	taatacatta	traggtrict	atgagaggaa	aaaagagtga	ttccgaaagt	180
atteageegg	tenetetent	108686666	agttttgag	aacgaagatg	agtttggaat	240
agtgactctc	Caatattat	acgccaaaaa	ageceeaac	aaaaatacaa	0088800880	300
gattcaaata	agcatctgta	gagaggagaa	aagccgaggc	aaaagcgcug	ggaaaggaac	354
tggcatagat	cgaaattcca	cttaaaacca	agccgtacaa	cgactggata	Laaa	774

- (2) INFORMATION FOR SEQ ID NO:367
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 686 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...686
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:367

tccccgggtt gagttttag tgttacctat atcttattga atatccaaca ggagacaaat gagtagggct aaaagaagaa gagcagaata gatggttgta	attgattcgt gtttttagaa tcatttctct gcggaagatg accccgtaac tttcggaact acagaaacaa cagctgatac cagcgaaagg	ctattccgaa tcaaagccag tccatagcga ctatttggtg aaccgaagga ttacagcct agaatgattg cgcttccact ggcaaattgt	ttttgagact ggcgcattta ttcttcaagt gtcttacgtt agaatcattg atttgcttcc tcaatcttat taattccact attctttcc	tttcgcacca cttcagccac cgaaaatgcg acgatcacaa caagtttttg ttatttgtct tgctgctgtt catgaactct gattggagag	caaaggaatt gattttagcc tcgaccagca ctgtggctat atgactgcag cagataacaa gcctgatatt attatcaaaa atagattgac	60 120 180 240 300 360 420 480 540 600
gatggttgta accaatgcat tggcagtgct	cagcgaaagg tgtttagatt	ggcaaattgt ctaatctgtt	attcttttcc	gattggagag	atagattgac	600 660 686

						900
totoooatot.	gaaaggcaac	agggcgaaag	gcaagagcag	ggagccatcg	ccaccaacct	900
6666666	8	888 8		accetatttc	CGSCCGCGSG	960
ctcgctcgac	aacatcaagg	cgcaaatcat	cagcactate	agegreetee	cgaccgcgag	
			cctatcaggg	actaggcagt	gagtacgata	1020
gcgttcgtca	cggcggagat	gigigicaalg	cccaccaggg	Beeggeege	gagtacgata	
						1057
CCCTECLEAR	cgttcgacag	ggaatgtgtt	CCCCCBC			

- (2) INFORMATION FOR SEQ ID NO:362
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1118
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:362

ccaaagacct	ttatggcgat	ggcagaaggc	gatccggaag	accacactta	cgccaaaaac	60
cactccttgc	caccacccag	gcagccatcc	tctcgggcta	ccaatccggt	ctcaaagagt	120
gtctgaccga	aatggcaaca	ctctatccgg	cagggaatgg	caagagtatt	ccacgggcca	180
agragicgct	tecettetga	accggcttgg	tatcatctcc	gacctttggc	gacaaatcga	240
ageageagae	aagaagagaa	caaaatgctc	atttccgatg	ctccgtctct	attgacagga	300
tcatcaacaa	GAGCGAGACC	cctttcgtct	atgacaaaat	cgggtacgca	tcgaacacga	360
aatgatgat	gaatttcaag	ataccagccg	ctacagtacg	aaaacttcaa	gcccctgctg	420
tocasasto	taactcacaa	cagtacaacc	tcctcgtcgg	cgatgccaaa	cagagtatat	480
accocttcco	aatoccoacc	ggcgtctgct	cacagaggtc	gtcagtcggg	attttgccga	540
accectede	gagtcaatct	accatataat	tggcgaagca	ctcccgaata	atcgagttca	600
acatoggaga	ctacaagcat	ctgccacaaa	tecttetete	aggctatgac	tcgcgaagcc	660
acaaccccc	caatacccaa	tcctaattgc	Cogaggagat	caaccgtaca	ttcatgcaga	720
gagacgacgg	tatagacaga	ttgtgccacc	ggctaaagta	gaccggcatg	gaagcgtctg	780
cctatgccga	LgLgggcagc	atcatcagaa	66000000000	ccaatctttc	gtggaggagc	840
cattatette	egregeege	actattatas	teastetaca	22222222	atactccttc	900
agatettgea	ggatetteec	cgttttatca	taggicigia	adadagagge	taccatactc	960
ggatattgct	attctcgtgc	gcaaaactta	taggetegeg	agatageteg	gecatgete	1020
tcttatcaac	ccgaaccgga	gaagaggact	attetetat	coogalgicg	ttatatasas	1020
tgtcgctgat	ggagcagcat	caattcgttt	tctatcgaac	ctactcaagt	ttatatccgc	1118
ccccaatccg	atgctttgcg	acagatcgcc	tacctgtc			1110

- (2) INFORMATION FOR SEQ ID NO:363
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 659 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369

tgtaacccgg	ccttccgaat	ccgaccaagt	aagatgttgc	catcggggcc	gtcgaagggt	60
acccactttt	cggtcctggt	tcgggcttgt	cttccgtata	gttggagcag	tggtctcggg	120
ttggcgtcgc	tgctccccga	tactcggtga	ggtgggacag	aggactgtga	tggagcaacg	180
gatggctgct	ctttggcgga	gccggccggg	gagataccga	tccgctcacc	acgggatttg	240
cgtgcgtgct	ccatgggtcg	gaggcggagc	agtcagtccc	ttgctaaata	aagcgcgata	300
ttcatcagcg	acaactccaa	caacagacgc	ttgccattgc	tctgcgatac	tgctggtcac	360
aggcattcag	tatcttgagc	gattggtata	agaagaagtc	gggcaacgtg	ctgccatatc	420
cacatatcgc	tgtatgacta	ctcggactgc	tccaacagcg	gcaaggtaga	agcgtcctga	480
gccatcatca	atcgcggaag	aaagaagcca	atccgctcac	gatcacctgt	ccgtcgaatc	540
cttggcaagc	aattcgtcca	acacgatcaa	tacggatcgg	taatcccctg	taaaaagaaa	600
tccgtcagac	ggaaataata	atcgtagtcg	aggatatcag	attctctatc	gtattggcat	660
aggtaatatt	gccttccgaa	aaacggcaat	gcggtcgaag	agcgaaagag	catcgcgcat	720
ccctccatcg	gctttgtcgc	tattatagcc	aaagcttcgg	cttcggcttt	tatcccctcg	780
ctgttgctac	gtagcgcaaa	tgttgctcta	ttcgggcccg	tggtattcgt	ttgagtcgaa	840
tatctgacca	gcgcgagaga	atagtgggca	ggatctttgt	gctctctgtg	gtagccaata	900
taaagatcac	ataagaaggc	gggtctt				927

(2) INFORMATION FOR SEQ ID NO:370

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...420
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:370

ggcaaagtcc	atcttcaccc	actccggtcc	catatgtctg	aaacgtcgaa	ccccatgttc	60
gccttaagtt	gcccaaagat	cgcctcgggt	tcaatacacg	tcgcttgcgg	tgcacaagac	120
cttactccga	gttgagccga	tccttagctg	cgctttgtag	ttgttgagac	gatgattcac	180
ttcgatgatc	ctattaccat	agcctgtctc	tctgctaatt	cccgaatctt	ttatggatga	240
tattttctga	ccacagtaca	cgtctgactc	atcgatccga	accaaaaatg	caccatttta	300
gttcgaattt	tctgaaaaaa	tggaacgaga	ttttttcgt	tgtgcgtgag	aattttttgc	360
tttccgcgcc	aaaccaaaaa	agttcccacg	cctggttttt	aggaagtgtc	aaaacgggaa	
420		-				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1119
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368

```
caagttgttg cacgatgcct atgcaaaagc tttagagctt cgnaagttgg ttccggacag
                                                                        60
gaggtogaaa atgtogttaa gactatotat aagootttao ggoogagaga tttoagooaa
                                                                       120
gatggtagag ctattgaagc cggaagggtg cgtgccaagg tggagatcgt atatcaaagt
                                                                       180
ttggaagget tgcateggeg atacegaate ateegggaga etggtattte teeggegatt
                                                                       240
                                                                       300
atccgcaccc ggaggcgctc atttggtaaa tgaagctttt atcagctaca tggagaggac
tatggcaaat aattatttcc agaatcgaaa gagtattaag aactatgaga gagcaaagaa
                                                                       360
aagcgacatt gatattggac gatggtagcc gttcgaaggc tattctttcg gttgcgaacg
                                                                       420
                                                                       480
tgctgtggcc ggagaggtcg tttcaatacg gctatgaccg gctatgtgga gagtctgacg
                                                                       540
gatccgagtt tcgcggacaa atcatggtta tgacctatcc tttggtgggt aattatggct
tccgatgaaa gcagctgagc caaacggcgt atcttgcttt atggaaagga cagaatacac
                                                                       600
                                                                       660
atggaaggaa togttgtgto ogactattoo cattotttag toattggaat gotgtogaaa
gccttggcga ttggctcaaa cgtgagaggt attcggtctg acgggggatcg acacgagggc
                                                                       720
attggccaag cacctcgcga acacggttcg atgaaaggaa agataattct cgaaggaggc
                                                                       780
gaagcattgg cttcgccgat ccttacacag tcaatcaggt agcggaggct tctgtcgtga
                                                                       840
                                                                       900
agtaatcgtc tacggcactg gaagcaaaaa ggtggtactc gtgattgtgg agtgaaggac
aacattattc gctcgcttct ccgtgaagat aaacgctcta ccgtgtacca tgggattacg
                                                                       960
                                                                      1020
actttcatcg aatagcatac acggtctctt catcagcaac ggcccgggcg accccaatat
                                                                      1080
gtgcagcgta cagtggaaca tattcgtcgg gctgtggccg gcgacaaacc tatctgcgta
                                                                      1119
tttgcatggg caatcagctt ttggcgaaag ctgccgggg
```

- (2) INFORMATION FOR SEQ ID NO:369
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 927 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...927

cgcaaattca aggagcaagg tattcgctct gccattattc gggaggattc cgactttatt 120 cgcacaacat caaagagcgg tacggctcga ctacatctgc acatcggagg cagaggtgga 180 aaatggcctg ctgacagtcg tctatcgggt accatagtgg atgcgaaggt caaagccgaa 240 ttctcgctc cctggccaag gagctatccc tcacccctgc cgaaataatt gccgaggcga 300
aaatggcctg ctgacagtcg tctatcgggt accatagtgg atgcgaaggt caaagccgaa 240 tttctcgctc cctggccaag gagctatccc tcacccctgc cgaaataatt gccgaggcga 300
tttctcgctc cctggccaag gagctatccc tcacccctgc cgaaataatt gccgaggcga 300
tggagccaat gatgtaccca tgcttgactt ctcggccggc agctcatatt caacagttcg 360
gcacatccgc cttccatgcc tcaactacgc atgaagccat tctccaattc atgggttgcc 420
gatagtcgcc gacccgatcc gatagaataa gaacctccgt gctaagagaa atttatcgta 480
cggaggtatg tttttggcgg aaatatattt actttgggat agaagagtag acccataaga 540
gcttgaatac gatgcgatcg tatccgaagg gcatgcgaaa tatagatcgg aaaggtgccc 600
gtattctttg gttttgcgag cttcttttt gactttccgt ggagtttttc ccctgatgta 660
tggccgaaga ggaagcattc gtgcctttca gggcataggg acaaaatttt taagaataca 720
attatcagat ttatccaatg aaagtaggtt tgttcatccc ctgttatgtc aatgcagtgt 780
atccgaagtg ggtatcgcca cgtacaaact gctgaagagt ttggacatag atgcgactac 840
ccgatggatc agacatgttg cggccagcc 869

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 703 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...7\overline{03}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:373

gtcgttactg	tttgcaggat	actctcccta	tcgtatctct	ctattgatta	gagtgcgttc	60
cgagaatgag						120
tttcccctct	tctttctgcc	tttcagccga	gagcctcgaa	acaggcaaaa	ggataaagga	180
tgcgcgacga	agtatcctac	aaagttccag	aaaatgatca	ccgtcgggac	tgcatatcga	240
atagcgaccc						300
aggaccgaaa	gcaacgacgt	aggccacagg	gtgcctatcc	cccaataaag	cattgtcata	360
gacaaacagc	aagaggagat	agcacgtcca	taaacggtat	ttgctccata	aaggtggtga	420
cagccacatt	gcgaacgaca	gcatgaaaga	gcgaatctgc	tcacagcgga	gcacgtgtcg	480
ttgtacccaa	tgaagagatt	gcatcccgta	cgggagctga	gcagatagcc	aatcatcacg	540
ccaaggaacc	ctcaccggat	ggcataatga	atatgcaaga	gaagaaaaaa	accgtgaatt	600
tgtagtttgt	gactaagaga	cttcccggcc	tttctacttc	gctctgtccg	aatgcccatg	660
aaccactctg	ctacagccgg	atggcctagg	cagggatgaa	ttc		703

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 647 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{3}41$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:371

ccaaatgaat	tcatatatga	atttctccaa	ctatttctat	ttctcttcag	gttcagtaaa	60
tatcttctat	gcaaaaggcg	tattttagtt	cgcaaagtac	tcatttataa	taagaaaggc	120
aaataaaacg	gcaagaaaac	gcctcttcga	gcataaaaat	gtcgcaagag	gtgtatgtgg	180
taatcagggt	acataaacag	ggcaaactcc	acctttcgtc	gtttgacgag	acctctgagg	240
actttccctt	gtatcggcag	aaagagacaa	attcacgata	gaaattcctg	tcgccgactc	300
tatcttccgc	aacagtcggc	tcttgggatg	cttgccgtat	ccggcaacct	gcctgtcccg	360
acattgtagg	aaaggacggc	aagcagaaga	acgttccatt	taaaacatct	gaagataggg	420
atttacaata	gcttcctaaa	ttcatctccg	ccaatctgtt	gatttcatcc	ttgtagattt	480
caaggtgatg	aggatgatgt	tctccacata	gataccgatg	gtcatatccc	tgtttctcac	540
gacatgacta	tctccgccaa	cgtgtcttgc	aactctttgg	caatatagtg	gtcttgcgat	600
ttttcaaggt	gttgcgacag	atgaaaagcg	actcatatca	cctttatcag	cctttcgcct	660
ttctcttctt	gggactcttg	aaaaatcttt	gacattggtt	cttcatttgg	acgttccgat	720
tcaacacact	gctctctaat	tgagagcgtt	ttatttcgct	ctcatttctt	ttcatgggaa	780
tacctgtgaa	acaagttccc	ggatggcaac	aggatctacc	ttgccgtttt	ggtctctgtc	840
atactttctt	aatttttatt	attacacaat	tcattgttca	ttcgttgcca	gtatatttac	900
cgatgaagat	gaatacatcc	gctatcgaag	aatgcccaat	aatcggcttg	taccagtagg	960
gctacatcct	ttcattcata	cctttctgtn	ggagatgttc	attagtgtcc	atcaatacaa	1020
tcgttcgatg	tatctgcctt	cgcacattcc	cacgttcgag	tgnaaagaat	caanggactg	1080
ttctttgaca	tacaccctcg	cctatatcgc	tcatcgaaac	gtgatgtatc	gaagacacat	1140
accatcaccg	acatattcga	cagtgcaaat	atatggtcgg	tgatgctgta	atcagcgtga	1200
tttcctttag	tgcgtacttg	tggcacgatt	tggataattg	tggcttcgtt	ctacctaata	1260
gctttgggta	caaggatcgt	aactttgcag	taagcgataa	gtcggtattt	catggcttgg	1320
	ttcgagagaa					1341
_						

- (2) INFORMATION FOR SEQ ID NO:372
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 869 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...869
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:372

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...574
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:377

ggctgtgttg	tccggctgtc	ctgtctttt	gaatttgacc	atgatgaaga	ttccggtcgc	60
ttctccggtg	tggagagtgt	ccatttgtta	tagtaagata	gaaatggata	gaattggcag	120
gtgccgactc	tgcaatatca	agatattcga	tgtcttatag	gatgcagcag	ctgggatctc	180
ttgagcttct	gtggtaggaa	ccccttcgtt	accgaattgc	gaaactttgc	ctgtatattt	240
ccgacacttc	atatccttgc	acattgatgg	tgggttttat	catgcgaatc	tttgtgccac	300
			cccttctgtc			360
			gggctgtcgt			420
			tgtggccgga			480
cactacatag	tgctgaagtt	gttgttgcca	ttgaatagtg	gtcgcatttg	ctctttgacg	540
		tggatttgat				574

- (2) INFORMATION FOR SEQ ID NO:378
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...384
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378

gggaaggcgt	aatgaagaaa	gaaattcttt	cagcagatta	caaaggcgag	ttgttcgtca	60
ttctgtagct	gattatgtca	aagccgaaga	cttcgctgaa	acattattga	gcgtcatata	120
			ccattgtcgt			180
			tcttgcatct			240
			gccgatcatg			300
			cttgcggngt			360
-	ccaggganag		2 00 0	000	-	384
000000						

- (2) INFORMATION FOR SEQ ID NO:379
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...647
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374

agatcccttt	gaatcattga	gactctcttt	gaaaggtcca	ctctagaggt	ccccagccca	60
	gttctgtcca					120
acaagatata	tgtttacaga	gttgcacaat	gaaagaatac	gagttgagcg	attattttaa	180
	cgttgaattg					240
	tatatgtttt					300
	tacgaaagct					360
	aaaacagaat					420
	atttcctgcg					480
	tgcttgcaac					540
ctttcgacag	ctattctcca	atgggagtgt	gcaagccctt	ctgtgcgagg	aagtttacca	600
	taaagatatg					647

- (2) INFORMATION FOR SEQ ID NO:375
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...486
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375

ccccgggaat	aggcggattt	tcgccggcta	tcgtactgta	tctgctgatg	ctatcgtagc	60
				ctccgctctc		120
				aataggcact		180
				ttcgccattc		240
tttcgacaga	agaagaactc	ttcacgacaa	ggaacagaaa	cctcaaaaaa	ccctctccgg	300
				tgaaaagacc		360
				aaccggatgg		420
tcagcagact	cggatccttt	tctccgatat	caccctgtcc	gcttggatac	cggatccgac	480
atataa				•		486

tggacgaagc	ccgccacaag	catccgtgat	gctgtcccaa	tcgtctgcac	agatagagaa	240
		ggcacaagcc				300
		acgatcaaca				360
		aacggaggaa				420
		gcaaagctgc				480
tgggcgatac	gtacgaatca	aaggacagac	ggctataggc	agtattatag	atatgaatgt	540
cgggaggcta	ccattgctct	cggaatgatc	aaaacgactg	tgccgatcat	cggttggaac	600
cggccaagcc	cgtcaaggag	cggaagtctg	agcctgttcc	ggggcatctg	cccgaatgat	660
catagaccgg	atccacgaga	agcgttggat	ttcaagcaag	acatcgattt	gcgtggcatg	720
cgtgtgaacg	aagcctccaa	gccgtcatgt	attttatcga	tgatgccatc	caactgggaa	780
tacccgcgta	cggatacttc	atggaacggg	aacaggtgca	ctcagaacgg	tgacagggag	840
		cgtaaggcat				900
ccggcatcac	tgtcgttgaa	ttgggatgat	actttcgata	cgatcccaaa	tggctgaaat	960
catctgc						967

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...494
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381

aggatccccg	cccacaggcc	gtatttgctt	acttgtattt	ataatcatca	gacaatccta	60
ccatataagt	gaacagcgaa	ttagtaattg	acgttaagcc	aaagaggtat	ctatggccgt	120
cctggaggat	ggcaaactcg	tggagctcaa	cgcgaaccgc	gcaatctttc	ttttgcagtg	180
ggggatattt	acctcgtaaa	gtgaagaagg	tgatgcccgg	tctgaacgct	gctttcgtgg	240
atgtagatac	aagaaggacg	catttcttca	ttatcttgat	ttgggcttga	ctttgatgct	300
cagcagaaga	tgatggagat	gatgacaaaa	agcaaatcga	ttcatccttg	tccaaagtgc	360
ccctcggcag	cgacctccct	aaagaggga	agtcgcagat	gtgctcaagg	ccggacagca	420
gatcttggtg	cagatagcca	agagccgatc	tctaccaaag	gcccacgcct	gactgccgag	480
ctttcttttg	ggcc					494

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 637 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...574
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:377

ggctgtgttg	troggetate	ctgtcttttt	gaatttgacc	atgatgaaga	ttccggtcgc	60
ttctccggtg	tagagagtat	ccatttgtta	tagtaagata	gaaatggata	gaattggcag	120
ttetteggtg	tagagagaga	agatattoga	totcttatag	gatgcagcag	ctgggatctc	180
ttgagcttct	tgcaatatta	agacattegt	accoasttoc	gaaactttgc	ctgtatattt	240
ttgagcttct	gtggtaggaa	ccccccgcc	tagetttat	catorogato	tttgtgccac	300
ccgacacttc	atateettge	acattgatgg	Leggiciac	cacacatatt	tttgtgccac	360
tcgtttgagt	ttataatccc	ccaacagttt	ccctctgtc	graceacact	gatctgctta	420
ttgccatgag	caagcattac	gaaatcggca	gggctgtcgt	agaagagact	tcaatagatt	480
tototaccac	aaattgagaa	acgcagcttc	tgtggccgga	gcattgaaat	cgagactggc	
cactacatag	tgctgaagtt	gttgttgcca	ttgaatagtg	gtcgcatttg	ctctttgacg	540
gaatgatata	ngccccttca	tggatttgat	agtc			574

- (2) INFORMATION FOR SEQ ID NO:378
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...384
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378

aaaaaaaaat	2210220222	gaaattettt	cagcagatta	caaaggcgag	ttgttcgtca	60
gggaaggcgc	gattatgtca	Pagecassas	cttcgctgaa	acattattga	gcgtcatata	120
ttctgtagct	gattatgtta	caaccccac	ccattetcet	tecceeteec	tacggagtcg	180
gaagcaagca	aatttaatt	tettgeatga	tettacatet	gtattgggtg	gagaagttgg	240
gaagcaagga	aaatttgccc	testestest	acceptants	acatocaaat	CopaagaCag	300
agctttcgtg	ctgcggtaga	tgctggtttt	gttgattatg	Caddacaaa	cggaagacag	360
			Cttgcggngt	Cagggacaua	tccagcacat	384
cgccggtatg	ccaggganag	ctct				30.

- (2) INFORMATION FOR SEQ ID NO:379
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

agtogttogg tgatcaaaaa ttotogotog totttttto gotttiggit ogagattigg aaaaaagaca acogtaaato ogaaatcatg gogogagttt ttocogattt ttogttogtt	agtcgttcgg aaaaaagaca tttgtctgtt	tgatcaaaaa accgtaaatc gcgactgctc	ttctcgctcg	acacaaattt	ttcccgattt	ttcgttcgtt	1080
---	--	--	------------	------------	------------	------------	------

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1169
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:384

```
ttcgccactt gacatcacgc gtaatcgaag gattatcact cttacgggca tcttgtctat
                                                                        60
ctcatcgata aagacaatcc ctctctcggc ctgtttgaat cgtagtctgc ggcctgcaaa
                                                                       120
                                                                       180
agtotggtga gaatactoto aatgtotoco coacatagoo ggottoggto agtacogtag
cgtcgactac ggcgaaggaa catggagcat tttggctatc gtacgagcca agagtgtctt
                                                                       240
gccggtcccg tgggaccgac cataataata ttgcttttct cgatctctac gccacgctgt
                                                                       300
cctcttgctg gagcaatcgt ttgtaatgat tgtatacagc gacgaaagaa aacgtttggc
                                                                       360
atcatcctgc ccgataacat acgaatcgag aattccttga tctctatagg ccgaggcaag
                                                                       420
tcctctctct tcagattgtt ctctcttccg atttgaattt ttgcaatgct tctcgaacca
                                                                       480
cctctcctgc cggagagcac attcatcgca gatatgagca tggactcctt cgagcatcag
                                                                       540
tttacctgcg ttctcggcat gccacaaaaa ctacagtatt cttcgtcctt ttctttgcca
                                                                       600
tgagaaatat acagtccccc tttgggtaac gagagggtac tttcgattct tttcgaggat
                                                                       660
tttatctatc atcccgtact ccaatgttcg ggggctgtca tccaatagtc ccgatcacta
                                                                       720
tetttttega eetgeegaeg ggettteeae tgtgagaaga gataategtg taaagetett
                                                                       780
tcttacgcgc agaatctcgc gagctgcgat ctccaaatcg ctggcctgcc cctcatacca
                                                                       840
ccaagegget gatgtateat caegegggaa tgaggeaaag caagegtttg cetttegtte
                                                                       900
ctgctacgag cagcactgat gccatagacg cgccatgccc gtacagatag tggccacatc
                                                                       960
gcaccctata tactgcatcg atcgtatatg ccataaccgg cataaacaga tccgccgggt
                                                                      1020
gaattcagaa gatggaaata totttaccgg ggtcggcgct atcaagataa agaagctggc
                                                                      1080
ttgaatgaca ttggccgtgt aatcgtcgat ctgagtgcca aggaagagat ccgatccatc
                                                                      1140
                                                                       1169
attagacgtg agaacacatc catttgtgc
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2717 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

```
240
tggacgaagc ccgccacaag catccgtgat gctgtcccaa tcgtctgcac agatagagaa
atcaaccgcg acatcaaaga ggcacaagcc gaaagggaga aaacgcggag agcagacagg
                                                                       300
agctgaacga cttcagggaa acgatcaaca aagaagagat cgaaaagaag agcgaatcaa
                                                                       360
                                                                       420
tcgggagata gagaaaataa aacggaggaa aaacggaagc aggagaaagc agcaagccgt
                                                                       480
teggeegaaa cacetgtaca geaaagetge aagaagtgee ceaaceceet gteatacaag
                                                                       540
tgggcgatac gtacgaatca aaggacagac ggctataggc agtattatag atatgaatgt
                                                                       600
cgggaggcta ccattgctct cggaatgatc aaaacgactg tgccgatcat cggttggaac
cggccaagcc cgtcaaggag cggaagtctg agcctgttcc ggggcatctg cccgaatgat
                                                                       660
catagaccgg atccacgaga agcgttggat ttcaagcaag acatcgattt gcgtggcatg
                                                                       720
cgtgtgaacg aagcctccaa gccgtcatgt attttatcga tgatgccatc caactgggaa
                                                                       780
tacccgcgta cggatacttc atggaacggg aacaggtgca ctcagaacgg tgacagggag
                                                                       840
tatttggcca cagtcaatgg cgtaaggcat tttgcagacg aaacgtccag ttcggaggag
                                                                       900
ccggcatcac tgtcgttgaa ttgggatgat actttcgata cgatcccaaa tggctgaaat
                                                                       960
                                                                       967
catctgc
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...494
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381

aggatccccg	cccacaggcc	gtatttgctt	acttgtattt	ataatcatca	gacaatccta	60
ccatataagt	gaacagcgaa	ttagtaattg	acgttaagcc	aaagaggtat	ctatggccgt	120
cctggaggat	ggcaaactcg	tggagctcaa	cgcgaaccgc	gcaatctttc	ttttgcagtg	180
ggggatattt	acctcgtaaa	gtgaagaagg	tgatgcccgg	tctgaacgct	gctttcgtgg	240
atgtagatac	aagaaggacg	catttcttca	ttatcttgat	ttgggcttga	ctttgatgct	300
cagcagaaga	tgatggagat	gatgacaaaa	agcaaatcga	ttcatccttg	tccaaagtgc	360
ccctcggcag	cgacctccct	aaagaggga	agtcgcagat	gtgctcaagg	ccggacagca	420
gatcttggtg	cagatagcca	agagccgatc	tctaccaaag	gcccacgcct	gactgccgag	480
ctttcttttg	ggcc					494

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 637 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...5\overline{22}$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:386

	tantatacaa	tctttcatt	tttcgcagcc	agttcggccg	aagagacgaa	60
ggccaaatcc	tyctytacya	coccacac	atcagcttcg	gacgttatac	tccagcttcg	120
atttcgtttt	gctgcttttc	Caccagette	atcagecteg	teettacaaa	agtaaattat	180
aaagatcgag	ttcctcttct	ccggtcaaga	ataattttt	estantan	agtaaattat	240
ccgcgccaaa	ctggcactaa	ttttgtgtac	ttgtataaag	agiaaaiaag	acagtcatta	300
cggagaaaaa	gatttggtta	tttttgtctt	cacagaaagg	ctgctctgca	taatgcttct	360
ctatattcaa	ggagccggta	atgaattgaa	aaagagaaga	ttgatagaat	tgcaaaacac	
agaaatgeta	ccactcatga	cccaccgcct	caatcaatcg	gaatateete	LLCgallgga	420
tataataaa	coatagacct	catcccegto	gggattgtag	agaacgaatc	catcagatat	480
tatgttgtag	cgacagacct	agcatcatag	catappacaa	8C		522
gcaaatcata	allgallgal	agcaccacag		0		

- (2) INFORMATION FOR SEQ ID NO:387
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...399
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:387

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...2717
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:385

```
60
ggcgcatgtt tttataccaa tggatagtac aagcagggat gattcggtat cgtgccagta
                                                                     120
gaattacaga tootttocat gogattotto atgottatog tatgotgato ggacacaaag
aagatgaagg ggggcactta gaggataaag ggaggggatt tgttagggcg gatttcaaaa
                                                                     180
aaataagggc tatctccgac agcccttact tccttattaa ccttaaaatc taataccatg
                                                                     240
                                                                      300
aaaaaactgt acaaaaataa ggcgatgtat ttctcgtgca actatattag gccaaaaggc
gcatattagt ccaatcaata tttgttttcg gccttatact cttttttctc ccatattcga
                                                                      360
acggggatca tacgccagaa agcgaccagt aacgatagcg ccagtcgaaa gtcagcagtc
                                                                      420
                                                                      480
tttttcgacg gatgacagcc ttactattgc ttgggcaact atcttggact ccatcagcat
                                                                      540
tggatactta cgtctcgtag caggggggta tcgacaaatc cgggacgaat ctccgtaacg
                                                                      600
tcaggtgtag gctgtctgtc gtggccaatt ggcgtatgga ttggagatgt gcatttggaa
gcgtttggtg gcggagtagg caggagcgga tcccattctc ttgttgctgc taccgaactg
                                                                      660
                                                                      720
atggctacta tttgaccctt tttccgaggc gaaaatagcg gtaggcggca ccgatcattc
780
                                                                      840
attgtataac cgataccgga cgagtggaag tatacatcca taccgctcat ttctcgatga
                                                                      900
ggtgggacag ccgttcagga gcatcggaat gcgtgatgtc tatacggctg tataaacctg
tgagggattc tcctgcttca atgcatcgag ctttgggtat tgcggccggc aacacctacg
                                                                      960
aaccaaccgc gagagataaa aggcgggcta catcaagccc gatgccagag gtggctccta
                                                                     1020
cgacaacgat cgtttggctt ccatgatttc ctgttatgaa atgaagtcca tcccacgaga
                                                                     1080
                                                                     1140
attttcgctt cttctgtcgt agctcctacg acagtgaaag ccttcattca cgtgggtgcg
ggtaggcttt gcgttgttct tcgaatgtct tcggcgtgcc cttagcgatc gatccggtac
                                                                     1200
gagcggatcg aaggtatgca gcaaaccctt tcgatacgat ggtcggggaa gagcgacaga
                                                                     1260
                                                                     1320
tctatgatgg gatggtcggt gggggagggg ctaaagtatg cagcagggga aattccagtc
                                                                     1380
cgatacttcc gtaatggctt caaggcacat tctggctcca ttggcttttc cgctgcagag
                                                                     1440
aatcctgcta tgtgaggagt cgcgatgtct gccaaatcca aaggctgagg tctatatcgg
gttctccttc ccagcaatct attacgaggg ttggagccat ccgcttttga cagcccgaat
                                                                     1500
aagagettgg gtateegete ggeteetegg caggeattga teaggatagg cettttgtet
                                                                     1560
gcacagctcg tagaaaagcc tcaccgatga ggtgataggt ggcgtgaggg tcttcatggt
                                                                     1620
gaggggaacg tggaatgaga taatgtcgca ctgctccacc agtcggttag aggaagaaag
                                                                     1680
                                                                     1740
ctattgtcct gctctgcctc cgaccgaggt ggatccagag caggaactcc atgccatagg
cggaggccaa acgcttcagc tcacgcctac atggcctaca cccactatac ccattacctt
                                                                     1800
ctctttcagg gaaaaccctc gcgcaaagcc agacgacaca ggcagcacat tacatactgc
                                                                     1860
                                                                     1920
gcacggccgt agcattgcag ccgggggaat tgcgccagag gataccgtgg cttcgcagta
ttcgcggtcg atgtggtcga atccggccgt ggcagtcgtt tcaaccgcac atcagtacct
                                                                     1980
                                                                     2040
tgcagaagag ccggtgtgca cttggtgatc tgcggacgat cagcacccgg gcatgacgta
                                                                     2100
togtatoggg agagaagogt cogagtgtag gtaagtaatg toogcaacag gatogacaat
                                                                     2160
acctctcaat agggcacgga tgcttctgcc actattttga gaggaccgga tagagagaaa
                                                                     2220
gcatttctta ggcttcgcct tttattttgg ttgggaatgt aaatgggcat ccgatacgcg
                                                                     2280
ttgctcggtg tggatctcgc cgtgttccac ttcgagcgat ggatattgtc cgagagagtg
                                                                     2340
gtcaaaagtc ttttggcatt gtcggagtca ggatgatgcg attttggact cgtgcggtgt
                                                                     2400
cacgattcgg aacatacgga tgaagtccaa gacaaattcg ctcggagagt gcatcacgat
                                                                     2460
aagagattgc agtagttgcc ctgagctatt tcttcgggca gttcgatgtt attgttttgc
                                                                     2520
tttcgttttc catttgttct tgaatgtttt aataagtaga tgagggaaag tgccaagctg
                                                                     2580
aataacgtat ggcaccgtta ccccctttga acaaagttac tcctttcgtc taaatgtgaa
                                                                     2640
taagggttca cgtgccagag tgaaattatt gcggttcgaa ttacggataa tgctcttttc
                                                                     2700
ccatccgtac aaatataccc tgtacgaaat acgctctttt tgccgaggca tacttgtaca
                                                                     2717
gggtaagtaa gcatgtc
```

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...346
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:389

(gccttagag	aaagtgtcca	tcgctaaggc	ggtgccaaat	taccattttc	gaacaccgag	60
(caaaaaagt	ctctaatacg	gtgccaatca	caactttgat	actagagaaa	aagctcggca	120
8	ataggctat	cgactcatcc	gaaaaattgc	ataacaatcg	caagctccga	aagccttatg	180
ç	gcgaaccaac	aaaaacaaga	cagccacctc	gtttgcaaag	cgaacaaagt	ggctgtccta	240
t	atgttgcag	ggctatggaa	accccttatc	ctcanagaac	gggaatcgac	gaagcngccg	300
٤	gctataatc	tgcgtcttcn	aagtgtactt	ctctgtgaac	gttcan		346

- (2) INFORMATION FOR SEQ ID NO:390
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...474
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

tgatgtccgt	gatgatgtgc	ctcatgttca	tgtttgtgct	ccgagcaacg	gcgtgggcgt	60
				gatctgatgt		120
				attcggcttc		180
				ctccaaaaga		240
				tttaccatat		300
				ggctaaagat		360
_	_			ggtgtccttt	•	420
ttcggacggt	gcaccctatg	cttgcctctt	ttcatcgtgc	gcgatgggga	gaat	474

- (2) INFORMATION FOR SEQ ID NO:391
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 514 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...3\overline{46}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:389

cgccttagag aaagtgtcca ccaaaaaagt ctctaatacg aataggctat cgactcatco gcgaaccaac aaaaacaaga tatgttgcag ggctatggaa ggctataatc tgcgtcttci	gaaaaattgc	ataacaatcg gtttgcaaag ctcanagaac	caagctccga cgaacaaagt gggaatcgac	ggctgtccta	60 120 180 240 300 346
--	------------	--	--	------------	---------------------------------------

- (2) INFORMATION FOR SEQ ID NO:390
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...4\overline{7}4$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

tgatgtccgt gatgatgtgcgagattgtt tgtttccataacggcgtgtc ataatgagcattcagtacgt tcctttagacttgctcatctt tattgcaaattcaaaaagta taacccttgggccgagaatt cggtttggagttcggacggt gcaccctat	atttgctcgt tctgttttag gtcatcattt tttcaggaaa	tgcctgcgac cacctttgtg tgtcgacatt ttcatcatgc	attcggcttc ctccaaaaga tttaccatat ggctaaagat ggtgtccttt	atttgacac atttgccgtt cgagaaatga ctgtcgtgga	60 120 180 240 300 360 420 474
---	--	--	--	---	---

- (2) INFORMATION FOR SEQ ID NO:391
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 514 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO

			antatagata	traaatceca	ttctgcgtaa	1080
caggtcaagg	tcgcaacgaa	gtatgtttgg	gatetegete		caaccactac	1140
		+ccorcadaa	PALEGECCEC	CECCAC	0 9	1200
tatgccatcc	agaacacgcg		+ 0 2 2 0 C C 0 3	toggggcgtt	cggcttgtcc	1260
tcctgtacta	aaaaaacagg	acaacaactg	Lgaaageega	2200000	cggcttgtcc atgcatccgc	1320
		or oadcavac	aaagaacaca	A	~ ~	1380
		OFFOCTATIO	Cagaalacaa	Euco Barrer		
aacaccgact	CLECCOOD	+	aaattootaa	ctgtgacggg	aaccaagccg caccttcgtc	1440
taactaaaaa	ccaaaatggc	Laaagaaaaa	addiccoods	totocastta	caccttcgtc	1500
		ttcagcgaav	PECTECTACE	Cu CC C B	_	1560
		COSTEDUUCL	PULECUERCO	Ecanama.		
tacaatggci	gaguargaga	00000000	CCGGTGCAGC	cggtgcagtt	cacggctgtt	1620
acggtaaggt	ccaggagatg	Caaagugaag	CCESCESCES	agentatant	cacggctgtt catgattccg	1680
осарораеда	gcactaacca	caacctttac	ggcatcacag	ggcctatget	catgattccg	1709
600666-60	aattgcggga	pagttgcta				1/07
aatatgtata	aacc8c888-	80				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...463
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:393

gaaataacat ttccaaatgg agaactgatt aaggacaaaa agatccggag gaagattata	60
agatgaaatt caagaatcta atttatactg ttccagaaac agaaagcacc tatcttacca	120
agatgaaatt Caagaatta attacagat gaggetatge aaagatgagg atcatgattt	180
agatgaaatt tagatacaa aaaagaagat gagcctatgc aaagatgagg atcatgattt	240
gtgcgaagat gatacgacga acatcgaaag cggatacacg gtggcgtaca ccacagaggc	300
+ tanget gact atteacatag tegagageta tegaces	360
	420
castagogta praagcator taatcaaaaa googoocoga cocaaagoag abbasis	463
tggataatgg tatcaaagaa atggctcact ggccaatcca gtc	403

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 632 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...632
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:394

gcattacccc	ctttcagaaa	aaagtactcg	ctcggataga	taaccgacca	tcgaaataac	60
ctccgacatt	caattgatag	aacagtgacg	atgccggtaa	aagacaagcc	gctgctgtat	120
	aggtggtgga					180
taagagagag	aaaggacgga	gcacgtatgc	cctcaccctc	acgaatgaga	aatccatccg	240
ccgtaaacgg	taataaggac	gcggattgaa	tgtcatctta	gctcgtactt	ccagaatcgg	300
tgatgaggaa	ctatgcgagg	aagatcggga	tcggcattgc	tgaattcaga	atatcggtaa	360
tactgccacc	gaagagactc	cacgtctctc	cagcggcaaa	ggattgcgct	cggccagcat	420
cacgcttgtc	tccacattga	gttgggcaat	aggtcgatac	tattggtcag	acggacaaat	480
ttatcatcgt	gcgagttgtc	gggccttgtc	cgttgagcag	ctccatcatc	agatcggtcg	540
ttggtctatt	ctttcgcgcg	tgctgtacaa	atcgaaagag	cgatgtccgc	ggataattgc	600
aaaagccctc	tttgcggagg	agaatagtac	ag			632

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 784 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...784
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:395

tgcgaatatg	aacaaagaaa	tcacttttga	taagctaccc	gaagcggtac	gtatctgacc	60
gaacaggtct	ccgccattaa	agaaatggta	tcagcattca	ccctcctgtg	cctgaagaaa	120
aatctctcat	aggcatagac	gaagcgtcgt	aattattcag	aaagctaaac	ctaccatcta	180
tgctttggta	cgcaaggaat	tgtccctgca	tataagcgtg	gcaagaaact	ctacttctac	240
	actacaatgg					300
tgaggagcaa	ctggccatga	tgcgtcaaga	ggtgcgtcgt	aaacgaaatc	tatcaagtaa	360
cgatgggcca	tggaagaaga	agctatcgtt	ccgaagtcct	tcttgacaaa	gcaatagagt	420
tgggcttgtc	gttcacgggt	tgacctttcc	tatcagcata	tttccctctg	agatacgaaa	480
catcattgca	aggtacatga	gtgccaaggt	tttcccatcg	attacatcgc	ctctgccatc	540
ttgtggcaat	tgctgtgggg	ataggaaata	ctcatcttgc	cgaactcaac	gcggctggca	600
ggaaagtacg	atgctctatg	tcgcattggt	cggacgtcag	ggacaaataa	gagtcatccg	660
ctaagctttg	cgatgaagcc	ttttctgatt	ttgactatca	ggaaaacaaa	ctatacgaac	720
gctcctatgc	cgaattgaca	acatcatgcg	tatgaatcgt	aaggagcgaa	tagagggagg	780
cttc						784

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 984 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...984
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:396

tggaaaacgg	gattctatcg	catcgccgta	ggagccggag	tgcctattcg	ctcgctgtga	60
tcgactatag	ctataaagaa	atgagcgtat	tcgagctgtc	acccctacgg	gcaatgaaga	120
agcggatatt	gcctacatca	gaagtcgtac	agggcatcac	aggcacggca	ccccgaaac	180
tttgcagaat	cagaaaatga	tcaaacacga	gagctctcag	ccattgagag	ttgctgtagc	240
tcaatccgga	tagactggga	ggataagcac	gccaatctac	gccgaatgga	gcgttggccg	300
aagaaacagc	cggtatggcg	gatgtcctct	tctttcccga	aatatgacta	cgggcttttc	360
gatgaacgta	caagctctgg	cggagccttt	cgagagggcg	aaactatcat	gaagcctgaa	420
gagagtgact	gctcgtcatg	gttggctctg	tcggctacga	tggccgtacg	ggagaacggg	480
aaattctata	tcgtgcctat	ttcgtgacac	cggaaggaga	ggtcttccat	caggacaagg	540
gcacctcttc	cgtgtagggg	gagagcatga	ggtgatgact	ccggcacaga	acgccggatc	600
ttcaactatc	gcggttggaa	gatcttcatc	attccctcta	tgatctgcgt	tttcccgtct	660
ggtgtaccaa	tacggatctg	gaatacatct	gctcgtctgc	atggccaact	ggcctgagcc	720
gcgtcgcgcc	gtctgcaaac	gctactccaa	gctcgtgcca	tggagaacta	tgcctatgtg	780
tgcgcatcaa	tcgggtgggg	gaggacggta	tcggtctgcg	ctatacgggc	gatcggctat	840
cctttcgcct	cggggcgagt	atcttgccac	ttgtgcccga	agagaggaaa	aggtggctgt	900
accatacgct	cgataagggg	gcgatgcaac	gtttcgcgac	aagtccctgc	gtggatggat	960
atggactctt	cgtcatcaac	atga				984

- (2) INFORMATION FOR SEQ ID NO:397
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...600
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397 "

ggaagcagtt		0000001230	aactotooaa	atgatgaaat	ccgctttgac	60
ggaagcagtt	ggaggacacg	Cagggacaag	tattatata	+tatcatatt	attgaaaaag	120
aagcggcttg	atgagaacac	gatgaaggtg	Latiglatga	+00000000	castograft	180
tactcatcaa	ttcatcagaa	atttcatact	ccgacticgg	LEEBaaaCEE	capegggace	240
202000000	acggaaaggC	agaacacgct	gatataagca	gtagaaaagg	Lagicalge	
nagectacat	tototatite	caagtatgca	gggggttcag	acacicgggc	gcagccaagc	300
atacettess	agaaacaagt	ccaatcggca	gcaccgatgg	agagccgtgg	ggacttcaga	360
atgecteegg	agazzatage	toooocaaat	gccacgtggt	aagcacggta	cggatatttt	420
atacaaggga	aagaagcagc	ccattaggg	attttnctca	cecttcactc	cgtgtccgnt	480
caaaagagaa	aataccgtag		accettaga	cacccctocc	pageetgttg	540
gaaaatctcc	aataagccaa	cggggttgca	CCCCCCgga	tateceegee	gagcctgttg	
catgaaggaa	cgggcaagct	gaaacaagtt	tcattttccc	tettategia	aaatcaggaa	
600						

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 556 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...556
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398

gggaacaagc gagttctca	t cacgggagca	acgggcttca	tcggcggctt	ctggtcgatg	60
aagccctgcg ccgtcaata	t caactataaa	caactataat	ccccacagcg	atcgctcacg	120
aagccctgcg ccgccaaca	L gaagugugug		acaacccatc	coatattoct	180
cctgacagac agccggato	c gatttgtgag	atcgactact	gcgacccgcc	chacacago	240
cgcttggctg ataagaagc	t cccgaaggtg	aatncgcatg	gcacttggtt	atecacaacg	_ : :
ccggttaacc aaagctcgt	g acacctcgct	tttnagagag	atcaatgcag	agcaaccaag	300
cgttttctga taggattac	9 20000000330	cactorroro	aacctttgtc	ctgatgagca	360
cgttttctga taggattac	a aggggcgaag	caccacca	attentent	cttccgtacc	420
gtatgggtag ctatggago	t cctnccgacg	acgccaacca	CLLCCCCC	CCCCgcacc	480
caaacctacg actgcctat	g ggagagcaag	ttgctggcgg	agcaatatgt	gcaaaccttt	
gtnacaatac ctataccat	a atacaaccca	caggagteta	tggacctcat	gaccaagaca	540
	.u ucucuucoou			-	556
tctgatggca atccgc					

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1078 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1078
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:399

```
cggccttcgg gaatcgcctt actcattccc cggtaaaacg ctccgcctga agaggatgac
                                                                       60
                                                                       120
cggccggtaa agtggcagtc gtatcctgcg caagggcttc gctccgatag tcgtaagcag
gacagoogat aaagtocatt ttttcatato gtogatagat tgattgtttt actttgtotg
                                                                       180
tactaaaaag agtcggaccc gcctttgagc gtcactttta cggtgcggag tttcttttgc
                                                                       240
aggagtgact cgctccctgc atcaccccgc gggccgcttc ggaaaggatc tggttttggc
                                                                       300
ggaggaagca aaggtgaacg aagtcccgac cgttcctccc atatggctcc cacttctttc
                                                                       360
agcgcggaga cctcttccga tccgggaata aaactccttc ctgtccgtcc gtatcgaagg
                                                                       420
cggagagctg aacggaaacg accgtccgcc atactcgata ctcgtgatat gaagcttcat
                                                                       480
ccggttgccg cgattcgggc ctgtgccatc agtcgggtat gacggggaat ggaaaggtct
                                                                       540
gcaggcgagc ggactccagc agacggagtt gtacgaagtc tccatgctca gggtggttgt
                                                                       600
                                                                       660
cctgtccacg accacccgca acgtattacg ggtgacgacg atgccggcac gtcggcagac
cggaaaccga agtttcgctc cttatgccgt actcggcgat aaaagccgaa tcgctcatgg
                                                                       720
gctgatccag agacgaacga ttgctttctt ctccggaaga agctccacag cgggtaaagc
                                                                       780
                                                                       840
cgccgttctg ctgtcaccgc tgtcttgggt gcgggagcat cggccgggcg ttctgactcc
                                                                       900
gggtgtatgc atcccgggaa tttgcatcac cggaggccgg gagtatttgg ctgccatccg
gtaagatttt togagoagtt ogagatgato gtotoctoot otttttooto ottgagagtt
                                                                       960
gcgagttcgg agcgtatcat tccagctctt ccgcagggct tctttctcat agtcgtatgc
                                                                      1020
                                                                      1078
ccggtggctg tagaatgaat gtaccatctg cgacgtttct tcataccggc ttaccgac
```

- (2) INFORMATION FOR SEQ ID NO:400
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 404 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...404
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:400

ccttcagcag	caaatcgaag	ttcggagcag	agaaaagcac	cttgccggca	tcgcatcgtc	60
aaagttttcc	aatgccgact	ttacatccgc	ttcggaatgt	tgatcccctc	tttgactttg	120
aagatetgaa	topppaagat	gggtactcac	catgccccaa	accttcctcc	gtggcacgta	180
acaactcctc	catcacattc	gaccttcggg	cgaagtatca	gtgccgtaat	tgatggaact	240
gaataaacct	gattgcctcc	accacactoc	atcgtattca	agttgtggat	gaagcttcca	300
tagastanta	catateetta	cacatette	ggaaaactgt	OPCAPAPCPA	tctccacctc	360
Laguetgatg	cgcacccca	cgcgccccc	tcgtccctca	tata		404
tgtactcgaa	aaagggaaag	acguiguaca	ccgccccca	cucu		

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- (2) INFORMATION FOR SEQ ID NO:401
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...427
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

cggatnaagc cgccgattag gattaacgcc gaagactgca aagcaaaatc gaattaacgg	60
ctcccggctg ccaacccatt tccgggacag gccactgttt tctgtttgct gcttttttcc	120
gtactttgaa ctgtattttg gaacaaaaat attccgttgg catncaacta aagaattttc	180
atcataaata tcccgtctct tccacctgat tttgatgact ttggcttcag ggcttatcct	240
catggtatct tgttcggact ggatatttac acgagacacg acagctctat cgtgtgccgg	300
agttgcgtgg caaagacttg aaggangcag ancgtttgct gtcaaccata atcttcgcta	360
caaacttgtc gattccgttt atgacaaatc ctggctccgg gtgtcntant nnaaatggtt	420
ccncaga	427

- (2) INFORMATION FOR SEQ ID NO:402
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 451 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...451
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:402

gacaacaatc	cgtacgaaga	gagattcgaa	gttgatgtag	atggagccag	ctcaccgtat	60
				gaaagctata		120
ctttagcggt	aagttcactg	tgatgtagga	ttcgatatgg	atggcaaaat	ccacgacttc	180
tecetectea	gccacacgaa	acacccggtc	tgggagccaa	gatgcaagag	tggttccgaa	240
				gtacagatga		300
				cagcgcgacg		360

cgagcctttt tggatgcaat ggatcgtgcc taagaggttt caaagccgct caaggcagtg cccggacagg ctcaggagtc ttcgaggcag c	420 451
(2) INFORMATION FOR SEQ ID NO:403	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 458 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS</pre>	
<pre>(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1458</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403	
taaaaggact cttaagggac gactaaatat gcttttcaat acgcccatgt ctttctat tgtttcccaa gaatgaagct tatatttccc tgaaaacgat cttggacatc ttcaaacaaa tacttctgat tagctttgag gctaagatat agtcggcctc tgattgaata atcacttcag caatagctgt ttgtatccca ttgcatcaat actaacaact gatccactta aatcaagact accgtactt cgggaatagc ttgtaattca ttgtgtttgt ctgtaactgt ctctgacaag acttaagctc acttgatcaa tccatgccga gagtatatat gtaacccagt cttctttggg agctacgcaa acgcttgcca tctatggcaa tagtttaccc tctaaaatcgc taatcaagtc tttccataa acactgagac agcgtaaaga gcaatgan	60 120 180 240 300 360 420 458
(2) INFORMATION FOR SEQ ID NO:404	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 650 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404

agagtttatc atcaacctgc aaacctgaca ctctccatta tcctttgcgc aataatgaga
tagccattct tgccactacc gaaatatcat ttgagaaaca catatcgcct gacaaaact

(A) NAME/KEY: misc_feature
(B) LOCATION 1...650

(ix) FEATURE:

60 120

atccatatto	ccapttgatt	ctcaatatat	agctctcagt	gtccgagagc	atttgtagaa	180
gttccttttt	cottatattt	atctctattt	atcttcattc	gtatcggata	atatttgctc	240
stanstone	accetaatet	caaacatata	atacattcag	aaaactttgt	gtttacttac	300
acaaaccaac	actettaaca	aggaggttta	tatctccttg	tgaagacagt	tatattattt	360
adactadatt	ggtttgata	ttoccantat	ttatacacat	tctctaaaca	ttgacgaaca	420
ctttgtattt	attatatta	coctttaact	ctgagaagag	caectettea	aaaccttgaa	480
aaattgaggt	teteatgega	gagittaact	tatattaata	aatatatttt	ttatctcaac	540
taatctcatt	cttaaagggc	Catttttgaa	tatattaatg	accatacttt	acacatorca	600
tctttttgat	tagtatcaag	ttgtgtttgt	acaattatat	ctactaatct	acacatggca	650
tagcagaaac	catactggat	attttctaag	caattagata	ataattatct		030

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 908 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...908
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:405

```
tgctcaacaa agcagccaaa gctcgtatcg accagtatac caaaactgcg gtatcggtta
                                                                        60
                                                                       120
cgaattgcta tataccgage taaccattta tttctcagtg gacgtgtctg ctcattcaac
                                                                       180
gacaagcaag tgcatagcgt actggaggtt caggcgtcaa acgcaagtct tttgcaggag
                                                                       240
ctaccgagtg gtattctgcg acttagcaac cgtcaagcgt gccatctcag ccatcaagga
                                                                       300
gggcaggata gcttgggggc aagcgaagtg acgctatctg acaaccccat tatttgcgtc
                                                                       360
ctgagcagaa agaagccatc gagcgcacgc tcaagcagtt ccgaaaggaa ataagatgct
                                                                       420
gtggaatgcc aagatgcgtt ttggcaaaac gcctgtgccc tgcgtgttgc caaagagatg
                                                                       480
gaagctgtgc gtacgattat ctcacgcatc gcccggtggt agatgccagc tggtttgagg
actttggtaa accttctacg accgtcctga gtggcactat ggctcccgta gcaaaggtgg
                                                                       540
                                                                       600
agcttcgctt ctctcgaaaa gcttgcttcc caagggaaaa agtgtgtcat tttgcctcta
                                                                       660
tgcaagatat gcgtggttcg aaggacgtag gaggtaattt gacaaaaaca acgaagtctt
                                                                       720
ctctacttca tgggatttag tgattgggac gaggcacacg aagggacaca gaccgagctg
gggaaaagcc gtattggtca gttgatgggt aaggatacaa aggcatttac atctatcggg
                                                                       780
                                                                       840
aacacttata acctcttcga tcagcacaaa gaggaggaaa gtctttacgt gggctatgtc
                                                                       900
atgggaacaa caagccaaaa tcgattgggg aantcaatca tctggcgaca cttacccct
                                                                       908
atgcctta
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{3}23$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:406

```
cggtgccggt atcggttgga cgatggcaca agcgtgtcaa gatgatacaa tgcctcagat
                                                                        60
ggtgcccttg cttaacggtg tcggaggggc tgcntccgtc tcgtggggat tttgtctctc
                                                                       120
gcagctatag gaatcaatcc gaataataca cggctgccga ctatccgatc ttttcgcaag
ctaccggtat gctggcctga ctgtcggtat gattaccctc ataggtagcc ttatcgccgc
                                                                       180
cggtagctac acaaactact gcctcagaga ccggtgatat ggcctaacca ctcgtgttta
                                                                       240
                                                                       300
cototttgct actgatcotg accgtgggat togtggtgct cggtctgttt ctatcgaagg
gtttcccctc ttctgggcta tcatcggagg acgtttttct cctctctt cggtttgttc
                                                                       360
                                                                       420
ttctctatcc gtgtcggtgg acggatatgc ctattaccat ttcgctactg aactccctta
                                                                       480
gcggtgtggc ggagccattg ccggtatggc tgtgggcgat attctactcg tagccgtaga
ggtattgtcg gtgccagtgg tctgttgctg acgcagatta tgtgccgccc atgaaccgca
                                                                       540
                                                                       600
agctcatgtc cattctgatg gcttcgggag caaaagcaca cctgccgcta caacgccgac
                                                                       660
tactgettea aaacaagaaa aaggagggtt geegeteetg eteetgeeaa ageagagaag
                                                                       720
acagceggta gegtatgege gatgecaage gagteateat egtaceeggt taeggtatgg
cattgeteag geacageace aagtaagaca getggeegat aaacttaegg etaeggtaeg
                                                                       780
                                                                       840
gaagtteget atgecateea teeggtggeg ggtegtatge eegacacatg aacgtgette
                                                                       900
tgtgcgaagc cgatgtgccc tatgaccaac tttcgagatg gatgccatca acggagactt
                                                                       960
cgctcagacg gatgccgtgg agtaatcggt gccaacgacg taatgaaccc tgctgctcgc
                                                                      1020
aatgctgagg tacgcctata tacggtatgc ccgtgctgaa cgtggacgat gctcccgagt
aatcatttgc aacttcgacc tgaaacccgg ttacgcaggt gtggacatcc gctctataca
                                                                      1080
cgagcaacgg gtgtattcct caaactcgga gatgccagga atctctggca gagatcatga
                                                                      1140
aggaaatgga tgccacaggc gatacgcagc tactgctgct cctgccaaag cagagaagac
                                                                      1200
agccggtagc gtacgcgcga tgccaagcga gtcatcatcg tacccggtta cggtatggca
                                                                      1260
                                                                      1320
ttg
                                                                      1323
```

- (2) INFORMATION FOR SEQ ID NO:407
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 529 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...5\overline{29}$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:407

ggactgagtg	ccatcatctt	tgttggcctc	attgatgacc	ttcggaaatt	ggtcggcaaa ttggttcca tgggcgaacg gaaactcttt tgatgatcca	120 180 240 300 360
tcttctctgt	ggtagccatt	gcttgcgggc	tttgcgagaa	gggcgactcc	ggaactggaa	420
2++00000000	offictttcta	catggtattc	cgtgggtaca tgatctatga	acciccicge	agccaagaaa	480 529

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...427
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:408

	cascccaata	gagaggtaac	ctgcgtaatt	ctatttctag	gttctacaaa	60
tgaggaaaaa	cgacccaacg	tattaggggg	ususccssso.	tocapataat	agctttgaag	120
ttgcccgtag	ccgacattgg	CCCggcccc	gagaccaatg	tttcaggata	agctttgaag	180
agctttgtcc	taaagtctac	cgttagttct	Ciccaigate	tteesettt	aagcgaaact	240
gataggttac	acctggtcaa	ccctcaaaaa	acgtacagga	ttagggtttt	gcagaggatt	300
accetataca	tostataoto	ctctccaaag	agagtgttat	Ctactcttat	aggatggtat	360
ccaccaaat	genetateta	taaatggaat	attcttttcc	tacaatacti	CCCaacaac	• • •
ttottoacat	gtaactccat	tentgagete	atatctgcaa	gggaagtccc	acttcttcga	420
	gcaacccca	-80-8				427
tggcaga						

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 992 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409

```
ggatgccatc gacgaaagta ttatcggtag cggtatcatt cgatacgaat aagcgcacgc
                                                                    60
ttcatttatc cctcgccgtt ggatggagtg gaatcttaaa ggatacggac aagacttctg
                                                                   120
ccgaccttgc cataggagac attcagacaa gctgaagccg gacgtaacac ctctccccgg
                                                                   180
aggaggagta tcattagctg gaaagttcct ttcttaagcc agttggtttc ccgattcgga
                                                                   240
300
aaacccccaa tcctcccgtt ggcgtagtca ttgcagacaa gttatggccg gtacatatcc
                                                                   360
cgaaaaggct gctatcgctg ccgtttatgt aagccatccg ctccggactc tactttccac
                                                                   420
ctcttctcaa gagcaacaca acagaagatt gcagaaggtg acaactccct ccgattggca
                                                                   480
ggccggaaca ggttgaggat caatttggat aagccgttcc cggtgaataa tgaccatatc
                                                                   540
tttttgccgg tatcagaatg cctaataagt acaagctcaa tcgtgctacc gttatgtaag
                                                                   600
aaatccggat aaccttttct ccattaccgg taagaagttt catataacaa cggagtctct
                                                                   660
ttcgaaggct acggaatacc ctcgctttgg gctatatggc tatcaaatat ctggtggtaa
                                                                   720
ataccgatgc tccgagatcg atatgtcgct tgtacaggag ccttatgcta agggaacgaa
                                                                   780
tgtgctccat tccccgaatt ggtcggcata tatgtctata agaacggaac attatcggca
                                                                   840
cacaggatcc atccgtcaca acttattcgg tttcagacng aaagagagcg atgaatacga
                                                                   900
aataaaactg ggtatataag gggatccggg ctttcgaatg ggcgttgctc aagattgaga
                                                                   960
ataacaatgc tgtccgttgc tatccgtctg tt
                                                                   992
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2585
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

```
agtgtaaaat gaaaggataa aggggataaa gggcctgctt attgcgaaag tcttcatacg
                                                                        60
acaaaagcaa atcctgaaga tcgatctgcg gcgaatggga aggaagagga agggaggggc
                                                                       120
ttatttgggc tgttgcccca ttgccttcga agttgtaggg gtgtattgcc gagcatcttg
                                                                       180
cgacagaaag cacagagtag ctgacagagg agaagagatt cttttccgct attgccttga
                                                                       240
gagacgagac ggatcggcca agtctgtgta gacatgcttg gccctttctt catgatccat
                                                                       300
ttgagtggcg gacaactgaa ttcctgattg aagtgacgtt tgaagaactg agcgacagat
                                                                       360
tcattttggc tgcaagctct tctgccgatc ggactccaaa tggtgtcgga atacgaaagc
                                                                       420
acgaaagccc ttgttctgac atggaatgag gagagaaagt tgtctaaaag cggcttttcg
                                                                       480
tagcgtgagc gaagatgcag aagagttcgc gcagtttcag ctcgaatatc tcggacgaat
                                                                       540
gggcatttct gacaaatatc ccatcacaga gtggagccag gagttcacat tgtctctcgt
                                                                       600
tgcaaggagg agatgtgaac gatttcggtt cgtctccgca ttctttctta ttgcccgaag
                                                                       660
agggacaaat gccgaggcat aaatgggcgt gggatggaaa taaaagcaaa tgagcgtagc
                                                                       720
cgggcctttt tcagcctaag tcttatacga agattggcag ccaaaaggac aacattatct
                                                                       780
cccgcaattg cgaattaccg gattccggcc cgacaaatac ggccggctct ccttgagcag
                                                                       840
gaagagcaaa gcatggctgt ctttggtcca gatttccaaa tcgctccttg tcctaccgtg
                                                                       900
tggagttcgg gcaatccgga cagagcagtg gcggtcggct gttgttcagg atgccattcg
                                                                       960
```

```
gattttcttt gggagagaca gctgacagat atgaatactc ataaggagga tggtcgggcg
                                                                      1020
ttatctttgc aaagcgagct attatgtgac gagctgcctt gtccgaggta ttgtccgtcc
                                                                      1080
gatgettttg eggatggagt egtateegga caactgtget tgtegettge ggaegaagea
                                                                      1140
tcaaggagcg gagacaaact tgcggccaac cttttcccgt gaacaaggct ccgaaaagtt
                                                                      1200
cgggcactac agccctgccg gcaataggtt ggtcagcgaa ataaaaggcg taccaaagca
                                                                      1260
atacttgaaa atcaattggt cagtcgacct cctcgaatat agtagcatac gacctgtggc
                                                                      1320
gtacgatcag tgcggtttcg agcgtagccg ttcctgaagt tacgagggct gcttgctctc
                                                                      1380
teggagtatt teatacgtge gteegaatae aaegggaatg egtegteggg caaaaatgga
                                                                      1440
gtatagteet gtategteag teegggtgea eggetatgae agggeggtag teegggaatt
                                                                      1500
getteateae aegeageata eaggeaaatt eteetteaet tegageaage gaetteeaca
                                                                      1560
gagaagggta cttgacgaga atctttggct gaccgctctt gctcttcgat cgtaggcgca
                                                                      1620
tgtgttgctt gacggcatca tagcacggat tgcctacata gatgacggaa aatcgtgtcc
                                                                      1680
ggcaaaaaaa totttotoga aaggcaagat gcagacatga gatcgacgta tttottcaac
                                                                      1740
gtcttgattc gccaggattt ccatcccaga ccttaggaga gatataatag actatcggct
                                                                      1800
tgccaagctc ttccgtacaa acggaagtac gtagcgcata ttgaagcccg ggtagtccac
                                                                      1860
tggatgacaa cgtcggggtt aaatgctcgc atctgctcct gcacatgttc gccgcgcggc
                                                                      1920
ggatgacacc gaggtgcgtg agtaccggaa tgaagcccat aaggctactt ccctgtaatg
                                                                      1980
                                                                      2040
aaagateggt egeteteegg tageetegge aagaaateee eecceatgaa tgeaaacaeg
gcttccgggt catgctcttc aaggcacgaa ccagattgga tgcatgcagg tcgcccgagg
                                                                      2100
cttcgccgct acgatgaaat agcgcatacg caataaagaa aatcagggaa aggggaagga
                                                                      2160
                                                                       2220
gatcagacgo tootottgag aagttootoo aagacaggta gataagtoto gaagtoatat
tcagtttgat gggagatagt gtaacgtagc ccgctgcatc agttccaaat caccctctat
                                                                       2280
ggtgccttta ttgatctgac gtctgtcatc caatacacag cattgccccg tgcatcttcg
                                                                       2340
gaagccatgt atcgtcgaca aaacgaccgt ccgtaacggc gcaaggcttt agccccaaag
                                                                       2400
gtttcccttc ggaacattca tgcttagcat cgtgtcctga ggcaagccat cttcaggatc
                                                                       2460
atacgactga catgcacggc ataggccgtg gcatgactct atcgcaaatc tcgctatggt
                                                                       2520
cgtccagcga aacggccaga gccggcactc acacacacat ccttccatcg cagcacccac
                                                                       2580
                                                                       2585
cgtgc
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 440 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...440
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:411

acacgaacta ccgg cgaagaatgg aaag gacagacaga tggg gattctcaca caaa ccggatcttt tcaa	gctcaa aaaaaaacctg caagag ttcgtccaac aactgt accgccgatc cgactc ctcgaaatgc actatc gggaatggat acaaaa ggtattcccc cttttc ggcaggatca	ttggcacgag gtattctggg agaaacagga tgccaagccg ctactcgaca	atgagtggta agatagaact agccaaccgt gatacacgtt atgcgaaaag	ggaacaagcc ctctttgccc cgacatgagc gtattcttca	60 120 180 240 300 360 420
tccttcatag acaa		gtggagagcg	LEGARACCEAC	gereage848	440

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1872 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1872
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:412

```
ggtgaagatg tagtcaataa gaacttcgcc gcagtggatc gaggtggcgt gtggtagaga
                                                                         60
 taacggtgaa acccgaatgg gctgacctgc ccgacgatcc gtggtacgcc acgagggaga
                                                                        120
cacggacttt gtccacaacg tggtacgccg atcaacgcac aagccggaga cgacctcccc
                                                                        180
gtatccgctt tcctcgacgc gaagacggta catgggattc aggaacggcc gcttccgaaa
                                                                        240
aacgcgtgtg gcagctttcg ttcctgtatg ggaagctgac aactgtgtac agtgaaccag
                                                                        300
tgtgcctacg tttgtcctca cgctacgatt cgtccgttcg tcccaccaag gaagaagagg
                                                                        360
agaaaaccgg cgtcaaggtg ctcaaggctg tcgaaaacag ttcccagaca tgggcttccg
                                                                        420
cattcaggtg aacgtaatgg atgtctcggc tgtagcaact gtgtggatgt atgtccgggc
                                                                        480
aataagaatg caaggctctg accatgcagc ctatcgagga gcagtacgaa gaaccaaaaa
                                                                       540
actgggataa gatgatctcc ggtgtgaccg gcaaggctca cttggtggca tcgcagccaa
                                                                       600
tgtgaagaac tcgcagtttg cgacgccgct ctttgagtct cgggtgcatg ttccggttgc
                                                                       660
ggtgagactc cctatgtgaa gctgataccc agctctatgg agaccgccag acagtggcca
                                                                       720
acgctacagg ttgttttcca tctactctgc ttcggctcct tctacacctt acacgaagaa
                                                                       780
cgaggcggcg aaggcccggc atgggccaat tcattgttcg aggacaatgc agattcggtc
                                                                       840
toggtatgca ottggcatat aagaagatgo gtogoogoot tggaatottg cagaagaago
                                                                       900
tcagcagtct ccctgctgtt cggacgagct gaagctctct tgagagaatg ggtagaaaag
                                                                       960
cgtcaggatg ctgtcgccag aaagttcttg ccgataagat caaacctctt gtcgctgcct
                                                                      1020
gcgattgtgc atctgcaaga gaatcggccg tgtcgattcg ttcttcatca agcgtgcaag
                                                                      1080
tggatcatag gtggagacgg ttgggcatac gatatcggtt tcggtggttg gaccatgtga
                                                                      1140
ttgcatccgg tatgaatgtg aatatcctcg ttctcgtaca gaggtttatt ccaatacgga
                                                                      1200
ggacagtcgt ccaagagtac tccgacggag ctatagccaa gtttgccgca gccggtaagc
                                                                      1260
gtatcaggaa gaaaacctcg gtatgattgc ttgctacgta tggctatgtc tatgtggcac
                                                                      1320
aagatctatc ggagccaatc cggcacagac gctcaaagct atccgcgaag cgaagcctac
                                                                      1380
gacgggcctt ctatcgttat cgcctactcg ccctgtatct ccacggtatc aagagcggta
                                                                      1440
tgggcaagac tcaggccgaa ggcaagagag cgttgagtgt ggctactggc acctctggcg
                                                                      1500
ctacaatccc gaactggaga agagggtaag aatccgttcc agatggatag caaagagccg
                                                                      1560
aactggagga attcaagaac ttcctcaaag gcgaagtccg ctatgcatcg ctgtacagga
                                                                      1620
atteccegag gatgeegage aactettega egetgegtte gaaaateeca atggegetat
                                                                      1680
cgtaactaca tgcgtatgag tgcggcagac tggtcttgcc tcttggtatt caggacatca
                                                                      1740
aggaagaaaa agactgcgat cactagcgta tctacgccct tataacaaaa tcgaggctgt
                                                                      1800
gcagctaagg atttattctt agtggcacag cctcgattgt ttctattcct acccgtattc
                                                                      1860
gtcctgctca aa
                                                                      1872
```

(2) INFORMATION FOR SEQ ID NO:413

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...342
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:413

ggtcttgctg gt cctcccggag aa atcactttta ta tattacattg gc ttatttgtag gc	igtgctctt iatggttac caaagtata ctacctaac	tttcggtatt atcattagac gccagccatg catatggcta	caaatggctt catctccaca aatggatatg	tggctaaaca ataccgatta actttcaaga	aatgtgttac ataagtaaaa	60 120 180 240 300 342
tgaactaaat aa	agctgacag	tcaaaaaagt	taattcagct	tt		342

- (2) INFORMATION FOR SEQ ID NO:414
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{3}00$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:414

cctgatcgaa	accggtacta	tgccgagtgt	tccattgacc	catcgacgat	ctttgtcgtt	780
ggagcgaata	tcacctgagc	atcctgcttc	agtgtaagtt	cctcctctgt	cggaaggatg	840
aggagggaaa	atcgccttcg	atagtgccgt	acagggtgac	gggtcgccct	gcagctgttc	900
caattgccgc	tcattgatgt	aactcacgtg	cggcgtttgg	tggcaagtgt	gatgaccggt	960
tcgtccttcg	gcggctcgta	tggcgattga	cacatttatt	gatgtcctga	agatcctgtt	1020
			tatctgcacg			1080
tacaccttgg	tcagctccac	tgtgacggga	ggggttgctc	gcagtgctcg	gaagagaaaa	1140
			tgtcggatca			1200
			tgcacaccgc			1260
cctctgtata	taccaggagc	ttatcgatgg	cgtcgatgac			1300

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 757 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...757
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:415

```
aggatococg ottgaagota ttgttogtac atgtogttog agtagtoggg catcaagott
                                                                       - 60
aatottggcg ctttgggcgt aaagaccaac tcccaaaagg acgccgcgat cagcaataat
                                                                       120
                                                                       180
aatttcctca tactttaaaa caatttaggt cgtgattcag agaaccacgg ccgggttaaa
aaaacaaaaa aaatcccaaa taagattcat ttcaagaaca atccaagaaa agaaaaggaa
                                                                       240
                                                                       300
tttaaggcaa aatgctacct tctatttcta ttggtacttt tctcaaggag ttttttgcgg
                                                                       360
cgcaatttag agaaaaaatt cgatttaaga agagtatcgg atttaaagaa catgttttca
atataagcga caagggatta accettataa aagetgteaa ttageetttt gecaaaatat
                                                                       420
                                                                       480
tgactgtaat ctgaaggaga aatgaaagag gaaaaggttc atgctccacc tcattaaaag
tcagagtctt taaaagtgtt gtctaacaac acttaaagtt attgtgttgc atgtatttaa
                                                                       540
                                                                       600
accgaaaagt agagcagacc aaggttaagt cagtccagca tgaggaagga gcggagggga
                                                                       660
aaggggaaaa aagatccttg actaaggagt cgggggttga tgtggaagta aagagttctc
                                                                       720
gggctgtaca ttgttcgaaa agacaaacgc cccttactga tatgataggt accattatgc
                                                                       757
tgagagaaaa gagggcacta tatgcgaaag agtaacc
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1324
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:416

				-+	2020002002	60
gactctagag	gatcccacgg	atgacatccg	ctacatgcgg	atcgcgctca	agaggcacga	120
acaactacta	acgaaggaga	gattcctatc	ggagccgtat	CKCCKCaaa	gggcagaccg	180
++acacatac	tracaacaga	gtggaaagct	aaacgacccc	acggerearg	ccgagacgcc	240
+ acceptesed	staarctaga	toccatageg	gggaaatacc	LUCELEALLE	Caceceguac	300
atascatcas	accetecte	atgtgtgctg	gcgcacttcg	Ciggacacaa	acaceceaec	360
+-+	acatecgaac	ccaaagtggg	ctacagguig	LLCCCBacca	cacacacac	420
accasatacc	acotagaagg	cggtatattg	gcgacgaacc	ggagaaccig	argegrager	
totttaccaa	acoocootae	cgagcaacac	attatatate	LLLELECAAL	acggcagcac	480
teagtataca	atattgggct	gcggatctgc	cctgccaacc	acacaccacc	accecteg	540
	acctacacaa	caaactctac	atgatcgatt	gcggagaagc	gcccagcgac	600
22++020202	cgaaaagctc	catttcggac	gtctcatcat	atetteatea	gccacccca	660
+ ~ ~ ~ ~ ~ + C ~ C	+atttraat	ctocccgatt	tatetecaeg	CLUBBLLLBL	1888856161	720
caacacccta	catotcateg	gccggaggga	atagagcgcu	LUCTUABLU	Cacaccagas	780
castctstca	ccgaatgccc	tatcaggtgg	agatacatac	gattgatgtt	cccgacacgo	840
cagicigica	gaggagaaat	ccgtcaaagt	ctatagcata	ccctcagcca	ccgcatccct	900
getegeacat	acctcttcga	agagaaatgc	ctgcaaggca	tctgaacaaa	gcggctgccg	960
geggeggee	tattccgctt	ccgaatatcc	cctcatcata	gaaggatccg	attacacgac	1020
agilitacaa	ggatcatcc	Caacceacac	ctcacgaccc	cgggtacacc	acccagacat	1080
accegatege	etcacece	gagttttgtc	cctccatcgt	ccctattttc	aaggtgtgga	1140
atgettactg	citggacacg	cttttataa	ggaggacggg	caagagccaa	agagactttc	1200
tttgctctac	catgaagtta	ccccacga	660660066	аррарсавав	cgcctcctca	1260
cacagtacag	ccaaagaagc	cgccgaacag	ccaaggtttg	ctopaagaag	cgcctcctca	1320
tcgggcatta	ctccgcagat	acaaggacgu	CLAAKELLE	~~66~~64~6	ctcaaagcgt	1324
atta						

- (2) INFORMATION FOR SEQ ID NO:417
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...588
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:417

		««ссаапасс	aageteggta	acaatgaagg	accggtgctg	60
gaacctcagt	tegaaggaca	gaccaagacc	augeteggea		220220008	120
tcgatatggc	tgtaagcgaa	gcactcgaat	actatctgag	gagcacccga	aagaagccaa	
actgatcgtg	gacaaagtcg	ttttggcgca	actgctcgtc	aggcagcccg	taaggcccgc	100
	-					

gaaatggtgc	agcgcaatcg	cccttgtccg	gtggaggatt	gccgggtaag	cttgccgact	240
gctcgccaaa	gacccggagc	agtgcgaact	cttccttgtc	gagggtgatt	cggcggngga	300
acggccaagc	aggggcgcng	accgcgagtt	tcaggctatc	ctgcactgag	gggaaagatc	360
ctcaatgtgg	agaaagccat	gcaacacaag	gtttcgaaag	cgaagaaatc	cgcaacatat	420
ataccgcttt	gggtgtgacg	acggaacgga	agaggacagc	aaagccctta	acctttccaa	480
acttcgctat	ataaagtggt	gatcatgacc	gatgccgatg	tggacggtag	ccatatcgca	540
cgcttatcct	tacgttcttc	ttcaggaata	tgcgtacgct	tcatacaa		588

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1340
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:418

```
aatgcatcca gatttagcgt aaaaatctca ttettaeeet gtatteatta aeegettett
                                                                        60
aggeteetat agaaatagtt gatettteta agtgettete tagtgtttte geaggtatat
                                                                       120
aaaaaagaat atccatacaa gcacagctgt atcaaaataa tcctcctctt cttttccatc
                                                                       180
tctcagggat atgataaaga gccaaacccc ttggattgtc tcgcaccaaa gttatggagc
                                                                       240
ataaaaagtt ggtgatgaga ttgttcacct cttctcttag tccagcattc tgaagcgtat
                                                                       300
taccccttca actggagtat tgacaaatgt tgctaattgt acctctgcca gttttcttca
                                                                       360
aatattottt tittattitt tattiggiot gggigtoaco aigotitata tiaggitoig
                                                                       420
atttageett gteeteatta gaaagtaaga agteaagggt ageateteaa eetettgeae
                                                                       480
tectaaette ettgtgegag getttttaat ttatetattt etttegggtt aetaeteatg
                                                                       540
gcaagaaata ctgcactttc gcatcagggc ttagcttaaa agagagttgt agttcaaggc
                                                                       600
teettettgt eeggggatga gacaaagete caatttteae eettatteee tttetttte
                                                                       660
tetteeteat acaetetgeg ageeteteat etttattttg aaagtattet ateeecettt
                                                                       720
cgataaagtt ttttttgttg tcgaagcagt tttctttaca aacctcttgc ctatctgtgt
                                                                       780
caagtaaact tgtcgagctt cggtttgacc tcggaggcgc gcagcgttgc cccgcatccc
                                                                       840
tggcctggaa gtggatgatg ggcgtatgct gttccaattc aattccaact tatacatcgt
                                                                       900
ggtctatgct ttttgttttg tattgtcctt aaatagactt ccatgagtcc cttattggtc
                                                                       960
tcaagcaacg attcggagaa ctctgccatt tattcaaatc ctttgttctt tctcgttcta
                                                                      1020
attogaacat gttttgtoto gtaattooto otttttgatt tttaatttgt agotocatta
                                                                      1080
atggctacga caataattgt ggcagtggct actaccacaa aacagagaag attaaagttt
                                                                      1140
ctatttccat gctatttct gtatttgaaa taatgtttat tgggaagtag aggcagatgg
                                                                      1200
caaatactat aagcgtaata atatcccacc caatagcccc catgtcgagg gacaagggtc
                                                                      1260
                                                                      1320
cccgatattg aagagcgagt gatgcatcct ttttcaacaa aagtgttgat gcctaaaaag
ccacaagtaa cgtgataggc
                                                                      1340
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1514 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1514
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

cot nangata	ctcttgagaa	ogattgattt	ggaagaggtt	ggccgaagct	ttccggctat	60
gatagagata	ctgaacggta	ccacatagtt	gatacctctc	gatctgcata	gcgtgatata	120
acceptatet	aatcattaaa	ggeteetega	taataaggtg	acagtcallg	ageteactac	180
geegetatet	atcctcgcat	capacetatt	cgatacatcg	taaacgcgca	aagtcaccga	240
tgtggattat	tcttcagacg	attcagcccc	atcagcatac	cctcgtagaa	ttcccatatc	300
cactettett	gcccgataga	gggagcatca	gtccgacctc	tatgcctccg	actgcgatgt	360
gctgggtatt	gaagccatag	ccotogaatc	gcgccgggga	tgcgtagttt	gtggcctgca	420
cgtaggggag	tagcagatat	accognites	ctttcatcag	ttcctcttcg	ctcaatccat	480
gggaagttgg	atggagtaga	acattteeta	tggccggata	atgtgttcgc	tcggatgaca	540
attititigit	ttttgctatt	gogocooog	egtttggacg	gaatgagcga	gtctgccctt	600
gcggcggaca	ttgtctggcc	gaagggttga	gcgtataata	tcatcctccg	acagaccgta	660
ccttgatttt	agtccataaa	caatctttta	gcttgcacta	cgtgtacttt	tgtcctgcta	720
ttggcgcgcc	agiccacaaa	actacogaca	tcagcacaca	cgtaatcagc	aggatataaa	780
CgCgtCtgaC	cggacccgac	gatctgtcat	potttcccc	tttcttttt	agtctattta	840
gacctttatc	cggaacacac	aacctaccac	taacgactct	gcggcaaatg	gttatcctct	900
ttattaggig	agatggggca	aactacotoo	gttaatgtct	tcgttataaa	tcaagccatt	960
ttgcaatctc	nagacat ggt	gettaaggtt	atcccggatt	ggtcattgga	aaagtaaggc	1020
tcaatatcga	ttaccarage	ttatcoactt	captoggttg	ctattgattt	gggttgtgag	1080
ctaacgacaa	catagacata	ttcgagtccg	tetagatetc	cgtacttctg	cgagctgcag	1140
cattettgeg	cgcgagcacc	accaccasts	agcaattect	tctgaatgcc	cgaagctgca	1200
tattgcaaag	graraged	atococataa	CANADCCEES	aactccgtat	ataaggcgat	1260
atcgaatacc	ctagaaggcg	tttatttcco	tatatacaca	aatttatttc	cgtatatacg	1320
aaatttccgt	acacatatac	ccaaatctco	ctaccttcgt	ggtgcgataa	aaagcaatca	1380
aaaaatattt	ctanactatt	taataaccab	ataattaagt	tattatgatt	aagattaaag	1440
aatcgagata	. gradagigii	ttcggcaaga	cagcaaacgc	ttggtaccct	gcaatcactg	1500
		. cccsscaasa	02602220	. 00 -	•	1514
cattcgatgt	. gaag					

- (2) INFORMATION FOR SEQ ID NO:420
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 822 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...822
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:420

tggccgtatt	tcctttcgtc	tctgtcgaac	tgcacccctg	tctggcggat	cccatccage	60
			cgggcatcct			120
			agcggcatat			180
atcgtccggt	agaaactttg	gccgtcgctt	tcttgaacca	cgtttcgcct	tcgcgatgct	240
tccgcgtgca	tagaccactt	cgtaaccctc	acggtatttc	gcatacagtt	ccggatcaat	300
tccggcggat	cctgcaagtc	gccgtcgatg	atcaccgtag	ccttcccctc	acatggtcta	360
atcctgccga	cacggctatc	tgatgaccga	agtgcgactc	aggttgatgt	agaagaaacg	420
gtcatcaccc	ttgcacaggc	tcgcaatagc	tccatcgaac	catcggcggc	tgccgtcatt	480
gacaaagatc	gttcgtagtc	ctccgttatc	gaagccgccg	ccgcactcaa	ccgccgcaca	540
gctcgggaag	ttccctttct	tcattataga	tcggcacgat	gatggaaact	ccttcgtata	600
agtcgtattg	acatccatta	gaattgacgt	ttagattttt	tcggcacttc	tcaggtgaaa	660
aatgaagtgc	ttaggtgaca	agggtcggac	cgttcctttg	tccgcttcgg	gatggaacca	720
gcggatcgta	ctgtccgtct	gaaccatgtc	atttgcttgc	gggcatatac	gcgactgttg	780
cgttgatccg	ccttacggcc	tctgcccgat	cgatcgagcc	gt		822

- (2) INFORMATION FOR SEQ ID NO:421
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 626 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...626
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:421

ggatccccgg	gaaaaccgct	gtcattgtag	taggagcagg	tccggcaggc	ttttcgcagc	60
actccggctc	atcgagcttg	gtctgaggcc	tattattcgg	agcgaggtaa	gtccgtacac	120
gaaagaagag	cagacatcgc	tcgcattcca	aagaggggca	cgtagacccc	gaatccaatt	180
acggatttgg	cgaaggggtg	ccggagcttt	ttctgacggt	aaattataca	cacgtagtaa	240
gaagccggag	atataaccaa	aatactacgt	attctctgca	aacacggagc	acagcttcta	300
tcctgatcga	tgcgcatcca	catatcggca	ccgatcggct	accaaagtga	tagaaaacat	360
tcggcaccaa	atattggcag	ccggaggaga	agtcacttca	gttgccgaat	ggaaagcctg	420
atcatacata	acggtcaagt	ctgggagcaa	gagacaacaa	ggggcgtgaa	tactgcggtc	480
			cgacatctat			540
			ggtgtccggc			600
	gcgctaccac					626

- (2) INFORMATION FOR SEQ ID NO:422
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1128
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:422

```
gccacatagt tgtgaaaagc ccggacaaag agcaccagcg aaagcacgta accaccattc
                                                                        60
ccgcaagaaa ccatgccgta ccgaacttga acgggacgaa acggaaagca ccaatatggc
                                                                       120
aatttgcagg attgtactga cagaggcttc gccttgtctt tggtcgtgta ccacgaggta
                                                                       180
tecacegege getttetece teacggaaga ttgccatata tataaactgt atcagcacea
                                                                       240
tgccgacgaa ggtatccatg cgttcagcca tccggcttgc aacgtggtga aaaagaaaaa
                                                                       300
tcactcatag tcatcgggaa tgatattgtt tttttaatgt gatagcgata cggcaaaaat
                                                                       360
cagggtatac accagattgt tccatccgcc cgtatcaaca gaagaaacgg ttgcggcagc
                                                                       420
gttttccaaa ggaaattgag cagatggtga tcaacggtgt tgcgaaaact atccaacgag
                                                                       480
gaaaagaagt tgcttttgca gcaccaatac agaaaagagc aaccatccga ttcccattag
                                                                       540
aaaaaagaaa aaccgcccaa ccagccggca taggagagaa aatggtcgtg atttcgggat
                                                                       600
gtccctgcga cgatacgatg ccgaaagccg ggaagaagca tgataagcac ctcctacaat
                                                                       660
tatacttacg gatagggaag caagcaccag caggetgttt ttegtegege tttettaace
                                                                       720
ctgagaaaca aatggagaat ccgatgatgt acagaaccgc cgccaacggg cctattatcc
                                                                       780
ctccgcaatg agacgctcca agggcactgt gcccatagaa agcagcagat cttttcccga
                                                                       840
tegggaatgg gttgtgtcgt aaaatacage aacatgtege egtatacate ageaggetae
                                                                       900
ctgccactcc cacataccct gtcaatctga gttcttatcc ataccttttt cttattattt
                                                                       960
gagttcgcaa aaatatacaa tagaatatcg tttgcaatcg ccaatagtgg ctattttcac
                                                                      1020
agcccggaac cctatttctt agggtttgtc gattcgtcaa tcagtaactc atatcctcaa
                                                                      1080
attcaacctt taataatctg tttggcattg gctctctgcc ggattgca
                                                                      1128
```

- (2) INFORMATION FOR SEQ ID NO:423
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423

aactccttta	a tagcggcat	g atccggtgto	c tgaccagatt	gcgccggaac	gcggtatcct	60
cattggaaga	a gtcccgtacg	g ataggtgati	t ttttggtcag	g cagataagco	tctatctcat	120
cccgtgtgg	atccagcage	g gggcgcagat	t accatcgtto	cgcttatagg	gcatcccgca	180
caggccgctg	g attecetted	tcgacagaga	a ttcagcacca	tggtttcggc	attatcgtcg	240
gcatgtgcgc	caccgccacg	g tattcgatag	g ccagttcttt	ccgcaactgt	ccgaccattc	300
gtaacgcagt	: tctcgagcag	g ccatctcgat	cgaaatcgac	cgccgcgago	ataacgaacc	360
gtgtcgaagt	cgatccgate	g gagcggaaca	tcagatctcg	g gcataggcgc	tccacgaaag	420
ctgcatcctc	: atcgctctct	. accctcggag	g gtgaaaattg	cagtgtgccg	ccaccgtctc	480
ataccccaat	cgcgcaatac	gcagagcaga	gccaccgagt	cggcacctcc	gctgagagca	540
ccagtacgag	geggteteet	tctcggaaga	gcttccgctc	tctgatcgcg	ttcggacacg	600
gtttgtcagg	g gaaatcttca	tcttgttgtg	, aatatatagg	gggaaaatat	cggcccggcc	660
atcctgccga	i tggaaaaaat	. ttcttgaaat	gaagaggcto	tttatccgaa	taagccgaat	720
gctgccataa	aacaagagag	aactctcgtc	ctctctcatc	agtcctgccg	gcatctccga	780
agaggccgaa	ccttatctcg	gaaaacttat	gcacctgtga	acccgaagca	tcgccggaag	840
cgaaaaccgc	ctacaccggc	ctcttactct	. tggggagctt	tagctcccat	ttcgggatcg	900
accatgatto	gtccgcagta	ttcgcagacg	agatttttt	ccgaagcttg	acgtccagct	960
gcttctgagg	aggaatcttg	tgaagcaacc	gccgcaagca	tcacgctcta	cgggcaccac	1020
ggccaagcct	tgtgcgcagc	ctttctgatg	cgcttgaaag	ccgtcagcag	gcgcggttga	1080
tcttggcttc	gagcttcttc	gccttttcgc	gcagtttctc	ttcctctgct	tagtctcggc	1140
aatgatggta	tccagttcgc	cgcgtttttc	ggccaaacct	cgctatgctc	ttccagcacc	1200
tctttcagag	tagctatatc	ggtctgcgct	gttggatttc	gacgttgtat	tccttgatct	1260
tcttttcaga	cagtggatct	ccagctcctg	aaattcgatc	tctttggaga	gattgtcgaa	1320
ctccgattgt	tgcgcacctc	gtcgagctgt	tttttatatt	tctccagcag	cgcttggctg	1380
tactgatctt	ttccttttcg	gtggttacag	cctgattgag	cgcttggatc	cggctgtgaa	1440
gttctccaaa	cgagtctgca	ttccggcgat	tcgtcttcca	gatcctgtac	ttccagcggc	1500
aattcgccac	ggagagtctg	atcttatcta	tttcagagag	ggtattttgc	agcttgctca	1560
gtgctgccat	ttttcctcta	cgctctgttc	gttctcaacg	atgatctttt	ctttagcatg	1620
atgctcaatt	aactaactac	aaatagttta	ccggattggt	tgcaacgatg	atttgtgggt	1680
ggcaaaggta	gggaatttct	gcgatattat	gcgcaaaata	gctcattagc	cacctcttcg	1740
ctctcgtaat	gaccgatcgt	aaccgcagca	gatgctcccc	tgcatcgaag	aagtcgttgt	1800
acttcgcctc	cccgtcagga	agaggtctgc	accctcctgt	gctgcacgcc	gccacatgaa	1860
agaccgctac	cgccgcatat	agccatccgc	ctcaacggcc	gttccctcca	acceaateee	1920
acaggacctt	cagaccgaat	acctccttga	tgtgcagcag	atctcccgct	cgcttatggg	1980
cgaaggcaga	tcccccacta	ttccgcctcg	gccgagggat	gatcgttggc	cagcgggatc	2040
aggctgacag	ccggcagccg	tacggatgag	ccgcgtgcaa	agcctgcagc	acagtaccct	2100
gcctgtagcc	ggcagtacga	ggctgatccg	ctcctccgcc	tcatggtgca	attcgctatc	2160
gctcccacaa	agggattggc	accctcggca	gctctgaaag	tcccttgccg	gcatggctga	2220
acgaacagca	atcgtaatgc	cccaaacggc	ctgcccggcc	tgccacaaag	cctgcctcac	2280
ggcatcggca	tactccgtgg	ggagaaggtg	accagttcta	agagettgee	ttgcagcggc	2340
tccagcggtc	gctattcagc	aagccgaagc	gttcggccag	cagcgcattc	agtccctgcg	2400
ggcgttgtcc	gcattggtat	gagccgcata	tagcaccaga	ccgtgccgta	ggccagctcc	2460
acgcatcgct	ccacgtagga	gctgccggtc	aatcgcttgg	cggtttgaaa	agaatcggat	2520
ggtgggcaat	gacgagattg	catcccagcg	aatggcctcc	tccaataccg	cttcggtaac	2580
atccacacag	aggagggacc	cgttgcctcc	cgcttggtgt	cgcccacctg	cacgccacta	2640
ttgtcaagct	ctcttgataa	gccctcgggc	agaccgcctc	gatagcctct	ataattcctg	2700
aatgatcatc	ttcgagtgcg	agccaagagg	ctctgtttgg	tttcttgtcc		2750

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:424

```
tggtgtaccc acgggagaac cggattaccc gaatatcggt atcgacgaca tttctctatg
                                                                        60
ctgcagaggg atatgcacaa gattcagaac cgtgtccgct ggngcatttt cgcggcaaag
                                                                       120
ccacctgccc cgattgtcgt gggatgcact caagccggat gctctgtgcg tgagaatagg
                                                                       180
cggacggaat atatcgagct gacggctctg actgtagagg agacgtcggc atttttcgag
                                                                       240
gggctcagct atcggaagac gatctacata taagcanacg gctgctggag gagaaggcaa
                                                                       300
geggetaege tteetgeteg aagtggggtt ggggtatetg acattgaeeg eetgteeaat
                                                                       360
acgetetegg gtggagagag ceagegeate agetggetae geagetegge ageagettgg
                                                                       420
tgggttcgct ctacgtgctg gcgagccgag tatcggtctg catcagcgag atacgcatcg
                                                                       480
gcttatcggt ttctgaagcg actgcgcgat ctgggcaata ccgttgtagt cgtcgagcag
                                                                       540
acgaggagac aatccggtca gctgattata tcatcgacat agggccgagg ccggccgcca
                                                                       600
aggcggcgaa gtggtctatg ccggcgagta tgaccgctag acaaggatac tccgggctat
                                                                       660
acggcggctt atctgacggg acgagaaaga tcgaactgcc acgcctgcgt cgtccatgga
                                                                       720
actcatatat cgaagtcggg aagcctcgaa gcacaatctg aaaggggtga atgtccgatt
                                                                       780
cccatgcacg tgctcacggt ggtgaccggt gtgagcggat cgggaaagag tacttggtgc
                                                                       840
gcgatctttt ctacgaagga gtaaaaagga ttctcgaagg agcagcacac aagggttagc
                                                                       900
ctgcgagggc attgtcgggg acatcaagtc ttccgagaca ttcagtacgt ggatcagaac
                                                                       960
aatttcggtc gcagcacccg tccaacccgg tcacgtacat aggtgcttac gatgatattc
                                                                      1020
gcaagetete agtgeattge caetgteeaa acagatggga taccageeet atttettegt
                                                                      1080
ttcaataagg aaggaggccg ctgcgaggtc tgcaaaggag agggcagatc gtggtggaga
                                                                      1140
tgcagttcat ggccgatata gtattggagt gtgaaggtgt catggcaaac gtttccgcaa
                                                                      1200
ggagattete gatgtggagt actgcgcgcg aatatttacg acttgctgga gatgacggte
                                                                      1260
aatcaggccg ttgatttttc accgatcatc cgaaagccag ctacacggac aagatcgtgg
                                                                      1320
agagctcgaa tgtcttcgag aggtcggact cgggtatctc aaactgggac aggcagcagt
                                                                      1380
acacteteeg gtggggaaaa ccaaegegte aagetggetg etatetggga caagecaaae
                                                                      1440
ccgcacccac gcttttcatc ttcgacgaac gactacgggc ttacatatcc atgatattcg
                                                                      1500
taccttgctg cacgcactgg tgctcttatc gacaaagggc attcggtagt ggtggtagag
                                                                      1560
cataatatga gataatcaag agtgccgact gtatcatcga cttaggccct gagggtgagg
                                                                       1620
tgccggtggt tatttggtcg caacaggtac gcccgaagag gtgatggatg cgatgcctcc
                                                                       1680
                                                                       1740
tatacgggaa agtggttgaa agagatattg ggaaagaaca aagaggttga acatataatt
ataatagtgt agtatggtag gatcgtattg ggttcgattg taatcggtgc tttggccggt
                                                                       1800
 tatatagccg gcaattgcgg cgagggaagt cattgggctt gttgctcaat attctcatcg
                                                                       1860
 gttggtgggt ggtgtcctgg gcggatacct tctgaatttg ataggcatat aaatggtgga
                                                                       1920
 tetttettgg egaggettge tacgtetacg etggggggeca egttetactg etgetggetg
                                                                       1980
                                                                       2040
 acctcctaag caaaaagcgt tgagattggc agctatctgt ttggcaattg gggggtacag
 cgccggttgc ttatattatt gagtgtctaa ttataaaatg aatgcaaaat gttaggatcg
                                                                       2100
 attttagttc cattattatc ggtgcattag ccggttttat tgcaagtaag ttacggaggg
                                                                       2160
                                                                       2201
 ccgatcgtta ggcttatgct caacattatt atcgggtttg a
```

- (2) INFORMATION FOR SEQ ID NO: 425
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 984 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...984
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:425

```
ccgatcgaat gcctcttcac gatggacgaa agagacgggt atgaccggtc gatgaaccta
                                                                        60
aagcccggat ttttcaatgn aaagatcctg ctcaacctga cagcgaagac gaaggagagc
                                                                       120
tcttcatcgg gtgcgccgga ggtatggaac catggtcgaa tttgcctacg aaaagcgcga
                                                                       180
                                                                       240
agcgacagac gactattcta tttcaaggta aaggtcagcg gtctcaaagg cggtcactcc
ggagggagat tcacatcggt ctcggcaatg ccaacaagat cctgactcgc tatcctatgc
                                                                       300
tcttgagcac gaattggatt ggaagctctg ctctttccag ggagaaacct gcacaatgcc
                                                                       360
attccgcgcg aagctcatgc cgttatcggc ctaaggctga tcagaaagaa cgtgcacgag
                                                                       420
ttatcttgaa cgaactcgct gtgcagtgga ggacgaactc aagcgagtag atccgggtgt
                                                                       480
                                                                       540
gaagetegaa tgaaateggt aggaaageet geatategta tegattgtga caegaagege
gtottgttcg cgccctgtat gcttgccctc acggcgtcta cggtatgacc atgacatcga
                                                                       600
                                                                       660
aggtttggtg gaaacgtctt caaacttggc ttccgtgaga tgaaagaaga tgataagatc
                                                                       720
tacgtggaga ccagccaaag aagctcacat cgtctcttat cagcgatata gccaatacag
                                                                       780
tggcatccgt attcggcttg ccgatgctaa aatcagcttc cgcgatccgt accccggatg
                                                                       840
gaaaccaate cegattegee gattttgaaa geggeatetg agtegtatga gegatttteg
                                                                       900
gtcgtaaacc tgctataaaa gcaatccacg caggtttgga gttggtctct tcctggataa
atacccctat ctcgatatgg tttcattcgg cctaccctcc gagatgtgca ctctcccgta
                                                                       960
                                                                       984
gagaagatcg aaatcaagac gttc
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...506
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:426

gtagcctctc	tcattcaatt	tatgagctaa	atccaaaatc	aaatcacaac	tttatcaggc	60
atgatacgag	agaaaaagac	aagacgcaac	accttggagg	agtataggga	gtatgacaat	120
gcaagggaga	aaacagagat	atgtcctgaa	gttaggcata	acttttacat	tctctacacc	180
ttgcccacac	aaagcacttt	cattgcttgc	ccttcgacca	aaagatattg	caaacttttc	240
aaaactcaac	tcggtatctt	cccttctcaa	cttctaaatg	aagatccccc	cctataccca	300
aagaacaatc	ttacgcttag	gaaagacaac	tttcaaaata	cgggcaacca	atacacattg	360
ccataactag	ttgagaaaat	tatgggagta	ttggatttat	taataagata	aaaggcaatt	420
tccacaatcg	ccaaggctta	gacgactccg	ataggtatca	actataatta	gtttgncaac	480
aaagtcccta	gccttttcgt	taggaa		••		506

- (2) INFORMATION FOR SEQ ID NO: 427
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 909 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...909
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:427

ggctttgatg ccggctgcca aaagatgatg agcaagaact aagtttctgt gtgttccttg tagtgtgccc agtatttatc atgttgtacg	aactgagaga gatagatcag aggactttct gactctgaag ctgatgcccc gagggctgaa tgttcagcgc agcagaccgg aatttatatc cgatccaccg	aggggacgcc attcagggat ctgaaacgga gctgagcagc aggaggttgt attcgtaggt gtggcagaag gaaatacaat gatcagccga atattccaag	gacgaaatct tgcctgcctc tttgttgaac aggggcggat agttgagctt ggcgaaaagc cctgaaaagt cgagggaaac ttgctgctat aaagatttct	cctccgccga	aattgcatcc accccatttg aatgcctgga tagcatgccg catgctaaag gggtagtaat cggccgtatc ttgccggtct atacattgcg	60 120 180 240 300 360 420 480 540 600 660 720
atgttgtacg cccactcata ccgagcaaga gtctctaatg	aatttatatc cgatccaccg gcaaaattca atgcacccaa tcgcgttgca	gatcagccga atattccaag gtccggaccg ggtttgtcga aaaaattgag	ttgctgctat aaagatttct atgaagtcat gggtggttag atcgataacg	cctccgccga tgcttttgct cagtcgcaca gagaaggctc	ttgccggtct	660

- (2) INFORMATION FOR SEQ ID NO:428
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428

gctccatagg	attcattgaa	aactgcaaag	tcgaaaagct	taccgctacc	aaaagctcac	60
		aaactgaggg				120
catggagtgt	agcagacctt	ttttcgagca	acggcttcag	cacgaccgag	tacgatacag	180
ttcaccacga	tcagtggatg	aagataccga	gactcttgtc	caaatccggc	atataagcct	240
tgatagcatc	tgcaatatcg	tcacngaaac	ctgcaatgat	gacaataaaa	gccggatacg	300
aaccatatcg	gggatgagat	tcttgaccaa	ggatactacc	atgtggagca	gatcaataca	360
aacatggtgg	ccagtcccat	actcataccg	ttatggccga	cgttgtcgtg	gccaacgtag	420
gacacatacc	gaggaggagg	agaatgtcgg	gttctccttg	ataatgccgt	ttataataac	480
actcaaattc	tactcattgc	gcttcggtat	tatctgngtt	agtattatcg	tagaatcagc	540
ggagctgcc						549

(2) INFORMATION FOR SEQ ID NO:429

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...428
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:429

ggggaaaacg	actctgacgg	aaaaattctt	gctcttcgga	ggcgccatta	tgtggcagga	60
gcggtcaaaa	gcaacaagat	aaagaaaacg	gctaccanga	ctggatggag	atagagcgtc	120
agcgtggtat	atcggtggca	acttccgcat	gggattcaac	tacaaggact	ataaaatcaa	180
catcctcgat	acgcccgtca	ccaagatttt	gcggaagata	ctttccgtac	gcttactgct	240
gtggaagtgt	gatcatcgtn	atcgactgcg	ccaagggggt	cgagacgcag	acnccaagct	300
gatggaagtt	tgtcgtatgc	gcaagactcc	cgttatcgtc	ttctcaataa	gctggaccgt	360
nagggacagg	atcccttcga	tctgctggac	gagtggagga	agagcttcag	atncgngtgc	420
nggcactc						428

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...397
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:430

	ctcacaacac	cotaoccata	taggctatca	gcacggtgaa	agaagcatcc	60
gcgaataggc	Cigacaacac	terageoutag	ccaccatccc	aatccgagga	taatcagcgg	120
tgccggcacc	tttcccgatg	Leggeaatag	ccattgaaca	taaraaaaat	ccgaataaac	180
aatggagaag	ccgagcagtt	cgctgaaaga	gcattgaacg	cgacgaagac	ccgaataaac	240
aa+aa	anangtorro	aagccgatac	Chankacaar	ggccaacacg	acccc66600	300
a a t c	cataatttac	ocatatogtt	gggggllgcl	Lgallaagaa	Bucceegee	360
ccaastatap	cggaagttag	catccagcag	acgacgggca	gcgcgaaact	cctggcacga	• • •
tottocaaca	cotctcttcg	actccggtat	gactctg			397
	06000		_			

- (2) INFORMATION FOR SEQ ID NO:431
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 844 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...844
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

aatcaagaaa caggatgcac ttgtttctca aaagtgtgtg tgcactatca ggctgctaca gaacaggccg agcgtcaggt ttggctcgtg aaagcgcatg ccaccgggcg	caggaaaagg gtctatacgc taagccttca cctattcata gggaaagaac ctctctgcct aaacggtaca aacttttggc gccacgcttc atggcaccat tatgctactg	gtacaccccg ccatatactt ttcttttagg atttacgaac gatatgaaaa gcaacggcaa accgatctct cctcgcatcc gcagctttgg gctgcccatg atggctactg	gattcttccg gccatcgaca atagatttaa ggcaattcgt gactgataac tacacaagtg tctcggccga ccggcacagc tgccgcggtg cgcaatacat ggatacggg ggtgcggacg	agcctcatac ccggtctgcg atggcggcag	aattatgtac taaagacata caccttgccc cctttctact cgatcggact accttcgtgc gcctgtggaa agccgaaatc cgcccgaag atcaggatgc	60 120 180 240 300 360 420 480 540 600 660 720 780 840
caaccccgct	atgcaacaga	gaccttcgac	ggtgcggacg	atggcggcag	cggaattagg tggcatcgat	

- (2) INFORMATION FOR SEQ ID NO:432
 - (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...723
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:432

gccgagaaag	agcaaatgat	tttttcgagc	gtaaaacgga	cgaattgcct	tcgtgttttc	60
cggaaaaatg						120
aagtgaaaaa	ttctcgcgcc	acgtttttcg	ttccgtctga	aacaatttt	tggaacgtaa	180
aaactcgaag	agggcggggc	ggatcaaaag	aaaataagtc	cgaatcggag	gaaaaaagca	240
gcaagcaatg (caggttcaaa	ggcaagttgt	gtcgttttc	aggcttctcc	atttctgtat	300
aacttccgtc	taatcccgat	cttggcagca	gtatcggtgg	agtgggactt	tcggacaatt	360
atcaacggtg	ctcaattcat	tatctttgca	gcatttagat	acgaaaaaat	aatctgaaca	420
ataatggata ;	gacaattcaa	ggaactctta	ttactacggc	cctcccgtat	gccaacgggc	480
ctgtacatat ;	ggacacttgg	ccggtgtcta	cgttccggcc	gatatatatg	cacgctatcg	540
cgattgcgtg ;	gcagagactg	cctgctgatc	ggcggttcgg	acgaacacgt	gtacccatcg	600
ccctgaaagc	caaagccgag	ggatgcactc	cgcaggagtg	gtagaccgat	accacgaact	660
gatcaagccg	ttcgttcgaa	gggctggtat	ctcttcgaca	tatacttaac	gtaccacaag	720
cga						723

- (2) INFORMATION FOR SEQ ID NO:433
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 562 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...562
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:433

ttccttgatc	ttcgtgccgt	cacgatagac	tgtataggta	tagcttgcag	tgaatcgtct	60
		-	ccggcgcgcg			120
ttgcctgctt	cgaatgtgaa	atcgtcaaac	gtgcaggctg	gttgcctcca	tctcctgcga	180
tccacatctt	tccggagcag	gttccgggtt	cgtaatgcaa	tagtcgtaaa	caccacçggg	240

taataaccca	caaatactcg gttgccggaa tattgtctcc tttgcaggtt	aagttcgcac tgacacttcc catacgttgt cgatcgtaac	tgtaaagatc gatgtattgt ctgctgcgag	ggagaagctg gatcggcatc cacaaccttg	aggacggcat ttccggtaaa caacaagaac gcttcgttgg gttttactta	300 360 420 480 540 562
cgagaacctt	ctgtcttctt	tg				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 569 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...569
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:434

accacateta	tetettecag	caaatcctca	gctacgggta	aaaggagttt	tttccttcgg	60
ggcacaccca			tactctcacc	acatcatcga	ttgtccctac	120
gcgtagttat	agacaaaann	acattgageg	Lactetegee	acatcatcga	thouse	180
gaaacaacct	tctcggtcga	ataccgtaag	ccgatgaaat	gttcccaggt	gaattegata	
gaatcagtat	coasottest	cgttccataa	agagagacac	accggtgtac	tgctccatct	240
gaallagial	Cgaageeege	08000000000	ncasatast	atratroott	ttctacggta	300
cctcctgctt	tcaataccgg	Caaagcggaa	IIcaaagcaac	accuceggee	ttctacggta	360
gccaataaga	cggaacggaa	ccggcaatgc	atccagctcg	aaaagagaaa	caaccgctct	
tottoctoss	agagrotart	caaatoggot	gtagacgagc	gttgcactct	ccctgaacgc	420
LULLULLUA	agagegeace	cantatanta	contrastor	aaatroatra	taaagcatca	480
catgcggctt	acccagcaca	cgatatgett	Caacgaaccc	aaaccgacca	taaagcatca	540
aaggcgagag	tacgtgcgcc	gatagcgttg	aggcgagtat	ctatggattg	gtaacccctt	•
	tacgtttgtg					569
Cgatttgitt	Lacettee	6466444				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 902 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

tggcgcttac	aaaacgaaca	ggatccggcc	aaacgtcagc	agatcatcgt	aaaattctca	60
agctgtatga	tgaccgtgtc	aaatacttcg	gagaagaccc	aagtatggaa	cggactatat	120
catggccagc	aaaatatcgg	actacatcag	tatatgggcg	ataaaacgga	ttatgacaag	180
			agcatggaga			240
			agctatcaga			300
			gccatggaga			360
			aactcagatc			420
tggtcttgca						480
			gcatgttcca			540
tccgctttat	ttccaagcca	ataaatacct	ctttgccgta	cagccctcgc	tatagctgct	600
			aatcgatcaa			660
aaaaggctat						720
tctgttggct						780
gccgagatcc	tgcgatgggc	gatgctctta	tcctgattgc	ccaaatgtat	gcacaacggc	840
caatactgtc	ttcccggtga	tgctatcagg	cacgctgngt	attttcctgc	cgtggacaaa	900
ct						902

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2107
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:436

```
ggccctattg cctttttggg gatagccgta cctcacttct cgcgcatcca ttcaaaagtt
                                                                        60
cggactaccg catactgctc cccggcacca tgctgtgcgt gctctgctga tgctcgtgtg
                                                                       120
cgacatgatc acgcaggtac cgggcaaggc tttgtattgc cgatcaacgc catcacctcg
                                                                       180
atgattggtg ctcccgagta atcatgacga tcgctcgcaa ccgcaaaaag cgtttaatct
                                                                       240
tcaacgaaca ggcgatgatc cataccgaca atgtgaccct gacgggacta tctacggata
                                                                       300
ccgaagcaag aaaacggagc gcatcgtatc gaagctaatc gactttccat gcttaatggc
                                                                       360
gaactggtaa tgctgatggg tccgaacggc tgggcaaatc cacgctcatg cacaccatcg
                                                                       420
caggattact gccacctatt tggggaatat caccatcgca ggacgcgaca cacacggtct
                                                                       480
ccgcatgaga agaaagccaa gatgctcagt ctggtactga ccgacaaaat agcagcgaca
                                                                       540
atctgactgt tcgggatatt gtcgtcatcg gacgctatcc ctacgtcatt atcggggtag
                                                                       600
cctgaccgca aaggacaagg agattgtgaa tgaatcgtca tagcatgccg actgatggga
                                                                       660
ttcgaatcgc gccaatacgg ggaattagcg atggagaaaa acagcgtgta atgatagccc
                                                                       720
gcgctttagc ccaacgactc ccgtgatgct tcttgacgaa cctacggcac acctcgacct
                                                                       780
gccagccgtc tggaggtgat catcatgctg cgcgaattgg cacgcaaaac gaaaagagta
                                                                       840
tcctcgtttc tacccacgaa atggatctgg ccctgcaatg ggggacacgg tatggctgat
                                                                       900
gaacagccaa ggggagattt gtcgtggggc acggaggatt tggtactgaa ccactgtttt
                                                                       960
gaaaaagtat teggeaaega actettteet teaatataga cageggagee tteteegtea
                                                                      1020
```

```
aacataaaag gctacacctg tttctgtaga aggacagggt gctgcctaca aatggacatg
                                                                     1080
agtgctttgc accggaatgg ctatgtggaa tctgcagatg cctccgacgc aaaatcaccg
                                                                      1140
tgggagaggg ctgctggatt ctgcaggagg gcgattctcg aaaagcttcg actccatcgg
                                                                      1200
ctccttgcta caaacgctgc acgctaccac gaatgaatgc ttgtgaaaca aacaattata
                                                                      1260
tgcaaaaccc tacgtagatt tcgacaaaga aacgcctctg ttttttagtc ctatgggcga
                                                                      1320
tecetttace actigaaaga aagtatgate gttegetteg caggaegeag agagtegtga
                                                                      1380
gcacctgcaa totcaacgge ggctaccgag aagacctccg cacgcottca acaacagttg
                                                                      1440
cgggagggac cccgacgtaa tagccaaacg tctgtaggga tgcgaggaaa gaccatgatc
                                                                      1500
gaacactacg ccgccttagg gaagaattgg gtctgcctct tgacaaaaca acgggcatgg
                                                                      1560
gtaccgctct ctgatcgaaa atacggcgac ctcctctcgc caataccacg gagtaacgtc
                                                                      1620
atggcggttg ccacggcagg tatagatgta aatggggggac gcgcagagaa cctgccgcat
                                                                      1680
acaacgaatt tacccaaaca gacctgatta agccggtacc atcaacgtat tcctgttcat
                                                                      1740
cgacgcctca ttggatgcag gaacctgaca cgcgccctcg tcaccgccac cgaagcgaaa
                                                                      1800
teggeageee tgeggaactg atggeaaaca geatgtatte agaagatttg geeaceggtt
                                                                      1860
cggaactgat tototgatng coatotgtaa taaggagtog gagatagtgo toagaatagt
                                                                      1920
ggcaaacacg tgcttttggg cgaaatgata ggccaaagcg gaaagaggct attacggaag
                                                                      1980
cettateceg acagacaaag atgaceete aegteagget tegategaat ggeagaceaa
                                                                      2040
acgctacggn ataacgagga agcgatcgtc tccgaatgcc tgcgcctgta tccacatctg
                                                                      2100
                                                                      2107
aaaaaag
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 719 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...719
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437

ccttttttt acgattt gggggtactg cttcaggg tcatcgagtc cattgcg tccggaggaa tacgaccg ttctaatagg aggactg taagctccct cttttcg ggctcctgca cagatca gtgtggtagg ggcaaag gaacgagaaa acaaatg agagactcgt cgatacc cccatcgnt agctttt gggaaagagc ctacggc	tc cgatcgtacg at aagtcgggca tc gcctaccgtg gg ttcgagcaaagc tc tcatacagac ccagtcgtgc ga caaagggcac ttg ttgccaatg	ggtggtgca atgaagcgtt gaaatctcgc cttggcggat ctcatgccca tgcatacgac gaccgtctca gcaaagcaga cggcctgggc	ttggtaccgg tgtccgaagc tgccattcgg gccgaagtgc tgatccgcac gcgcttgtgg acggacgtat caaagcctcg agatcgtcat	ccggcagcaa agatgcctac gacataaccc agatctccac tattggagca agctttatcc cgacagcgta tcatatatca agaggaagat	60 120 180 240 300 360 420 480 540 600 660 719
--	--	---	--	--	---

- (2) INFORMATION FOR SEQ ID NO:438
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 492 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...492
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:438

cactattgtc	cgggttgtag	ccacggagtt	gtgcacaaac	tcatcgcaga	gtaatcgaag	60
aaatgggctt	gacggaagaa	actatcggca	tcgcccccta	ggatgctcag	tattcgccta	120
tcgctacatc	gatatcgact	ggcaagagct	gcccacggcc	gtgcaccggc	tctggctaca	180
gcagtaaagc	gtctgatccc	tctaagctgg	tatttacata	tcagggcgac	ggagacttgg	240
		ccatccacgc				300
		cggtatgacc				360
gtatgggtac	cggntacttg	ccctcaggga	agaacgtaga	gctgaaccgg	tattccgctg	420
aagattgccg	atatgcttgc	tttgctcgac	ggtacttggc	tcgtaacgcg	ccaagaaccg	480
tgcacaatgc	gc					492

- (2) INFORMATION FOR SEQ ID NO:439
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1699 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1699
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:439

gatttctttg	aaagcatatg	atgactttct	accatcggca	cgcaccaaca	cagctctccg	60
gaaggcaata	catcggcaat	tatggcatcg	aaacgccctc	cttattttgg	aagggatggt	120
			acgagtgtga			180
ttctatgtgt	ctgtaggtga	acgcatctcc	tgcataaaag	agcggaatat	ctctatacga	240
tctacgaatg	ccccagaatg	atccggaccg	atgtaggatt	ggggagatag	ctcgatagtc	300
gctttcgttg	atattgagac	cgacacccag	aatgctgtag	tcgggttgct	gcccgtcagg	360
ctgtgctcga	tcagtatgcc	tgctattttc	cttctccata	gtatatatcg	ttcggccatt	420
			gtcgtagagt			480
			gcaggaagca			540

```
aaaaggtcag gttcaagccc ggagacgcga accagctatt gccctgcttc ctcgtcccgc
                                                                       600
agtotgattg totgtoatga coacggtoca ogcaggtggt ogggatoctg catcaaaaga
                                                                       660
toggacagat agggagttgg tgctggccgt ttcgggcaga tggatcagat accettcaga
                                                                       720
ccaactgttc ttcttgactc catcgaaagg cggttgtgta cggatgtatt tagggagttt
                                                                       780
ggatcaacga gagcgtacga atgtcggatg agccgtgcaa tcagatcggc agggcatccg
                                                                       840
agtocaaago tacgotgtto caatgiogtt tgttoatatg aaagooccog tgataccoto
                                                                       900
gtagtgcatc cttaaatgtt cggaccgatc ggatcgcatt tgagtgcgat gactttcttt
                                                                       960
teggaateaa ggggtateag geaaacattt tgeeggetae ttteataace aaegtaacat
                                                                      1020
catcgaacgg aaactctcct ccacctgtgg cagtgacaag catagctctc gagcttgcct
                                                                      1080
atgtccatat attatttat ttttgctacg ttatgaattt cgctccattt tgcttggggc
                                                                      1140
acggtctaac aaaaataatg gaaaaactca tttttgcaca aacaatccac ataagctcaa
                                                                      1200
cgagattcgt catattcttg agggaaggtg nagattgtcg gnctggacga aataggttgt
                                                                      1260
cggnaggata ttccgaaacg gccgacacan tacagggaca atgctttgct caaagcagaa
                                                                      1320
tttttcacaa acgatatggt ttaccttgct ttgctgacga cacaggcttg gagtagaagc
                                                                      1380
tettgacaga geanceggeg tecaetetge aeggtacgea gagaaeegae caatgeenat
                                                                       1440
gccaatgtac ggaaactact cnaagcattg gcagtgtacc acatcccaga aaagcatgct
                                                                       1500
teegtacegt gategeecta tegatgatea tggaaaacae ttettegaag ggaagatega
                                                                       1560
aggtaccaag catnigaatg cagaggatcg ggcggcttcg gctatgaccc cgttttctcc
                                                                       1620
cggagggaca cacgctcagc tttgcagaaa tgggagaaga aaccaaaatc aaatcagtca
                                                                       1680
                                                                       1699
 tcgtgctttg gcggtggca
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 917 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...917
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440

```
ggctgcgatg tctataccac tctcgacatg gatatgcaga gcatagtcga gtggagttgc
                                                                        60
gcagcaagct cgaagaggtg cagggagaaa gtggaacccc atcctcatgg aggtagctac
                                                                       120
agggcaggta aaggctatca ccaatctcag cgcacgccct ccggcggata tatcgaatcc
                                                                       180
aagaactacg cagtagcgat atgtcagaac ccggttctac gttcaagacc gtgtcgatga
                                                                       240
tggtacactc gatgccggca ttgtgcatcc ggaggacatc atcgaaacgg gcaaggtctc
                                                                       300
ttctccgtag gcaagcgtac tgtaagagac cataatgcac acaaggaggg tatggccccc
                                                                       360
ttacggcagc tcagacgatt tggtactcaa gcacgtaggc gtagccaaaa tcattctcaa
                                                                       420
aggetttgcc cacgateceg aaaatacgtg gaggeggtea ggegaacegg tateaeggae
                                                                       480
aagttoogto ggaaatacco ggagaagoto oggoogtagt gogcaagogt googacaato
                                                                       540
tgaccgctgg tatggcacga cccttgcatg gatgtcattc ggatacgaac ccaaatcccg
                                                                       600
                                                                       660
ccgatccata cattggcttt ctacaatgcc gttgccacgg tggtagaatg atgcgtccct
                                                                        720
acttcgtaac gaaagtgatg gatagaggga ggtcgtacag gagcaccggc cggtagtatt
acgcgattcc atctgaagca ctctacgctt atcgccatac aggatatgct ctcgaacgta
                                                                        780
gtggcaaagg gaccggctcg ccggtcaaaa gctctacggt aaacatcagc ggcttgaccg
                                                                        840
                                                                        900
gtacagegea gateteacag ggeaaaageg gttategtge agtggeacea tgeacttggt
                                                                        917
attctttctg tggttat
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 680 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...680
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441

```
cggactggca cccgaacgac aaggtgtctt tcttcttcgg acgtcagtag cgcgtttcgg
                                                                        60
agggatagaa tacgacatga accccgtaga gatctaccgt acagcgacct tgtggattac
                                                                       120
atgacctgct atacttcggg cgtgaactcg catggaactt ccaccccgaa cagcagctgc
                                                                       180
agctacaggt actcaagctt acaacaaccg cttcgccgac cgctaccacg tgacacccga
                                                                       240
tgtcgtaccg ccacgagcta cccgctcctc tactcggcac agtggaacgg tacctcctcg
                                                                       300
gaggagcact gcatatgcgt tacgccgtgt cgatggctca tcagcccaag agcgtaatat
                                                                       360
gtggtacttc actgcgggca acctgttcaa tcgggcaaac ggatcaacgg atacctcgac
                                                                       420
ctcacctact cgatcgaggg atggacgaca aaggcattat gactgctcgc tacggcaagg
                                                                       480
gcaagaccet acggacgtca agtactatge tetggtateg aagtggaact teegcattte
                                                                       540
gatcaggtca atctcttcct caaaggcatg tacgagaacg gctatgcgct gcccaatacg
                                                                       600
gcgagagcag ccacacgcgc caactcctac ggctataggg aagggtggaa tattacccct
                                                                       660
acggagacca actttccgtc
                                                                       680
```

- (2) INFORMATION FOR SEQ ID NO:442
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 855 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...855
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

	ctttgatcaa					120
	gtactcagcg					180
tgctcgttgc	atctctctgt	tgcaaattga	ccgtttgttc	ggtctgcttg	catttgcgtt	240
tgggcattgc	gggcagttgg	aagagtccca	atgccagaat	caaggcttta	gccttaaaag	300
ctttttcatt	gtttgatatg	ttttatgatg	ttatgaatat	gttctgaaca	tatgataaga	360
tctcggggaa	ataataaaga	gggacatggg	ccatctttt	gcgaaatatc	catggaggga	420
tttaccttcg	gtttttcacc	tcaacccgat	aaccgcccgt	aaaattagaa	gaaatcatca	480
	aataaacctg					540
caagaagtat	cttttcggta	tcgtttttgc	tcacctatag	agtgtatcca	caagtcatgg	600
	agaggtattc					660
aatctcccgg	aaaatgccgt	gcgacatctt	atctatcggg	ttcacagctc	gcacggaacc	720
tccacttccc	gatccgccat	ccgacacaga	gcagatagca	tcttccatca	atagaccata	780
gtatctctca	taggagacca	taatatcctc	tcataggaga	ccatagtatc	ctccatgtga	840
gaccatagta	tcctc					855

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 904 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...904
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:443

```
60
gtcgttgatc agtcccacta cgcgacaacc tttaggcgta tgtttacgga gaacttactg
                                                                       120
cttggctgga agattatagt cttggagaaa tttgggagaa aatatcattg gtggacaacc
                                                                       180
ttgggctaag tagtgagatg gggaatagaa aaaacggctt gtttttattg tcgagggaga
tacagaggtt gccttttcca tgaacgtgtg atcccatacc taatgagcaa aggctaccgc
                                                                       240
aatgcatgaa tgcccagaag atcaccacca ataaatcgct tcataaaaag ggtgtatagc
                                                                       300
                                                                       360
ccgcttcgaa tacttggaaa atgaagttcg aagcgtagca gccaaggaga tatcttgatt
actactttgt tagacttctt caggctacca acaattttcc taactatact gcggatagcc
                                                                       420
                                                                       480
ataagatttc ggatatagag caggggttag acaaggtatt gatggggtta atgtttcgct
                                                                       540
tttctatcca atattcagcg ccacgaacta gaggcactca tgtacacgag tatggatggt
ttgagatcgt ttgtgacgaa aaaagagagt tagatcagct gagagcaatg tagagggtta
                                                                       600
                                                                       660
cgataatccc gaagatatca attctggggc tgaaacccgc catctaagcg ccttatcaag
                                                                       720
attttcccaa aatatgagaa ggttcttatg gagaactgat atttgaggct ttggagattg
                                                                       780
atgctatacg agctcatgcc cccgtttcaa cgattggata caaatccttg aggacggatt
                                                                       840
aaagaaggat acttttaagc cagatttttt attatacttt tttaagggac tttagctctt
                                                                       900
gtactctttt cgataaagaa tatcgctcaa tctatgcttg cacgcccgac aatgcgtaga
                                                                       904
cttt
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1071 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1071
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:444

gcgtcatgaa tgctgcgaaa gctttagccg agatcggtct ggaatcgggg aacgaatcgg 60 tatctattcc cccaatatgg tacactgtct gtataccggt tgggggcctt cgccatgcgg 120 ggtgtagtag tgcctttgta tgccacagct caccggaaca gttacggttc atcgtggagg 180 attcatccat ggagacttgt ttgtcggaga gcagttccaa tacaacaatg cttatcgggt 240 acagaagaat atggtacgct aaagcgcata gtcgtattcg atgagcgcgt ggtgtcaatc 300 cggaggataa gacttcgaaa tacttttccg aatttgttcg tttggtgatt ccatgccgaa 360 cgagacgaag gtcaaagtct cttctcgcga agcattcctt ccgatccggc actgatcatc 420 tatacatcgg gcacttccgg tggagcaagg gcgtcctcct cctgcacagc aatctgatgt 480 atcagatgaa gtccatagcg agcatatccc cgtctatggg ccgggcgagc tgtcgatagt 540 ttcctgccga tgagtcatat tttcgaaaag gcatggacac tcttttgctg acgacgggaa 600 cgaggattgc catcttgaga gatccgaaga aagtattgag gcactacctc agatacgccc 660 atcgctcatg tgcaacgtgc cacgctttgg gagaaagtgt atcagggcgt gaatgagaag 720 atggcctcct ctcccgcatc ctgaaaggtg tctacaggcg tgctatggcc gtaggccaac 780 gctacgtctc gactattgga atgaggggaa gcgtgcgcca ctgcttctga gtagcaatat 840 gccttttaca actgcactat ttttaccctg ctcaagcgcg tatgggacta cagcgagggc 900 gttatttccc cacggncgga gcaccgctat cgatgagatc aacatcttcc ttcagtccgt 960 aaacattccc atcattgtcg atatggtctg tccgaaacga ctgccacggt atctttctat 1020 ccgcagcgag attcaagatc ggctncatgg gcaaagtgat gccgggctgg a 1071

1

- (2) INFORMATION FOR SEQ ID NO:445
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1999 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1999
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

catcgtcttg cgcttgaaga aatcatcatt gtcgatgaat aaacctgcat gcgggccgac 120 tggatggaag ccactttgat gatcaacgat ggtcgttgtc gttaatgatc atattgatgc 180 cggaaaggcg tatcactcgt gcaactgatt gcgacgctca ttgatgatgc catagcgggg 240 cataaaatgc gcacctcgtt gcctcgctcc tgaatggtct gaggcaattt gcgcaaacga 300 ccgatatgtc cgtttccggc aagtagggga aaatttcttg ggaatgtaaa gaatttttt 360 ggaatccatt cttttaccgt catctacgtt tctgcaaagg tacaaaaaaa actcatcggc 420 aagataagga agaagtacgt aagccctctt agataagtat aaaaagacca aatacctcaa 480 gaatcgcact caaaggctac cataaacaag ctcccaaaac cagacctaaa cggaggagac 540 aaagtgcgaa tcgagagaca aaccactcaa ggatgagcac ctgattatag aggattaagc 600 caaaagatcc gacaagatgg gaaaagaaat agccgaaaag aaccggctgg ggatcgccac 660 cttttcacga gccaaaaaac ggcgaccacc ggccctaaaa atgcggcgcg taaaagtttt 720 ccttttggtg cgagaaagaa aaatttacgc gccacaacga aaaaaatctc gcgtcacttt 780 toccaaaaca ogaacogcaa togcagottt tgoggttoog gaattgtogg agacggotga 840 ggttcgagac agacggttgg gcgtattatt cgtactttcg tgatgatttt cacacgctgc 900 accggattat tatccggggt tagtccacag gtgtctgaat tiggaatgca gagaatcata 960 tagaatacag aacgagaaca agatgagcga agagctgcaa cacttgtcac cgggtgaacg 1020 tetetatece tetecacega tatgaaagag gtteeegate gttatttgca eggggaaggt 1080 acgaccatga gcagagtgat gagatcggga gagaggaaga agacttttc ctcctatgcc 1140 ggaggaggtt tccaatgaga tcgaagctcc gtctctcata cgccggagga ggttttgcta 1200 cactattggg gctaccette gttcageetg tgcageteee gateategaa teegttttgg 1260 cagggaagga cacatgggac tactgcccac gggtggtggt aagagtatca cgttccaagt 1320 cccgggctgc tactgccggg tttgactctc gtggtaacgc cactgattgc tcgatgcggg 1380 accagatcat gggattgcgc caaaagggga tcaaggcgac accgttcatg ccggaatgac 1440 gegegageag attateacea egetggacaa tgtatttaeg geegetaeaa atttetatae 1500 gtttcgccg aacgtctggc tcggaacttt tcctcagccg tctgcatgct ctcagggtaa 1560 1620 gtctgctgtc gtagacgaat gtcactgtat atcccagtgg ggctatgact tccggccgca tacctotoga tagoagacat cagggaggoo otgooggatg ttooogattg goattgactg 1680 ctacggctac acggccggtg atcgacgaca tacaagcatc ctccgatttc cggagccgaa 1740 cgtgctgaga aaaagctttt tccgcccaat ctgtcgtatt ccatccgccg gacggcagac 1800 aaagagacga tgcgctgcat atcctcagnc gcgtggacgg ttcggccgtc gtatactgtc 1860 gcaccgagat aaggcgcgcg atctggcacg cttctcggcg aaaacggctt ccggccgatt 1920 tctatcacgc cggtctcacc atgtgacacg ggaaatacgg aaaaaagctg gatggaaggg 1980 1999 gaacgccgga tcatcgtct

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...465
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:446

			+-++a+aaac	aatctcctca	agcaggcgat	60
papccagato	ttctttggtg	agccagccat	tattgtaggt	Autocoocc		120
	+	ctatoaccoa	tacaaaaagg	aagcaccege	~~6~6~	
cttcaagcci	LEGUELLE	c cu cga c ga		ctggagacgg	agctgcttgc	180
totetaccte	tatccagcca	ggcaaaacac	gccccagucg	Cragagaces	agctgcttgc	240
50-00	ctcctgttga	ctgaggttat	ttccaattcg	ccccgcgccg	atggtttgac	240
gaagcatgaa	CLCCLECGG					

atctgtgcta	catcaagtac	atcattagas	tagaaataga			
tcttcggctt	ttccaattt	t-t-	LagadaLaga	gtcccactac	tgcgagttgc	300
		LLLCCAPPC	Leargaactt	OCCO+ 2000+		
	- Borragear	catteacata	atgccgaaaa	tootooccat	accetttee	100
gcatcggcaa	ctgccgaccg	agcatttagc	tgaagccatg	-88-88-64-6	acceletee	420
- 00	0 0 1 9	-Bearings.	cgaagccacg	cccgt		465

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 532 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...5\overline{32}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:447

accaagacat	ggcgcagctc	tatcastasa	.			
0004-444	PPopulation	rgreggigga	tgggatatct	atatggcacg	aaaggctatg	60
Cogtotttac	ggtggatagt	CgCggatcto	CCaatagagg	not cot t	880000	00
tcatcotcot	ttagagaga	9 99	ccaacagagg	gergettteg	agcaggttat	120
	0000~~~~	CCEGEGLELL	Varragator.	0000taba-		100
agccaatcat	gggtggtgcc	gatagaatag	Sastasat -	0-88-8-864	cccccaag	180
teactconst	000-00-00	Bacagaacag	gaglacatgg	ctggagctat	ggtggcttta	240
	00+	CACACEECEA	LVICTTCAAA	atcacactes		
gtcatagact	ggaatcgata	tsasstate	-8	greggagtag	ccgggggcct gcgccacagg	300
-	00	- Faractate	Lacourgage	Ott+++00		260
aaaatcccga	aggatacgat	gctgccaacc	tatcaaacaa	600000	tgaaaggacg	360
acttatocto	attentages	8-18-014-0	egecaaacga	gccggtgatc	tgaaaggacg	420
		CALLEALLID	VICUITORES+	000000		
cttgatgctt	Cgtgaappca	Cacacctate	0 0 00	Pergentite	acticitite	480
2 0 -	9 - 9 - u 8 6 c u	Seacciate	crgactetta	cgtctatccg	ag	532
				- 0	0	222

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 902 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...902
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:448 *

```
ggaaaactat catcaagact atttggatca taaccetege ggttattgta tategateet
                                                                        60
tetttatteg aattggegag gaaageeaat eeggeeagtt etacaagaag geegatgatg
                                                                       120
                                                                       180
cagagetteg tgeceggett acceeeggea gtatgeegte acaegeaaca atgecaeega
accggctttt gacaacagta ttggaatgaa tttcgagaag gtatttatgt cgatgttact
                                                                       240
                                                                       300
acagggaacc gctatttctt tctactgata agttcgactc cggctgtgga tggcgagttt
cagcaagccg atagggaaag agctgatttc cgagcgtatc gatgttcttt cggaatgact
                                                                       360
                                                                       420
cgtacagaag tgcgtagtac gaccggcgat gccatttggg acacttgttc aatgacgggc
                                                                       480
cactggaaga aaggcggact cgttattgca tcaatagtgc ctcccttcgg tttattccca
                                                                       540
aagaggatat aagaaagaag gctatggcag tcttcttcct cttttgaaca aacgatgaga
tgctcttgta gcatataatg attcccaatc gtctcagata agactaactc caatggcata
                                                                       600
tctcggaacc aaagccaagt ggctgttact actctcccca tcgtgcttct tgcaatagtc
                                                                       660
ggagtotgga tttttcaata ttooggtatg gggagogatt ogaaattgto gaogaattgg
                                                                       720
                                                                       780
gtggcaatat ctttcgtccg ccatactgtc ggtggccacg accgatgctg aagtaatcaa
accgtcgaag gcctgtacgt gggcaatccg aagtccgtta tcagtattcg cctaaaacgc
                                                                       840
                                                                       900
gaagggccaa tagccgtgtg cgtgtggaag tagccgaaac gcttttttct cccaggggga
                                                                       902
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1731 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1731
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

atccttcggt	ttaggggttt	attgccaaag	ataaagagaa	gtccccgtaa	tttgtctgca	60
attatccaga	tagtatgact	accaagggag	gaataccacg	tcgatgtcct	gcgagttctg	120
gcaggattga	tggtaatcgg	catccatctt	cgggagaata	cgttctcgaa	ggagtggctg	180
agggtgcaaa	ctttatgccg	gtctatgctg	ggaggcggtc	gtgcagccgg	ccgttcctat	240
attcgcatta	tcagcggggc	ttttgtcttg	ggacgcaatg	agacgtgggg	agattctatc	300
ggaaacgaat	accgcgactg	ctggtactac	tcgctttttg	gctccgttct	attggctgtg	360
gctgtggctc	aagggcgatg	atataggttc	cttcttgccg	gcttttggca	gggacgctca	420
ttcgttcatc	tgtggtatgt	gtgatgctgc	tgggacttta	tgcagtcgtt	cctctgctca	480
acgaaataat	cgcaggtgcg	aagccgatgg	agagaaggct	gctcgtaaac	gactttggat	540
ctctctacca	tattgctact	gctggggata	ttgtccaaca	cctacgatac	atactcggtt	600
acaaccgctt	tttccctttt	ctttggccgg	attatttgga	tatttccttg	tgggttatac	660
cctgaagagc	catgctccgc	agcgtttta	ccggctcttt	ccttgtacgg	actctctacg	720
atttctcttt	tcttccaagt	cggtacgctt	tcgagcacgg	cgaagggcta	tacttctacc	780
gtaactctct	cctttgattg	ttctttctgc	tatcagtctc	ttcgcgttct	tcgttcttgg	840
ggaggatgtg	gaggaaaatt	ggcgcggatc	gggaaaatgc	aggggatatt	ttaggaatct	900
acttagtaca	catcgctgtg	ctgaacgtgg	tacaaaaata	cttgtactga	ccacccccag	960
cctgatgcaa	tgcgcatggc	caacataccg	atccgtgtag	gattggtttt	cttcgtttct	1020
tggggagttt	gcggctgatg	aagcggttgc	cgatatgccg	ctatttggtc	tagatcagcc	1080
gataccggtt	ctattgtacc	cgtttcttcg	acctctctat	atcgttcccc	gtttcaggac	1140
agacggccat	ccccttgtca	tcgaacgaca	agcggtaccg	gcgcggctta	cccaacçgat	1200

cgaggagacg cgaggattga	ccttcgtgca tcacgttggt	aatgagtggg aaatacacaa	gcggtattcg	aagaatagtg gattttcttt	caccacggtt gcattggctc cataaaggcg tcttcgcata gtcgtacctc	1260 1320 1380 1440
aagtgagaaa tgtgggatgg	acgacattcg gtgccatacg atcataaaga atgaggcatt	cgtgtaccct cctgctatca	gaccaagcac attegcgate	cgacctcggc acaaccgtct	tccgcacatc tctactacgc	1500 1560 1620 1680 1731

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 424 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...4\overline{24}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:450

tgggcgataa tcctgctgcc gaagcgccgg ctgttcattc tcagggtatc	gacccgtatg ggttcgtggg attcgacacg gatggtggac	gagcagcctc tggcgtggca atctttgtag ttcttcctgc	tcgagagaag cgcaagacgc agacggtagg	gagatccaaa aatgccttta gtgagaccat angtgggaca	catcaagcan gggagtattc ttcgtcccag cgtgctgtgt gagcaaactg gggatgaact tcaataaaag	60 120 180 240 300 360 420
cgga			0 6	gracicateg	ccaacaaaag	420 424

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2521 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

	,		

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 610 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...610
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

gagcataccg	cccggccagc	gttctaccac	atagggcatt	cccactgatt	ggccaattcg	60
		cttcttcgtg				120
ccataccctt	aataacttcg	gctgcttgtc	tactttagca	actgttttgt	gcaggtcgat.	180
aatatgaata	tcgttggctc	cataaagata	tacggagcca	taagccggat	tccactttct	240
cttgagtgtc	cgaagtgagc	accggcttcc	aataattgat	caaaagaaat	tcttacattt	300
tcgtttacgt	tctttgtaat	gattactgtt	tgcaatccaa	accgtagagc	agactcgaaa	360
agaaatgaat	tacccccgaa	tgcaatccga	tgatttagat	actaaacgcg	agaaatatcc	420
tctaaggaca	ttaacgctta	cgaattggaa	tctcttgcga	gctttgggac	gtcccggttt	480
cttacgttct	ccacgcgagg	atcgcgagtg	atgaagcctt	ctgaacgcaa	agcgggtttt	540
cgtccggatt	gatcttgacc	agtgcacggg	ccgatagcca	agcgagcact	cgttctgacc	600
tttgaaacca						610

- (2) INFORMATION FOR SEQ ID NO:2
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 628 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...628
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

tcttccgctt tttttggaat actcattcgc atcgaaagct ctacagagct caaggatgcg gagaggatta gtttgacacc cgctcaaagc tattttgcga bcgggtgttg cgctttctgc

60

..120

cattagtcaa tttggatagc ccgagggtgg cttacacaac atcggtacac gtacttcgat	actttagaaa agccgtcagc aattcttcat gacatccgga gccgtagtac cgttctgaat	tgcccttccg acattgtatg gcagtagcat aaccgatggt gccttcgccg aatcaaagtg tcttcttcgg cggttcgggg	aacaaagtgt cggtggcaac acggaaaacg cttgcccaat gagtccgagc aggcgaatcc	ggaaatacgt agtggctgct aatcggattc ttggtcggag agcgaatgga agaaactttc	gacgggagcc ttggaccctt aagcagacat ctgcagaagc ctcttcagca agcgtcccca	180 240 300 360 420 480 540 600
	tagtaggcta atgtagtaaa		gtgatcatca	tgcacagagg	atatatcatc	600 628

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 970 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...970
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

```
gacttettta eccegetaaa agtaacetta etgatgegag gaegtteagg acaatgattt
                                                                        60
tcagatagac tttattgccg acatatttat ccgcgatgtt cgcacatttg agaagtagcc
                                                                       120
                                                                       180
ctgacgcata attctattca cggcagcgac atggcatctc caggaatcag gacttcatca
                                                                       240
cctacagcca agcctgaaga ttgcgcaaga caaagtcatc gaaagacctc attccctcga
totoatagat gotatggtot tatgaatagg ottggoatag gatatttoag ggottatata
                                                                       300
                                                                       360
tggatctccg tgaggggtca gatccgagga ctgtcctttc aggtccctat gctggcgcag
aagagagetg ctaeggeaat aatetttttg taatagtett teteaaatga tteaatattt
                                                                       420
attttctctg agagcgattt gtcgctggtc ttgccgaatc gacgctccct cgatgaatat
                                                                       480
tottotatgg tgccttcaga cagtcggcat caaagtccgg ccaaagcgta tcggtaaaaa
                                                                       540
caatteegta taggeeattt geeacataag aaaatgetga taegetteet ceacetgtae
                                                                       600
gaatgaagag atccggatcc ggaatgcccg cggtggaaga tgatcagaaa ccaaatcgac
                                                                       660
atttatatct tcaggctcca cacttcatcc cgaacctttc gagccaatct acggatgaca
                                                                       720
teggteattt cecaggagaa etgtagetaa gggeeaaaae caaagteage eeegtgttte
                                                                       780
cggcgtctct cgaataccct tttctaacga ttcacggaca tcctcgggga gccactgaaa
                                                                       840
tegeegatag ceaagaggeg aatgttattg gteateaagt eegeatetea tteatgataa
                                                                       900
gctgtaacga aaaggcccat cagcgccctg attcctcttt cggacgattc caattcttcg
                                                                       960
                                                                       970
tactgaaagg
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

agccgcacga	ttggaaaaga	aactggagca	actcacagcc	taacggcgca	gagcctgtgc	60
ttgagacgct	gcagaagacc	gggatgattc	tccggatccc	tgaggtcaat	gtctgggaaa	120
gattctttc	ggatacgatc	agtagcagtc	tcccacttgc	aagtgcatac	gccctttcgg	180
tacacgataa	gccctccctc	ttcgtaccag	gatgacaagc	tcttcatcac	gaagagaaag	240
attcacagca	gatcgccatg	ggacagcatg	gaagcatcca	ccactctctc	ctccacttgg	300
ttcccgtctc	ttccggtatt	tccacaccga	acaggctacc	tatggcggcg	aaggaatatc	360
cagtccgagc	caacgtgcta	cctgggagat	cgactcccct	gtacgagcag	agagagtatg	420
gtaatgaaga	agacgacatt	gaaagctgat	ccgctccggg	gatattatcg	atcatgggat	480
aggtggcaaa	atgataggaa	cggctccgcg	caatccgacc	cagctgagaa	aggtcttacc	540
ctgaatgata	ttttgcggaa	gggaatcagg	cagaaa			576

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...588
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

```
gettteatet etatteteet tttttattet attgtgtttt tttcatatte tetteggaca
                                                                       60
tagccgtttc cgcatacaag gcttcctctt cccatccggc atttccacaa actcccctc
                                                                      120
cgcatcagcc ccgcgatcga gacaatatcc aatagctcca tggcgtaggc cgtttcccgg
                                                                      180
acggcttcgt cccgatgaga gcgatcccgt tcctgttgga cgaaagtcgt cccaccgtat
                                                                      240
tragereace greatesta tggeragtge caaageraca caagetarag ceretagegt
                                                                      300
accaaccgaa gcgacaaccg ccttgaagga tgccggacac gatctcccaa ctcgccatct
                                                                      360
tttccaagag aactttgtcc gaatcatctt cctngcccgt ttcacgctca ggaagaccga
                                                                      420
tcaaagcccg caaaagctgc agtccgaatg atagggagcc ggatccggca atccettcag
                                                                      480
caagcaatac gctccaactc ctcttgcgga aaatggtacc ggcataaaaa ctttncagtg
                                                                      540
ccggtcgatt ttattctctc ttacgcatca tcttatcacc tcctagct
                                                                      588
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...473
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

aacacaaaac tt	tagaaggg	agtcttacac	ttcgtcccat	cgagtgtctt	cctttaccgg	60
tagtttcatg ag	tagesaga	ccactaccct	gaatgatgtc	ccatcaaaat	caatagcaaa	120
cagattatgg cc	cggcaaga	ntacaacaat	cccactagag	totappappt	atettccett	180
cagattatgg cc	ggagatti	acacgacgac	cccgccggag	assuscuata	acatoattao	240
ccaaatactt gg	atctcgta	gntgaaatac	CLLCgaaggc	aaagacgacg	categateat	300
taaggctttt ac	gtcacagg	ggtaggacga	ttgttcaaaa	acctcgatat	cattgattat	360
atgacttcat gg	atttgtac	gaaaggcaac	atgtctcata	atataccgcc	ggccttcaag	
tactggttct tc	ccaaagtg	tcgtttgcag	gccagtatgt	attgagcaat	ccgaaaggcg	420
agtacaacaa ca	cacacgct	cgctaacaca	ggtgcaggta	gcattctgac	agc	473

- (2) INFORMATION FOR SEQ ID NO:7
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 625 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...625
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

tcttattata { agtggtgagg { atacctctgg tatagataac { atacatttcg	gctaccgctt taacgatgcc ggacatgctg	tcgagagctc ggtactttga cagcagaaaa	atccacggca ccagcaattt gcgcgagtat	tatcgtattt tgaaaacggt tgcagcggat	gacaatatct tcttccgcgc	60 120 180 240 300
tatagataac s	ggacatgctg	cagcagaaaa	gcgcgagtat	tgcagcggat	tcttccgcgc	
atacatttcg (gcagaatctc	ttcgaacagc	aaaaggacca	gtggccagga	taattggaaa	360
ggataacgat	ggctacatta	atcacattat	tccgatcaga	atagtagcta	atagctgatt	420

cgaattgtct	aataaattgg	aagcgcgatg	tcggaagagt	gattccgttc	gcggatgttc	480
tgcagatcga	cggctttagt	gaaaaataag	ccacctcaca	ggaggacata	aaagccgaaa	540
gcaaagaaga	agcaggtcga	taatgaaagc	cactatggct	gctgcaccat	aggatgaccc	600
gaagcccttc	aaaaaatcag	tataa				625

- (2) INFORMATION FOR SEQ ID NO:8
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 962 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...962
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

ggggatttgg	ggcaagataa	gttactttgt	agagcttgaa	tggcaaacag	ggatttctgc	60
ctattttcca	aaaatctgca	tcgtcgattc	ttgaaacggt	tgagagccaa	cgggggcgca	120
aggagtttgt	tctggttggc	cacccgagag	cttcgtctcc	ggggagagtt	ttaattatct	180
tatcgggcaa	cttaaagcag	ctatcagttc	ttgagcatga	cagagttgta	tgatcagagg	240
ctaaaatagg	cacaaagaaa	ggcgtcaagg	atactcataa	gcccgaaaca	cctgcccaga	300
aggaccatct	ccagagggac	ctgaagctgg	tttgtaatta	gttatagaag	ctcaccccag	360
tagaggtagc	gagttttgct	ggggtgagtg	tcatctgtta	ttgtttagtc	attacgaccc	420
aatagatggg	tattatcaaa	atccatatta	gatatgctta	atgcaattta	tttttaccga	480
ttgtctcatt	gctttatcgt	catcatatcc	cgatattgcc	aaagttaatc	acattgctct	540
cttcctcatt	tataatagca	agatacctcc	tcaagctaag	ataggcaagg	atctaagttc	600
ggttatggag	ggataagtgt	tgtggtacat	catgactggt	gataggagaa	aattgtagta	660
ttggtcacgt	tgttactata	ggaggagtaa	ttcgaagtat	ccaggagtcc	ctgttatagg	720
aaataatgtc	cagatagccg	aggaagtgtg	gtttttggcg	ggataaccat	tggtaataac	780
gttgtatagg	agccaataca	gtagttaatt	ttcctgtccc	agacaatgct	gttttgaagg	840
caatcctggt	cgtattgtgc	atattaagga	aagtacatgt	tacatcattc	ctcaaactta	900
aaacctattg	ngaacaagaa	ggcttcaaag	gtgggatccg	tacgatggat	tgaactccag	960
gg						962

- (2) INFORMATION FOR SEQ ID NO:9
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 605 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...605
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

200200000	COOCCAACEE	aaagcttcgc	ccccatggc	ggcacgaata	tttcgataga	60
cacataagaa	ppgctttgga	aagacgagcg	accacgtact	tgataatgtt	ggctccccc	120
ttcacgacac	gctgtttcag	ttctgccact	gctcgttggt	cagcttgtcg	gtaccgatca	180
gatcogtcag	aggcgtccgt	ttaccttggc	cgtgctggcg	aaaacagcca	tetgetegee	240
atgactccat	aagtacgcgt	gttggtcacg	agactttgtt	tgatgccgaa	gtgctagcca	300
gttcgctttg	cagacgtgtg	ctgtccaaac	cggccaaagt	agtacctgcg	aaggcttcag	360
cccggagtag	ataagcgtaa	caagaccggt	gagtcagccg	gattgaagat	gatgatcacg	420
tocttacagt	cgggacaata	gtcttgatgt	ccttgcccag	ctgagcagcg	attteggeat	480
toccettgag	agatcctcgc	gggtcatacc	ctctttgcgc	ggagcaccgg	ccgaagaaac	540
atatatttgg	catctgtaag	agcctcttga	tgtcngatgt	aaaagtcaat	tcaggccttc	600
gaatc						605

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 688 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...688
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

- (2) INFORMATION FOR SEQ ID NO:11
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1593
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

```
ggtcgttcag ctccgagtag gcgttggcca actccttgcc attgaccata gctcgaatcg
                                                                        60
ctctgtcagc tccggattgg tgcggtgctc cttcgtcaag gcgacatttc tttcggatag
                                                                       120
tctgtgatga aagtaggctg gatatagtct tctcgcactt ctcgccgaag atctcatcga
                                                                       180
tgagcttgcc tttgccatcg tttcattgtg ctctacgccc agcttgtcgc atacctgacg
                                                                       240
cagctggcct cgttcattcc gctgatgtcg atacccgtat gctcatggat ggctcgatca
                                                                       300
tggtcactcg cttgtagggg gccttgaagt cgatcaattt ccccccacct tcatctgagt
                                                                       360
agtacccage acatecatae agatgegtte gacatetget cegtaaagtt cateatecag
                                                                       420
ttgtaatcct tatacgccac aagatctcca tggccgtgaa ctcaggatta tgcgtgcggt
                                                                       480
ccatcccctc tttcggaaat tgcggctgaa ttcatacaca ccatcgaaac cgcccacgac
                                                                       540
agacgcttca gatacaattc gttagcgatt ctcagataga gcggaatgcc agagcgttat
                                                                       600
gatgcgtgat aaaaggacgc gcagctgcac ctcccggatc gattggagta caggtgtatc
                                                                       660
cacttegatg tateegeact cattgagaaa etgegeateg aaatggaata eeategtacg
                                                                       720
cttgagggaa aatgttttga catgactatt gacgaccaga tccacgtatc gcttgacgat
                                                                       780
aacgtgctcc ggatccgtga agccatcgaa gacctcccca tctttttctt ttacacagga
                                                                       840
agggggggga tagctttcga caagaaagtc atctcctgca cagcaccgat atttctccca
                                                                       900
totgagtgog gaataogtao cotttoacto cataaaatoa cotatatoog tacaottott
                                                                       960
gaccaccgta ttgtagaact cttatcctca cccggacaaa tatcgtcccg agtaatatag
                                                                      1020
atctggatag cccctcagca tcttgcagct ccatgaatgt agctttcccc atgatacgcg
                                                                      1080
gctcataata cgtccggcaa tgcttacttg acgtttggcg acattctatc gccattgaaa
                                                                      1140
ttccttttga tctcggcgga ataggcattg acggtaattc cgctgcagga tatggatcga
                                                                      1200
tccccaaatt acgcagttgc tctaactgtt acggcgtacg acttcttgtt ccgaaagttc
                                                                      1260
gagtatgttc atgcaaaact tctaatttat attcccctg cagcaacttg cttgctctgc
                                                                      1320
tgctaaccga cacgatcgga gccattcgtc cgagggggaa aaaccttggt tccaaaggta
                                                                      1380
acttatttct atcagatacg ttccagaacc aaatcgataa gccctctata cttccctgat
                                                                      1440
aggaggtatt catcitticg gatticctgc tgcgatgata caacagaccg tgatggctic
                                                                      1500
gtgccccatc agggcagccg accggccaaa gaggagcttt ccatttcata gttcgtaata
                                                                      1560
cggctgcctt gaagtcgaaa gcctgtatct tcg
                                                                      1593
```

- (2) INFORMATION FOR SEQ ID NO:12
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1422
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

```
teggteatge cetecaeggt atgttteeeg eccageagta teetttgett eeggtaegaa
                                                                        60
tgtggcgcgt gacttcgtcg agatgccgtc tcagctcacg aacattgggc tatggatccg
                                                                       120
gaagtgtttg ccaactacgc taagcacgga agacacagga gcctatgccg gccgaattgg
                                                                       180
tcaagaagat tcaggagcga gcgacttcaa tcaggcttat tctatgggag aaaatcttgc
                                                                       240
agccgaagcc tcgatcaggc atggcatacg ctcacggtcg aagagncgga ggccttaccg
                                                                       300
acgtggccaa gttcgaagaa gaagccctgc gcaaagtcgg tcttacaatc cgcagatacc
                                                                       360
tectegetat egeteetett attteegeea taetggagea atggttatge ateeggttae
                                                                       420
tacgcttatc tgtggacaga atgctggatc acaacgttta tcaatggatg gtgcaaaacg
                                                                       480
gtggtatgac ccgcaaaacg gacaacgcct tcgggatatg attctttcgc gtggcaataa
                                                                       540
caggatttca acgtgatctt caccgcgttc accggtctgc aaaagcctac atcagggatt
                                                                       600
tgctccgcgc tcgcggtctc atgtaataca gcaatagcga ggctgtgctt tcaggttcca
                                                                       660
agatcctgca agagcacagc ctctttttat tcaccctata ccaaaaacga aacagctacg
                                                                       720
atgaaaaaag gagattactc atccttctga tcattatcct gatgttgggg cttatgcttt
                                                                       780
cccctggaca tcggaaacat tcaactccct cagtcgccat tatccttatt atacggtttc
                                                                       840
ctgaagtttg ccatcttggc taccatcggt gaagtactgg ccgacggatc aaagcccaac
                                                                       900
gatacacctg ccccacctat ctatgggtgc gattgtgata tggggcattg tcggtatact
                                                                       960
catcgtette aacttegggt gtacgaagee ggtatacgag gtateatege aagaggaetg
                                                                      1020
ctccccgact cgacagttcg gtctatacgg ctttccttat ctcttccgcc atgaatctac
                                                                      1080
atteggeeeg geetteatgg eegeecaceg cateagegat acatategga gaataaaget
                                                                       1140
acaggacggg gaggaagcat ccggctcgcc gttgaagagt ggattggaat cgctttatga
                                                                       1200
ctttcgtcgt tggcaagacc attccttctt ctggataccg gcacatacgg tcaccttttt
                                                                       1260
acttccaccc gagtccgcgt ctttgtggct gcactcctgt ccatcgctct gggactgatc
                                                                       1320
ttgccttggc ttcctcccga catgcaaagg cgtaaaacat cagggaccga caaaggattt
                                                                       1380
                                                                       1422
gataccaaaa tgatgaaaat gccatgaagg aactgaaatg cc
```

- (2) INFORMATION FOR SEQ ID NO:13
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 713 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...713
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

to a standard cacagattt	caccataccc	60
ggcagtagcc tgttcggcag canccgtggc ctcacgatcg cgcaggtttc	tccgttgtac	120
togtattoga gtgctnccac acgattggcc agctctattc gcgtacctta ctgctccgat gctatccaaa tacctttgct ctggagctct gctcttcggc	ggtcgttctg	180
ctgctccgat gctatccaaa taccttigct ctggagctet gctatogg-	80 4 0	

1

catggctttg	accttggttc	gcgtcgcttg	gcgttgagtt	ctccgcggag	ttgtacttcc	240
					aactcgtgcg-	300
		ccaacaaggg				360
ttgagcacag	ctatcagacg	cgcctgcacc	gggaagtgat	gatctcctcg	aaagccggca	420
ccacttcgcc	ggaagccgag	gagcgatctg	cacttctcct	ttgtccaccc	gccccaaacg	480
		gccttggatg				540
		atgattgagg				600
		gaatcggttt				660
		ccatgcaaac				713

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1244 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1244
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

```
ggcatgaatc agttcaagga tatcatactc ggaaataccg aggctaaatc actcgtgtag
                                                                        60
cagactegea gaagtgtttg egtgtaageg geaageacae gaeetegaag aggtaggeea
                                                                       120
tgacacctat catcatacca tgttcgaatg ctcggcaact ggtcgttcgg cgattacttc
                                                                       180
                                                                       240
aagaaagaag ccatcgatgg gcttgggaat acttggtgac ggtgttgggt ctggatcccc
                                                                       300
agogttotat gotacogtat togaaggcaa coccgaagaa ggcottgaco gogaaacgaa
                                                                       360
gcggcatctt actgggcaca gtttctgcct gaagaacgaa tcacaacggc aataagcatg
                                                                       420
acaacttctg ggaaatgggc gataccggtc ccgcggtccc tgctcggaaa tacatatcga
cctgcgttcg gacgaagagc ggcccaaata aacggtttgg agctgatcaa taagagccat
                                                                       480
                                                                       540
ccgcaggtca tgagatatgg aacctcgtct tcatgcaata caatcggaaa gccgatgctc
cctgacgcct ctgccacaca aggtgatcga tacgggcatg ggattcgacg tctgtgtatg
                                                                       600
gccttgcagg gcaagacttc caattacgat acggatgctt tcagcctctt atccgtactt
                                                                       660
tggctacgat gacgggaatc ggatacgtga ggattctacc tcggatatag ccatgcgcgt
                                                                       720
                                                                       780
agtageegae cacateggae tategeettt gecateaegg aeggeeaatt geeeteeaat
                                                                       840
gccaagccgg ctatgtcatt cgccgtatcc tgcgccgtgc ggttcgctac ggcacacctt
                                                                       900
cctacactgc cgcgaagcgt tcatgtaccg attgctgccg acctgatcga tacgatgggc
gatgcttatc ccgaattgca agcacagcgc gactgatcag ccgcgtgatc aaagaagagg
                                                                       960
                                                                      1020
aagagagttt cctgcgtaca tggaaacggg tatccgcctg ctggagaaaa aaatagccga
                                                                      1080
caataaggca ccggctccac cgtattggac ggtgtcgctg ccttcgaatt atacgatagt
                                                                      1140
teggatttee cetegacete acagecetga teetategga aaatgggtga eggtggacga
                                                                      1200
atcaggette gacaeggaga tgeagaagea aaaagaegtg eeegtaatge egetgeegta
                                                                      1244
gaagccggcg aactgggtag tgctagtgag ggtgaatcca aatc
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1845 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1845
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

```
togottgaag cagcacgcac atcatogtag otgataccca gttogtotac aagtotacac
                                                                        60
tcatctctct gctcatcctc accaaatagt tcagctgcta ttgcgcggat tgcgctgctc
                                                                       120
cttgccatct atatagatct gattattctg atgctcaatt cttgtccggg catacccaca
                                                                       180
cagcgtttca catagtgtcg cgtctgtcca cggggcggta aacgatctcc ccgtagaaat
                                                                       240
                                                                       300
ceggatacte caaageteet ecegteetae gagtttette cacatataat aateggattg
                                                                       360
ggctgcttga cggccaccgt atcgcctgca gggaagttaa agacaccaaa tccccctcct
                                                                       420
tgacgtgtcc gaaacccttc agtcgcttgt acgcaagaga ggtttgtccg agaacgattt
gccaccegte aatggeateg tttgtgegte ageggeacae egageggagt cataggegaa
                                                                       480
                                                                       540
cgcggtccgt cgaaagcttg ctcacgaaga ggtagtcgcc tataagcaag gtcttctccg
cgaagaagtc ggaatggcga agttctgaaa caggaaagcg aagataaagt aacggctacg
                                                                       600
acacagtaga taatgtctgc cacccagctg caaatgaccg aagcgtcttg tttcggatat
                                                                       660
                                                                       720
tcttatacca gccccatttg ataataggaa gaaataataa tctacgatca aaggcagaaa
aatcagccaa aacggccggc ccatatacaa aaaaggaggt aaagaatagt aatggcaacg
                                                                       780
                                                                       840
cctttatacg acgccatggc gtcaaatctt tccaatggaa ggtcatatcg ttatctgttg
                                                                       900
ttataagctg attaaatcgt tcatcgtcag aaagcctttg tggtggcagc atattcggca
                                                                       960
gccaacacgg caccaagagc gaatccctct caccaaaagc ttcgtggcat atcgtcagcc
                                                                      1020
gatccacctc ggatgtatag atatgctgtg cgtacccggg acttcgcctt ctcggatgga
ggtgatcgga gttcgttctc ctccggtgtc tccgtcagtc tccaagcgtc cagcgaggag
                                                                      1080
attoggotat caatoootog gooagtgtaa tagoogttoo gotoggaogt coaacttatg
                                                                      1140
tacatgatgg atttccgtca ggtgaggacg atactgtcgt gccggctcat caatcgggca
                                                                      1200
aacatacgac tgagcgagaa aaaaaattga ccccgatgct gaagttcgaa gcccagaaga
                                                                      1260
gggtctttcc ctccgtcggc agcgttcttc cagctcgggc agacgctctg tccacccgt
                                                                      1320
agtccgcaca ccaccggcac ggacttatcc atacagcgcg agcaattcgc atggccgcat
                                                                      1380
ccggacgggt aaattcgatg gctacatcgg ccgaacgaaa cctatcgaat cgaaacgatc
                                                                      1440
                                                                      1500
ttcctctccg gcatcgatcg tcagcaccac tcatgccctc ggctgcatgc aatccgttcg
                                                                      1560
atcacatgtc ccatcttgca taccctatca gtactatttt cataggattt tcttcttgga
                                                                      1620
aaaacgaacg tacccggccg caagggccaa aggtacacag atttagcgca agttcatccc
gtgatcttgc ggtacagatc cagcgcgtat atatcggtca tgccggtata tagtccagcg
                                                                      1680
tgcactgtat cttaccgtag aggetetect eccgttgttg tactgcgtae ttacccgact
                                                                       1740
                                                                       1800
gagcagcgtc cggctatagg catgtccgga ttggtgaggg cctgcatcat cttatctatc
                                                                       1845
agogoacoga atactgatgt coggoaagot coacatocac caogt
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1193
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

```
aaggcaacgt ggttgactgt atcgaatgcg gttcgtgcag cttcacctgc cggccaaccg
                                                                        60
tcctctgctg gattatatcc gccaagccaa gaagactgga tgggtatcca aagagcacgt
                                                                       120
aagcaataag aaaggaaata agcgatgaaa ataaaattat catttctcct tcaccgcaca
                                                                       180
tccacagcgg agacagatca aaaagaatat gtatggtgtg ctgattgccc tcttgcctgc
                                                                       240
cttggcatgt cggtatatca gtttggaatc ggtgcggtga tcgtaacggc agtancggtc
                                                                       300
ttaactggtn gcatcgngga atacctgatc agcaaatata tgtgggcaag gagcctacca
                                                                       360
tcatggacgg ctcagctatc ttgaccggcg tatgctggct ttcaacctgc cgagcaacct
                                                                       420
gcccgtttgg atcattatca tggtgcagta gtagctatcg cattgggcaa gatgtccttc
                                                                       480
ggcggcttgg gaacaacatc ttcaaccccg ctttggtcng tcgtgtattc ctcctgatcc
                                                                       540
tttccctgcc cagatgactc tctggcctac cgaaggacag atgacttcta tctggatgcc
                                                                       600
gagaccggtg ctacgcctct cggcctgatg aaagcagaat gagcggcgac acctcggctt
                                                                       660
tggctaatat ccccacagac ctgcactgtt tatcggtgaa gcaggttctt tgggtgaagt
                                                                       720
cagtgctatc gcattcttct cggattggtc tatatgctgt acaagaagat tatcacgtgg
                                                                       780
cataccccgt gtctatcttc gcatctgtga tcgtactggc aggtattctg cactggccag
                                                                       840
ccccacatcc ttcccggcca ctccgtggtt ccacctgttc tcggcggtat gatgctcgga
                                                                       900
gccatcttca tggccacgga ctatgtgact tgccgatgac caagtccgga cagatccttt
                                                                       960
acggctgtct gatcggtttg tgaccgtcgt gatccgtaca ttcggggctt atccggaagg
                                                                      1020
aatgtcattg ccatcctaat tatgaacggt atgacacctc tgatcaacac ttatatgaac
                                                                      1080
ctaaacattt tggaggaaag aacaaatgaa aaagctaaaa tcttcacccc caatatgttg
                                                                      1140
ctctctttga cgggcttctg tatcgttgtt tctgctctct tggcatgatg gac
                                                                      1193
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 756 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...756
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

ggttgtccgt	aaacgtggaa	ccgtgtctgg	cacgtgtatt	ggtcgtagga	aaccgacaat	60
					accacaaagg	120
atatacccct	tgcgccattt	ggccaaatct	ccagtggcac	taatgaagcc	tatggagaca	180
attcgcctct	tgctgacgtt	atgcctcaag	ttgggcagag	gaatcgatag	ccgccggtgt	240
agcatcaaca	acgtctatgg	gtatgtcaag	gcagacatgt	ttgacaatcc	tgtgcagcaa	300

				agtacagtet	ataraaaaga	360
ccaagatgca	ggagaaaaag	acggacttca	atctgaacca	agigigatic	atacaaaaga	420
		actactttac	pottatetec	cgagagtagt	cttgcgtgca	420
atcgaccgta	aattttaaaa	actactette	66000000	- and togeth	gaatttcagg	480
aaatacgtto	ctcatggcat	cccggcgtga	agccggatga	agguiggaic	gaatttcagg	
uuucuogooo		anttraaaaa	atacetagac	aatccggttt	ctgccggtag	540
gtagaaagat	agiciggage	ageceaaaaa		sattagtagt	acanotopat	600
gctctggccg	acagcatcaa	gaaggcgaaa	gctgacaatt	Callegical	acaggtggat	
gccccgg-a	tntnong	ttctattaca	aatcgcaaat	tattatgcca	tccctattcg	660
tcgtcagtca	tggaatacag	LLCLALCACA	uu coguuni		cctcgtacga	720
ccatttcgat	patgaaaaag	ctcctacaaa	gattcctacg	ggcgtttcgg	cctcgtacga	
CCaccegae	66- C	atanaatcca	ttacag			756
aacaatgagt	atateteteg	gtaaagtcca	ccacag			

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

	aagcattta	ctgaaagacc	tctatgacaa	tggcgagaaa	tcattcgaaa	60
acgaactgaa	aaguguuug	ccgaagas	totattaact	tctacaaccg	tttctcttcg	120
ccagcagngg	cagategati	Cgcccgaaa	testttess	ctctatcaat	troortater	180
atggagagtg	agatagccca	agagctgaag	tgatttttt	the et actor	toggotatgo	240
+actacette.	atccaaataa	cacagggtag	ggatteegtt	LIBULUBUUB	-99-9-9	300
0.0000000000000000000000000000000000000	taagccagtc	ggaaataaac	aagctaagca	Catggatggt	caces cace	
gaaageegga	agtgcgcctt	atcatagaca	ataatcatag	gtacaaccat	aaacagtaat	360
agaccaagaa	aguguguutu	ttottotog	agageeetge	tettegetec	ttaaggggta	420
gcaaatgaaa	ttaaaaagta	LUCLUCES	agageeeege	tcaggagat	ctggatcgaa	480
gccaaagccg	acaaaggcat	gggctcctca	acgaactcaa	Caggagaac	ctggatcgaa	540
tocgtgagct	ggctttacct	cccgtggatt	cgctctacag	tttcgacaag	ccgtccatgc	
4	00					549
atgcccgtg						

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...300
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

gagttctgct tttttagctg aatccaaata cattttcttc cgttttttac gtgttaaaca 60 ataactactt ccgctactac ggtcgtagat ctggccgcaa gataatataa ttccctatac 120 cacagcgcga atctgtttct tcgctctgtt ataacgatgc cgttggacgt acggatctac 180 attgggccaa gcattcagga aaggtgaact cgcccttctt tgcatttttg ggtccaaaaa 240 caagcaagaa agccgagatt ctatttactt ttgtgcactc tttgaacgaa aatncgctta 300

- (2) INFORMATION FOR SEQ ID NO:20
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 746 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...746
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

gaagcaaaat	ttgtcactgc	angcatgtaa	cagtattttc	tgcaaccgaa	tcaccgtctg	60
caaacttgaa	tcaaagagat	actaatcata	agcaattatt	tctcaataaa	ataatcatta	120
cttccatatt	tagtcatagc	tatcatggta	cttatttcaa	attcctcagc	cgcaacaaac	180
tctacacctt	cgttacatcg	taggctttgc	cctctcgctc	atattcgtct	tgctgcttag	240
cttcttgtac	ggcgcgaaca	gcaagccgat	cgtattcata	ccgattacaa	acgttctatc	300
agtacaatgt	cgagagtaag	aataactgga	gcggatttat	ctgtgctatc	ctgccggaac	360
gctcattcgc	gagcaggtac	ccgatgtgga	aggatatgcc	gcatcagcga	atacaacgac	420
aaggaataca	tctttatcgg	tccgacaagc	aaaacgggtt	gattgcctcc	catctttcgg	480
tcgaatccaa	ttctttactt	tcttcgacgg	ctataaactc	cttgagggtg	atcccaaaat	540
gtcctttccg	agcagaacag	tgccgttatt	tcctccgcgt	tggcagccgt	atcttcggta	600
acgtgtctcc	catcgggcag	gagatttcgt	ttttcgattt	tccaaaaaca	agcagacctt	660
tcggatcacg	ggcatcatgg	agccgagccg	gataactgcc	atatcagacc	ggccgaactc	720
cttttctatc	aggagccaaa	gaaaac				746

- (2) INFORMATION FOR SEQ ID NO:21
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1804 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1804
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

```
gcctcaatan agcgatcgga ctcttcctcg caggtgtggc agccgtgatg ttcccctgtt
                                                                        60
cgatacattc aacctcccac cctcgctccg ccctctcgca tcccctatta ttgggtacag
                                                                       120
gtgggaggcc tcttcctcgt cacggtatca atgccttcaa gcaattctat gacggcatga
                                                                       180
gcgatacgcg caccccatgt atattaccat atcgggcaat ctcttcaatg tcgggctgaa
                                                                       240
ctaccgctga tattcggcaa aggcggtctc cccgaaatgg gactcctcgg tgcggctatg
                                                                       300
ccaccetgtt gageegeetg etgatgeteg teaceategt cettteetet ategeagace
                                                                       360
ctcatggaca gcgatccgcc acgccttctg ccgcagatgc atatccgtcg cgcctaccgc
                                                                       420
cgcctattct ccgtcggact cccgttgccg tccagatggg actcgaatcg gcctctttca
                                                                       480
ccatcgccgt ctttttgtcg ggcgactcgg cgatcaggct ctggcagcac accagatcgc
                                                                       540
tgcgtcatca ccacgctcgg ctacctcgtc tattacgggc ttggtgctcc accaccatcc
                                                                       600
gcatcagtca cttcaagctg cacggcaaac ccgacgagtc cgccgcgtag ccgccactgc
                                                                       660
ctaccgaatg gccgctttga ctgcctcgtt gtggttgtac tgcttttgct cacacggcac
                                                                       720
agcttttcct tcctctcacg cccgacgaag aggtggcgca catcgttgcc cttacgttga
                                                                       780
tecegtigte gictaceaat teggagatge ectecaagee atetaticea atgietgega
                                                                       840
ggaatggage gegttegttt tetggeteeg geageagett tegecaegta ttgetggeae
                                                                       900
cgatactete etatttgetg ggattegtat tatateggge aataegeeca tgeagttgge
                                                                       960
eggtatetgg teggeettte cateageetg acactgeteg geatectett etacagetae
                                                                       1020
ttccggaagt aacccgataa actccgcaga ggaaagccct tgttcgtctt tcggggaaca
                                                                       1080
atcetttte eggtegeece tetecatttg etceatggeg getgtatgaa agtgaaaace
                                                                       1140
acagacgaag ccgaccgata ttgccatccc tttgcttctc ctctgtcgat aaagtgaaat
                                                                       1200
                                                                       1260
tcatttcctg aaaaaaacat gataatacgg agagaatagt atagtcttat ataagaggat
actatggtct catagagagg atactatggt ctcatatgag aggatactat ggtctcatac
                                                                       1320
gagggatact atggtctcac atgagaggat actatggtct catacgagag gaactatggt
                                                                       1380
ctcatatgag aggatactat ggtctcatac gagaggatac ttggtctcat atgagaggat
                                                                       1440
                                                                       1500
actatggtct catatgagag gatactatcc ctctatatag accccttagg gatgtactcg
                                                                       1560
 aagatacccc ttgaaacata aaaaggctcc tccgggaagt ggcaagccac ctgcccgaag
 gagccttgag gaataagagg aataaggcag ccggaggcta ctattcgttg cggaagagat
                                                                       1620
 tgatccgtct atgcaatcga tgaggacggg acgtgtactg tccacctatc ggccaagagt
                                                                       1680
                                                                       1740
 gccttgctca agctcgttga ggacgaatcg ctgcagactc gcttcacagg acgcgctccg
 aactgcggat catatccctc gcgaccggca aaggtcaccg acagcctccg tattagtgga
                                                                       1800
                                                                       1804
 gcac
```

- (2) INFORMATION FOR SEQ ID NO:22
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 999 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGÍVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...999
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

aggtgtggaa	gtcgcaggat	ctgaatatct	ttcagattat	ccagcgcaaa	gcaagggact	60
	_	gggacttggt				120
tttgagaatg	ccatccggca	gcgttttctc	catttacgga	tttccctctt	ctcttcatat	180
cggctatgac	caaacaagga	ttttcaaagt	gttggagacg	gtcaatcagg	tctatgcaca	240
ccgctgactc	gtattcccac	acacaagctg	aatgaagtga	tgctacccat	tatcaggcta	300
cgccaccacc	tgctaccaaa	ggtaaataca	tcaagataaa	atagtgatgc	agcttccgac	360
ggcagtgcct	tcatttgcct	tttttgccaa	tcgcctcagt	gggtgaaaga	gccttataag	420
cgttttttgg	agaatcagat	tgtgcccact	gggatttttg	cggtactccc	atcaacattt	480
ttatccgcga	aagtagggtt	tgcccctgct	caatacgttt	aagtcatcat	agaagaataa	540
atgatatgga	atggaaacgt	tttagatttc	tgaacaatgt	cgtcggttgg	gcgtttttgc	600
agttgcagct	atcgtctatc	tgatgacaat	cgagcctcag	ccagcctgtg	ggactgtgcc	660
gagttcatag	tctgcgtaaa	caagttgaga	tcggtcatcc	gcccggagca	cccttcttca	720
tgctcgtcta	taatacatat	cgcatttcac	gagcgatccg	tcacaggtgg	catggcttgc	780
caatctacca	gtgcactggc	cagtgccttt	accatcctgt	ttttgttttg	gacattaccc	840
accttgtccg	ccgcgtactt	gtaccgacag	tacgcaatgt	atcggattgg	aagagccgtc	900
aaggaaaata	tcctttccac	gagtaatcac	gtactcggca	gtggagtcgt	tggagccttg	960
gtctatacgt	tcagcgatac	ttctggttca	gtgccgtcg			999

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1132
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

gctcatgcac	caaacaatac	aactcttcac	tctgcttcgg	cgtaagcgac	ccatatcgaa	60
ccacaactcg	ctgacagggc	cgtagcccgt	gaggatcttc	tgacctgacg	catattgtat	120
tggtgatgtg	ccggagtaat	ccgatcacat	tgtgatcgct	gatcggattg	gcttccggga	180
aatgccaatc	aataaggaga	agtaaacgcc	gaacttcata	cccgaacgct	cacaagcatc	240
gctcattcct	tcatcacatc	gcgacgcgaa	ggagtggcct	ccactatatt	gaatgagtct	300
cagccgagcc	atacatgcag	aagccatcgt	gatgcttgga	agtaacacga	tactcttcat	360
ccctgctttc	cgagctaagg	ctactatggc	atggcatccc	atctgtcggg	gcggaaccgc	420
ttggccaccg	gctcgtattg	ctcatgtcgc	gtattccgaa	agagtagatc	tgttcgctat	480
atccgttctt	actggtttgc	cttgccaaac	ccctccaagc	tcactgtaga	agccgtaata	540
atgaaaaggc	tgaatttgtc	acgatgccaa	cgctcgaagc	ttccgaattc	gttgagccac	600
gaggaataga	gacgagaaac	aaacggctgc	cagtgacgca	ggatacggag	gaaacgggtc	660
ttattcatca	tttattttgc	agcagggtgg	cctcttcttt	gcctttgaga	tagcggtaga	720
tagcagcttg	tgctccaccg	gtttctcatc	gctattgtgt	ttgtaaatgt	tgttgagaga	.780

				+-+	atantantat	840
agaacgatcc	ggcaagcctt	gatattgtcg	cgaagctgga	CCCCaacac	gtcataatct	
26226			aggeagtete	gagcogttot	atagattgcg	900
ctcttcgtaa	agcaggatec	agcacagggc	aggeageece	646-66-6		0.00
cttcatccag	tcggccgaag	agatgaatac	ccttctttcc	ccccgttgtg	gaagcaccag	960
Cilcatctag	CCEBCCEAGE	agacgaasas		neatatatta	caactetata	1020
atacggctat	gctccaaata	atatccacca	atcgagtgac	acguatatig	cgactctgtg	
		agatacette	gcacgatcag	atcgatctnc	acaccggctc	1080
gcatatcggt	accaaacagc	agacaccccc	Beardaran			1132
GG 2 2 GC C C G 2	tagagetgtg	tgatgaccat	tctttgtcct	gcaagccgtt	са	1132
854465556		0 0	-			

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 665 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...665
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

				ananatatta	tetteagaac	60
attacaagga	aacctcttga	tcgtaagcgg	atcggcagac	gacaatgtta	CCCCagaac	
accatacttt	ttacagaggc	actegttcag	gccaatatcc	cttcgacatg	gctatctata	120
acgacgeeee	ccacagagge		*******	testetetat	actogcasag	180
tggacaagaa	ccatagtata	taccggggga	ataccegeta	tcatctctat	accegeaaag	
caaagttttt	gttcgcatct	tttantacag	nttttctcag	ttgcttgatg	gggcgagtgg	240
	b t t at t a not	tactccattc	gacagtggtc	totaataget	ctttttgaaa	300
cgaaggggtt	ttigittatt	LECTICE	Bucagegge	tctaatagct	- 1	360
aaactatggc	gcaacacgtc	aagaaacccg	aatggttgaa	aatcgtcttg	gtgggaatga	300
	gagactasas	acattatoa	ggacattgtc	tgcatacgat	ctgtacaagt	420
gaagtttact	gagactaaaa	gcattgccga	Secure			480
ggcaaatgcc	ccaatatggg	aagtgctgga	gtagggggac	tgctaccttc	atgateggeg	
stantateta	acacatacct	atrostttto	caacacttte	acggggcgtc	ccaaaccgcc	540
gigalattig	acacgegeee	Beegaeeee	· · · · · · ·		annost set s	600
aatgaagcag	aacctactca	cgtcgcattg	agtatcaaac	tgatggggtt	aaccatgctg	
+aataacaaa	cattaaccac	gatgacttgc	ccgattaggt	gccgcacact	gggttaagac	660
rggrgacgag	CECCERCE	6446444		0 0	300	665
cattc						005

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

```
tttttgaatg tctgccggac tgagatttga tcgtaatgct cttttgggaa ggtgatattc
                                                                        60
agacagtegt atgtggageg aateetatee agaeteteeg gaetgetgea teggggagte
                                                                       120
ctaccatact tgagatagca acctcggtga tattgacttc gacggtaacg gtaagggcgt
                                                                       180
ctatgctgtg cagagcgcgg caaaggtctt tactaacata ataaagaaac agggtgcgaa
                                                                       240
aggacatcgg agactgtagc ttgcacggcg gctacggata tttccggctg tgtcatgtgg
                                                                       300
atagtatatg gaaggetgte tatgecatat egetegagaa gtgegatace tgteegatae
                                                                       360
tatccgatgc cacacgtccg ggcaaagcca actcctgatg agtttacgga gagatgagtc
                                                                       420
cggtgcaaag agcgagagag tagggtttcc ggctttgtct ttccttcttt atctctccat
                                                                       480
actttcaatg tgtagcggta gtggagtcag gcttgttcgt gaagagcaaa agcacatctg
                                                                       540
teceetatae caggaaagag tgaaagateg etgateaata teettgaeag gaagteegga
                                                                       600
gccaaacggc cgactgcgta cgacttattc cggctaagat ggaatcaaga gacgggggaa
                                                                       660
gccggtgcat cgagataccg gagcgggaat gaggtctatg tcgaaaaggt cgtattcctc
                                                                       720
cgctaatctg tttatccggt ggcatcggga tgggaaagat agaagtcaag ggctttgagc
                                                                       780
cgcagtctct gaaggctttt gctttggagg ggaagtcggt ggttcggaga tgacctgata
                                                                       840
gcgatggatc tcttcttctg cagtttgcat gaactcgttc aggtggcatg tgtacttcct
                                                                       900
ccttttattt taggcaggag gggttggtcg gatcgagagt gattttaata tcttctcct
                                                                       960
tttcaggata gagccgaagc cgttattgcc ctcgttgaaa tataatagaa tgcgactaac
                                                                      1020
ategeettta tttegtgteg aatetgtgee ttgggegaag taaegtgtat etettetgge
                                                                      1080
gaaaggagcc ttccccttca attcgcagag ccagaaccga atcgcctggc tgagattgga
                                                                      1140
gagattcagt ttgaggtggc aaacatcaga tgctctctgc atgaaagaga aaggagcagg
                                                                      1200
acaaaacctg ctactatata atatatatgt tggatggctt ggacattggg acggagtgtt
                                                                      1260
tcatgattcc gtagaagtcg gagcaggtat tcctctacag tttccggata gtgtgcatat
                                                                      1320
tccaagcgtg gattctttgg gccagcgtat ccggagtatc ttccggaagg acggacagac
                                                                      1380
tgcttgacgg aggattttgc cgtggtcata atgtccatcg aaagatgaat ggtgataccg
                                                                      1440
ctttcttttt cccttgcagc aaggacggct cgtgtacgtg atgtccgtac attccttttc
                                                                      1500
cgccgaactt gggcaataag caggatggat attgacgatc ctgtcgggga aggattccaa
                                                                      1560
gtagggtggg ttatataaca catatagccg gccagcacga tcaggtctat ccctaatctt
                                                                      1620
tcaagagggc aatgggcttc gatccttcga gcatctcttg ggtagtaacg aataagccgg
                                                                      1680
tattttcagc cgatgggcac gtgccataac tcctgatcgg agtgattgct gaggatcaca
                                                                      1740
gccaagettg ccgaacetet ttggcaaaga aatgacacag attttctgca tttgagecat
                                                                      1800
taccggaagc taaaccgcta cttttctcat tttatttact atttttgctg cacacaaga
                                                                      1860
gttgattgtg cagattttct ggcgctgata atggactaac acggtatttt cgtgctaaat
                                                                      1920
ccgctaaaca gcgctaaatg aagcacaaat ataagtaaga gattattagt aataaccatt
                                                                      1980
ttaaagaaca agactatgtc tgaagtagaa aaaaagtgat cgacctcgta gttgacaaat
                                                                      2040
tgaatgtaga agcttctgag taacgcgtga agccagtttc tcaaatgacc ctcggagcca
                                                                      2100
gactetetga tacagttgag ttgatgatga atttegaaaa ggaatteaae atgtetteee
                                                                      2160
tgacgaccaa gcacaggaga tcaagactgt cggcgacgct atcgatatat cgaaaaaaaac
                                                                      2220
ctgaagtaaa atactccgat ggaactgaaa agagagtagt aacagggtta ggagccatta
                                                                      2280
ctccgcttgg caactctgct cccaaacgtg ggaaagctta gtggcaggca
                                                                      2330
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 557 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...557
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

ggggacacgc	atcagtctgc	atagctcggc	agagaaggtt	tcacgcgtcg	gcgaatgccc	60
agcgatccgt	ccgaagcgat	gagtgccggc	gccacgcctt	ggcctgagga	tagatgatgg	120
tcagcggttt	ggtcgtcagc	tcgatcaatc	ccaggccaac	tccggcactt	cgtccatgag	180
goottggago	ttcgctccga	atcgatgaag	gaccaagcat	gctctngctg	teegetettt	240
ctttcgccgg	taaatccgct	ggacggcttc	ttcgttcgtg	gcatcgcagc	ctatccccaa	300
atggtatctg	tcgggtaaag	gatgattccg	cctttgcgca	tgattcggcg	gctttcttcg	360
cttcacttct	ctgaatatcg	ttgagcatat	cgtgggtata	tctctatttt	ttcgagagag	420
ccgagtgcgc	tcactccttc	agggcaaaag	tatgaatatc	tgccgtatca	atgctttaat	480
atgtcatttc	tagtcttcat	cggttatttc	tgtctgtttc	tttattttat	aaatgatcat	540
tccggccgga						557

(2) INFORMATION FOR SEQ ID NO:27

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 672 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...672
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

ggctgcaagt	atcgcgtccg	gatcagtgca	caacggtatg	gtttcattcc	atcgaatgct	60
gttgtttac	ccegtcatca	gggagacgat	ttgggtggtc	acagctgatg	tattcccgtt	120
tooragaaag	caaactttcg	cccaacggct	gtcgcgtatc	ctctactccc	acaagcagat	180
gaatcagcag	ttcgacggaa	gcaaaaggaa	cgattactat	ccatacaggc	aaagctgttt	240
tcctctacga	caaggaacaa	caacctgctt	atcgcacttt	cgagcagtat	atgcgtggga	300
aaacatccct	aagtatatgo	tcaacagcca	gcaatcatgg	cgatcttcgg	attagatacg	360
gtttgtatgc	ttctcgataa	ggaattgctt	gatttgccta	ctctcttccc	ttcgaatacc	420
gctacggaaa	gcgtatctat	gtgatatttg	tcgtgaactg	tatggcgaga	aaggcatttc	480
tttttcggac	atttgaacct	gcatggcatt	atctcttctc	ctgtttaccg	actcaaacgt	540
ctctaaagcc	tttgcttcga	ccatttatac	cccgtccttc	gatttggaag	gcgatattat	600
ceetttteea	acggatcatg	caacctgtat	taccgacggt	agagcaagga	cgacgtttcc	660
acccgacatc		J				672

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2497 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...2\overline{497}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

gcctatctct	gtgatgacaa	agtcggtact	gactcttttg	tcccaggagt	tgacgttgcg	60
cttgatctca	tccgtaatat	gaggcaccac	ttgcacggct	tgcccaagta	ctcgcccttg	120
cgttccttgc	ggattacgtt	ctgatagtcc	tgcctgtcgt	gatattattg	gcacgagtag	180
tgggcgtatt	gaggaacgct	catagtggcc	gagatccaaa	tcggcctcat	gtccgtcctc	240
ggtgaatagc	attcgccgtg	ctcataagga	ttgagcgtac	cgggatcgat	attgtatagg	300
ggtcgaactt	ctgaagagct	acgttgaaac	cgcgagcttg	gagagtttgc	cgagagatgc	360
tgctacgatg	ccttttccaa	gagaagaaac	caaccaccgg	tcacgaagat	atacttagta	420
tctgccatag	cgcgaaaaga	tgtattgttg	atactttgat	cgataaatca	ggggtacgga	480
aagctacccc	aacggaccag	cctcctccga	ttcgtgcgca	aatatacaaa	aagaacgccg	540
ctaaaagagg	caaatacgac	agctcttgcc	cgatgccggc	acatcaaatg	agaaatgagg	600
			ggcaaattac			660
gcggttcgta	aattctcgaa	aacacggcga	gattttttcc	gttttggttc	gggaaacaaa	720
aaatttacgc	gccaagcgaa	aattttctcg	cgccacgttt	ttacgaacga	caatggagcc	780
gatttggaac	cgagacggca	atatgagcag	catgccccac	gagtcgtttt	ttctctcgca	840
ggataaggta	tttccttagc	tggataagaa	ggaaatgaca	ccaccgattc	atagcaaaaa	900
gcatggtttt	cattccgaca	acaaggtgtc	aatgatgagg	gcaaactcga	tcgtaatgct	960
gccggcacgt	tgttcgaatc	gcacctgcga	tcaaagattg	gctgtttggg	aaaaagcata	1020
taaatttgga	ggaaatttca	gagtttcact	cctaatacta	catcagaaca	tggctgtctc	1080
atcaatgaag	tttccaggac	gttcggcgaa	tatcttctta	ttcccggctc	actacagaac	1140
agtgcactcc	ccaaaacatc	tctcttcaga	ctcctccatt	aagttcaatc	gcgatgagag	1200
			tcggccatca			1260
acgctggcca	tcgattggca	cgcaacgggg	gactttcgtt	tatcttcgga	tcgcagagca	1320
taggagtcag	gccgaaatgg	ttcgtcgtgt	aaagaaattc	aaggccggat	tttcaccagc	1380
gattccaatc	tcagaccgga	caatacgctg	gccgatgtat	tgatctggtc	aaaaggacag	1440
gacataataa	tataggtatc	actcacgacg	ttcgtccaat	ggccgtctga	tgggtatcgt	1500
cacgagcaga	gactatcgct	cagcacggac	tcaccctcga	agccggtcaa	agattttatg	1560
acgccgttga	gagacttacg	gtgggcaagg	tcggtattac	gctgagcgaa	gccaacgtat	1620
tatttgggaa	aacaaactca	atacgctgcc	gatcatcgac	gaaaatagaa	tctgcagtat	1680
ttcgtcttcc	gtaaagatta	cgacagccac	aagaaaatcc	gctcgaactc	tccaactaca	1740
cggacaagac	cctcctcgtg	ggtgcggtat	caatacacgc	gactataagg	agcgagtacc	1800
tgcactggtg	gagccggtgt	ggatgtggtg	tgcatcgact	catcggacgg	ctattccgac	1860
tgcagagcaa	tacgatccgt	tggatcaagg	agaaatacgg	ggacagtttg	ccgtaggtgc	1920
agggaatgtg	gtcgatcgcg	atgggttcaa	cttcttgacc	aggccggtgc	ggacttcatc	1980
aaagtaggga	tcggaggagg	ctccatctga	tcacacgtga	gcagaaaggg	atcggtcgcg	2040
gtcaggcaac	ggctgtaaag	acgtagccaa	ggcacgtgac	gactattacc	gacgaacggg	2100
cacttacttc	ccatctgtag	cgatggaggg	ctcgtacatg	actaccacat	ggtgctgcat	2160
tggccatggg	tgccgatttc	ctgatgatgg	gacgctattt	cgctcattcg	acgagtcgcc	2220
gaccaagaag	atgaagatag	gcagcaatat	cgtcaagaat	actggggcga	aggatcgaac	2280
cgcgctcaga	actggcaacg	ctagacagcg	gcggcaccga	gacgctcaag	ttcgaagaag	2340
gagtggacag	ctcgttccat	acgccggtaa	gatgaaggac	aacctgctca	tcacactcgg	2400
cagatcaagg	ctacgatgtg	cagttgcggt	gtcattacca	ttcccgagct	caagagaaag	2460
ccaagattac	cctcgtgagc	agcaccagta	tcgtcga			2497

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...630
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

		ttcatatcat	toacocaagt	ccatcgaaga	60
cgaggtagcc ctgctttgtc	tgtccactca	LLCatatoat	-646666-	cttcgaatat	120
	- ttcatcttgc	P C C C C C C C C C C C C C C C C C C C	gcaagcaccg	0 0	180
+ + catacaa	agggtaccca	agagggttta	ggcacacgc		
ctgtcccagg cccatacgg	, 4666	gcacgatttt	ggacacaata	cctttatttc	240
ccgtctgcga ggaacgcata	tectetigae	gcacgacce	bbattageta	tataacttto	300
	- coccaactte	gatettege	LLCCLESCUM	200	360
AAAAAA AAAAAACCAAA	· acceatter	CCCCCEarge	LCLALCLAGE		
gtagttcagc ttcaatctco	. ++aaaatact	togataatto	accgcaacag	ccttaatcaa	420
gtagttcagc ttcaatctc	Liggagige		tcacattgaa	atcaagagct	480
	- forccaatca	CLLAALLEEA	CCaca cc6		540 ~
+++aacaaa	- ++0c+0cc00	ccttaattaa	CCCaacaccc	446-46	
tacgccacag caggttttg	ctttaatcaa	gttctggtag	cttgtcgaca	gacgcttcat	600
tacgccacag caggiring	CCCCGGCCGG	8000-00-0	0 0		630
gaagtggtgc tgccttttc	g cgtatgtttc				
0 0 0 -					

- (2) INFORMATION FOR SEQ ID NO:30
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{3}22$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

		anagastata	ggtacgtcgt	gtccacgaat	60
gcaaactctg aatgatccgt	ccgcacatag	Caccgacgca	gg cac g co g c	eseastetes.	120
	cccctaaaga	aarocotaut.	alliackace		
ctcagcitcg ccargoauge		2422222	* hoogtacaga	cagatgatgg	.180
gcaatgctct tgccaagaga	ggtcttacca	Crcccggagg	Propression Pro-	- 0 .0 .0	

```
gcgacttcat atcgccttca tcttgaggac agccagatgc tctatgattc tctctttac
                                                                       240
tttctaagac cgaaatgatc tctatccaaa acggattggg cacgcttcag gttgaattat
                                                                       300
ctttactgaa tacgccccac ggcagactga tgatggtctg tactactgca tctgtacgga
                                                                       360
gtagtcgggc gattgaggat gtagccgttc cacttgcgga gttctttttc gaaagtttct
                                                                       420
gctacctcgc tgctccactt ctcgtagcag ctttggtacg cagctcctgc acctcgatgt
                                                                       480
cgtttatatt ccacccagtt cctcctgaat cgtcttgatt tgctgctgca ggaagtactt
                                                                       540
ttctgctgct tgtccatctc ctcgcgcgtc ttcatctgaa tagaagcttc agttccatta
                                                                       600
cctgaagctc cttgtgcaac aggtagagaa gacgatacca cgatccttca tcttgctgat
                                                                       660
ttccagcaat tcttgcttga cggctagctc gtggatatat tggccgatgc aaagttgatc
                                                                       720
tgatacatcg gattctgttc cgtctcatcg agaggataag ctcccgaggg ggtctctcga
                                                                       780
ccatagctcc atcatcttca gactcatatc ctgtatggtg gagacgagtg cttgaactcg
                                                                       840
tgatctttgt tcttcccggg gagaatgtct gggagcagct tccgcgaccc ttcataaaag
                                                                       900
gttccgtagc cgttatctcc tgcagtgcaa acgctggcgg ccttgtacga tagccgtggt
                                                                       960
agtaccatcg ggcatctcca caccctgatg atttcagcca cgaccccgac atcatacaaa
                                                                      1020
teggeacgae eggtteetee acatecatat egegetgtga aaeggeaceg aaatagaece
                                                                      1080
cttcttctcc acgtagcgga tcagcttgag tgatttttct cgtccgacat gataggcatg
                                                                      1140
                                                                      1200
gccacaccgg ggaagagaat catattgcgg agagccaaat cggcatctcc tcctgcatat
gatettettt cacetgaaat ceteacttet teacaaaegg aaageaeegg aaagaataeg
                                                                      1260
                                                                      1320
gggaaccatc atcccgtcgt cctctccagg cgtatatatt tctatcatca tctttagtct
                                                                      1322
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...454
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

catccccggc	aatcccagcc	acatatacca	gaacataggg	gctacaactc	atcgctcaga	60
ttctccgaca	aagtctccaa	agctgccgtc	ctgacttctg	cgccgacaga	gcagccgtat	120
cgcgccctac	gattcgcgtc	acctgttgcg	cccttcttca	agcgaacgat	cgactgcttc	180
gaataccata	cgtactcacg	aataagggta	gtacctgcca	aacagaagaa	aatggccgat	240
agccaaataa	gagaagccac	agcaaatgca	acagcaatcc	ggaaaaaatc	gtccgcaaaa	300
tggtataaac	acagacaaaa	acaagtccca	agaggatcaa	taggtcaaaa	gaaaaacggc	360
aacgatatag	aacaccgaca	tgaaggcgcc	ttcacctgcg	gtagtttcct	ttattcaatc	420
tttctctccg	atgcaatcat	ggaccgaagc	cgac			454

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1317
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

```
tcactctcca cttcgagcat attgcccgcg aagtgctcca cctgctccga ctaatggcta
                                                                       60
tgatgcggtg tccgttagcg gtcaggctat tcaccaccta ctgcgctcgg cttcgtccct
                                                                       120
gatgcactcc aaacaaacga togcatacgc gaagccacac acatcatcac attggtatga
                                                                       180
tagatgggag caccatcgca tctgtggcgg taaaaatcaa tcctttgtag tccaattccc
                                                                       240
gacaaattcc tctaatacct tcggattggt acgttcggaa gagcagcagt aagcatacga
                                                                       300
ttgaccctgt ccaataccat actgcccgtg ccttcgagaa aacattgtcc cgctcgtagc
                                                                       360
cggagagatt gatgatacga tccaccctt cctttcacca acagtagcca gtacgggcaa
                                                                       420
tttccgctct tgctgcctgt tggtgcatac atgggataaa gcaccaattc gcctgtgaca
                                                                       480
tgcgtgctga ccaattgttc gggaatatcg aatccggtgt atgaggtgtc ttcgaatccg
                                                                       540
aatgacccat acatctaccc cgtattcgcg caatagattg acgtagtttc aaactctttt
                                                                       600
ttcgcttccc ttgctactgc ttcgggtact cccgtttttt ctggaagctg ttgtttctgg
                                                                       660
ccgtttcggc attaaatcca aaaagaccgg gcgcaccatc agcacccggt tcgtggcctg
                                                                       720
cttgcgaata agagcatgaa tggttactct aaaaccttga tggattcctt gataatctcc
                                                                       780
acggttgcgc cagctcctca cgtgtgatac aaagtggcgg agccaagcga atgtatggcg
                                                                       840
atgcgtcggt ttggccagaa ggccgcgttc ggccattgcc tccacacgtc ccatgcctcg
                                                                       900
tgtctattgt gcggttcgat gacaatagca tgagcatacc tcgtccgcgg accaacttca
                                                                       960
atagaggget cttgattttg gcaactetee tetgaaatae tgeeceaget ceteggetet
                                                                      1020
ctccggcaac gttcttcttt taccaccgta agggcagcca tcgccacttt gcaggcaagg
                                                                      1080
ggaatccccc gaaagtggaa ccatgctcgc ccggcttgat cgtaagctaa cctcatcgtc
                                                                      1140
tgccaatacg caacttaccg gcaatacccc gccggaatag ctttaccgag cacaacaata
                                                                      1200
tegggacgaa egteateatg ategegeaga geateegtee egttegtgeg ataceggtet
                                                                      1260
gcacttcatc agcccaaaga gggcatggta cttgcggcaa agctctgcag cacgacg
                                                                      1317
```

- (2) INFORMATION FOR SEQ ID NO:33
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 895 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...895
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33 **

```
60
ggaaaacagt cggctgtacg cttccacctc cgccacgtcc gcacacaggg gatctgatcg.
gaaggatgac gggcaaactg atgatgaagc cggaagagtt tcttccctgt tggccgactc
                                                                       120
                                                                       180
cgctttctgc gattcgctgg gattcgacca cactccatcc gcagcctttt tctgcccgaa
acatacgaag tggattggac attaggccaa aggacttggt tctgaggctg aaagagatac
                                                                       240
                                                                       300
tacgacgcta ttggacagca gagcgacgga gtctggccga ctcattgggg ctgagccgat
                                                                       360
ccaagtatcc attatcgcat ccatcgtgga ggaggggtcg ggaaatccga tgaatacccg
cagatagecg gtetetatat cegtegettg eggaggggat getettgeag geegateega
                                                                       420
cggtgaagtt tgcgatggga gcttttccat ccgtaggatc ctgaatgtcc atttgcagac
                                                                       480
                                                                       540
ggattccccg acaacactta taaaaacgaa ggactgcctc cgggcccgat ccggctaccc
ataccgcgac catggacage gtgctccgag cggatcggca tggctaccgt atatgtgtgc
                                                                       600
caaggaggac ttctccggcc gtcaccgttt tgcccaccct atgccgaaca ccaacgcaat
                                                                       660
                                                                      720
gcggctctct atcgcaaagc actcaagaaa gggggatcaa atgaccgaag aaacggaaaa
gcccctcatg gacggagttg ggatgagagg acggagctgc tcataggcac ggaagcagcc
                                                                      780
gacageteeg geactegeat atactgateg teggeacegg eggagtagge ggcatgeage
                                                                      840
                                                                      895
agagatgete tgegtgeaga gtgggeagae tgaetttggt ggtgeegatg tagtg
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 685 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...685
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

gcc	gtctggt	tgaaaagggc	aagatgtctg	ccgatgagca	gcaagccgta	tggctcgtat	60
ccg	tacgacg	atggacttca	atgacctgaa	agatgccgta	tcgtgattga	agcgattgcc	120
gaa	gaaatgg	aaataaagaa	acaggcctca	gtgctgtggc	ggaagtggta	agcgagcaat	180
gta	tcatcgc	taccaaacat	cttcattgag	tatcacagct	ttggcaaccc	gaactcccta	240
CCC	cactcgt	gtgatcggaa	tgcacttctt	caatcccgtt	cccgtgatga	aactgtagaa	300
gtt	atcagtg	cccagcaaac	ttcggacgaa	gtgatgaagc	aggactggac	ttgtgcgaaa	360
tgc	tcaagaa	aacagccgta	cgcgtgaacg	aactccgggt	ttcgtcgtaa	accgtcttct	420
cata	accgatg	atcaacgaag	gatcggagcc	tatgcccgac	ggtgtggcca	gcatagagga	480
aat	agatcag	ccatgatgct	cggtgccaat	cacccgatgg	gccctttggc	tttgggcgat	540
tta	tcggttt	ggatgtctgt	ctggctatca	tggaggtatt	attcaccgat	tggtgatgcc	600
aaa	tatcgtc	ctcatccttt	gcttcgcaag	atggtcggca	ggacagcttg	gccgaagacc	660
ggc	aaagctt	ctacgactat	agcaa				685

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1591 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1591
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

```
taagatteet eegatgatat taeeettgtg eectacagee gtagettgge gaaatgaggt
                                                                        60
atcicattgt aggggatgac ggtcttgttt tcgatttttc ggccagttcg cctaagccgc
                                                                       120
tacccagtat tatagccgtt ttggcatgcc cggtagacga gaggacagga aagatgctgc
                                                                       180
ctcgtggtaa tgctgtcttg gagtttcata tgcggtatgc ttataatttc attcgtgtgt
                                                                       240
tttgtggcct ttgccatcag tttgtatgca gcttcagctg cgccggccaa tatgcttcct
                                                                       300
ctccgggtac tttacgtccg cgcatcagga tcttcccatc tacatagtcg tatccactgc
                                                                       360
                                                                       420
actgctattg gcagaataaa ccaagttgga tagaagttgt gacagggagt catttccggg
                                                                       480
atgtccagac gtatcagaca cgatctgcca agcgtcccgg agctatgaca ccggtatccg
tacccatgat cgagctccat ctactgtcgc actttcgtat atgtcggttg ctttcactgt
                                                                       540
gtagcatccg aacgccaagc tttgccgaga aaggcggcca gcttcatgcg atgatcatat
                                                                       600
                                                                       660
ccaaattgtt ggaagaggag catccatcgg taccaagcct atgactattc cgcgcttgcg
catctcgtca tagtggaagc ggtagcggag gctaatttca tattcgacgc ccggattgtg
                                                                       720
                                                                       780
taccacetta cageetgage tgecageaag tecattteet cateatecag ecagatgeta
tgagcaagat tagttgggcg atagtatgcc cagtttgtgc agatacctga cagagtggta
                                                                       840
ccgaacttag cgatgcagtc ccggacttct ccttctgtct ccataggtgc aagtgtatca
                                                                       900
                                                                       960
gcacattttt ctcattcgcg aagcgatgac aaattgcaat tgctctccgc ttacggtata
                                                                      1020
aatggcatga ggtcctaccg aaattggatc ctgtcgctat aggagcagaa tgcttcgtgc
                                                                      1080
agactgtaga gcgttctctg tcgatgcgag cccgctcctg atctcctctg tcgaagaggt
ggatgatagt acggcacgca agcccatctc ttctactgct cgtgctgggc aagggtatga
                                                                      1140
                                                                      1200
gcgtacatgt cgaggaaagc agtcgtaccg ctcttgtcat ctccagacag gccaatttag
aaccccagta gacatettee tetgtatetg tgettecace ggecatatee agtteteaag
                                                                      1260
                                                                      1320
ccaatccatc agtccagatc atcgccgtag cctcggaaga tagtcatggc cgaatgagtg
                                                                      1380
tgaagttttg caacccgggt ataacggcca tggaagaggc atctataatt tctcggcatg
                                                                      1440
acagocaato googgagoaa cotocacaat acggttgooo tgatootgat atcotgaogg
                                                                      1500
acaccttcca gcagtgcctg ttttatcaat tgcccaatgc agtattcttt taatgaaaga
                                                                      1560
gggtgcgaca ggatttcctt tgccctgtat gcaccctcta cggtttcttc ttacttgtat
                                                                      1591
atgcggtaaa ctcggctacc gattcgattc c
```

- (2) INFORMATION FOR SEQ ID NO:36
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2239
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

```
tcaactatcg tccggattcg tacgttctca ttcctcgcgc tttgtacgag agggtagagc
                                                                         60
 cgactattgg ctgaggactg ccatccacct gccggacgag gcaagggcgt agccgtcatg
                                                                        120
 gagtacaacc tgcctcatca ggataagtgc tgattttggc ttgggacaaa gcctcttcta
                                                                        180
 tgaattncta agaaggcaca gatcggaaca gagttcaccc ccggctttat ccccttttc
                                                                        240
 aaagaacgga gcgacagagc aggcaacata cggccaaaag agttgccctc aatcccggca
                                                                        300
 tgacaaactc gacctcttcg tattcgaagg aggtagtctg ctcttgccaa tacatacagc
                                                                        360
 ttcacggaca atcaaggcgt tcgctccatc gagaggaagt ccttttctat ctggtcaccg
                                                                        420
 tctggaagag cttacggttg gtatagagca tgaccgtatc gttatctgta tccaacaaaa
                                                                        480
 tatccgcgac actctgtcgg aaaagatgat ctcaggcaaa tattggagcc gttcttccgc
                                                                        540
 atatcgaact gtgcaaagag ccggtgtaac gccatattcg aactctctct ccacttcttc
                                                                        600
ccctatgcgt gtaatcagag gtaaatacgg acacagggtt tcgatgtacc caaaagcttc
                                                                        660
aatgcccgtc ctacaacgga ttttgcaaag agaacctctt caacatccta tccaaccgtt
                                                                        720
togatttoga aggacttogg ctatogacot attotooggo acggggagta tagcattgga
                                                                        780
attatatete ggggttgtte tteegteact teeatagaaa aacgeegtga geageageet
                                                                        840
ttattcgcaa cctcattaag catctgaacg aagaaaactg ctgagagtct tcgagacgga
                                                                        900
tgtattttta tttctggaac gcaacaaagt agccaccgct atgacttagt ctttgccgat
                                                                        960
ccaccctacg ccttgacaga ctggagcagc taccgaccaa agtattagaa agtaacatac
                                                                      1020
tggcagaagc gggcttttca tcctcgagca ccctaaggat ttcagcttta cagaacatcc
                                                                      1080
cgattcgagg aacatagagc ctacggttct gtcaatttca ccttcttcgg taaatcttaa
                                                                      1140
accccaccga caaatatttt tcataaatcg gagctagggt acgttgtaat ccttttggct
                                                                      1200
acatctaacg tactcgtccc ttgatccatt gcgttacttt tttatgtttg acgtctcatc
                                                                      1260
ggatgtogga goottogaag otgaaatott tgaactgaga agtgaaatao gotgacaaac
                                                                      1320
agctattgca tgtttttctt cagatcgaat cctcattgtt ttatagccgt tcgaatatac
                                                                      1380
tccgaagggg ggtcgagcta cgccctacag cgactcgggc tcgccgtaga gcgtaccgag
                                                                      1440
ctgcgctcta cggctcttcg agctacgctg agggctcgct gcgccgggct ctacggctca
                                                                      1500
gctcggccac ctctacggcc ccggagcgga actctacggc tcggctcgct acgctgtagg
                                                                      1560
gcgtacctgc cgagctctac agcgtagctc gaagagccgt acgggatagc tcgtcatctc
                                                                      1620
tacggagtac cgccatctgc cctgtggtat agcccatctc cctataggac tgcaacattc
                                                                      1680
ggtcaaaagc aatccgaatt tcaatgttgg ttcgaccagg cagaagcagg attgcccct
                                                                      1740
atacaattgc ctgaacagaa caactataac ttccaaaata ttagtgcgtt aaccgctaat
                                                                      1800
cttggaacga ataattggcg ttttcttacg ccgaactgac gttaaatcta taaatcgggt
                                                                      1860
cttcccgttt gtttatattt gtatctcatt atcacctgac agcataatcg cccgaataca
                                                                      1920
atactcagaa aatcggaaca gacaatcaaa aaacctgaat aacgaaaaat atagggcaga
                                                                      1980
gctgcaagag ctggaagaaa gcgggagtcc aggcagctta ggaatctgat acacgatggc
                                                                      2040
agctacatca togaggagaa agacgaatgo toaacctoto otogaacgat tatotoggac
                                                                      2100
tgactgccgg gaagatctga tagatgagtt ttatacctct atctctggag aggatcactt
                                                                      2160
ccgggcagct gttcctcccg tctgctcacg ggcaatagta cggcaatgac agattggaga
                                                                      2220
ggatgatagc ggaacgatt
                                                                      2239
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 771 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...771
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

		gattgcagta	tgaaaaacaa	tttttacaga	gaagcttatt	60
ccgaatttgt	gaaaataaat	tarageagea	tateettta	оясяряавав	cagtgataag	120
ggcaatgagc	gttttttcc	tcggcgcatg	LECCCCCC	gacagacac	araagtgaaa	180
caggatgatc	cgatcttgct	ttatcctttg	ggactacatg	glattaccac	acaagegaaa	240
	agactecett	cgtatttcgg	gtatateege	Callegigies	agaagaacas	
	2212003300	tcaagagata	caagtggttc	acaaagaccg	64446444	300
t	agageetttt	tacctatata	gaaaaggagg	Laagectate	ccecaeae	360
agaccccgat	ggagcccccc	atgateteac	agagaggttg	gcgacgttat	accccttccc	420
tgacggcttg	cgactgctct	acgaceceae	abababaaa	gacaacggtC	attgaaaaat	480
gtcaaccaag	gtacagccgt	cagggctttt	CCCacgggac	tateacetas	attgaaaaat	540
ccacaatcaa	gtcggtgggc	gtgatttggt	tcgacaagtt	Lattgettga	attattattt	600
	catagccgga	gcaaggtaag	cttgtcgaag	Laallgadal		660
+	tacccaatat	gaaaaacccc	ttccatagga	actactgree	accaea	
Lagageteau	ttactccast	getttteagt	gatgacttcc	gatacaaagc	tcctttctgg +	720
tcccaaacca	-theorteen	tatggcattc	caaatagtat	gaccgctttg	t	771
gacggacgtc	CLEguatgee	Cacescacco				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1548 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{5}48$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

	acagagtat	ctcttcgttg	gtcccgaaga	aatatcgggc	aagtattggt	60
tcaagggtaa	guagaaguau	cacgtataac	gaacotaaag	atcttatcgg	caagcccgtt	120
gcaacgcagc	gacggcaatc	cacgcacaac	gaacgcaacg	cctgaacgaa	gaagtggggg	180
acagtcatgg	cacatactcg	ctatgccatc	taccetcaca	ассраярасс	tgatcacgca	240
gaggtatcga	ttcgctatcc	tcagcggaga	cacceteacg	agttggcacg	antgncngga	300
ggtagcaaag	gagaaataga	ctacaccttt	gccgacgaac	+000C39900		360
ccctactacc	gcaatataga	catcagtttg	aaagtaggct	ccgacaaagg		420
tcgtccgcaa	ggacaatcat	tgtctggcgc	gggggtgaac	cgatgggggg		480
соясяяряяа	tcgtaccgag	catacagaag	cgatacttcg	agacgagcaa	gagegaegae	540
canatcasa	ggagcagtcc	gctccccgac	ctcgcatcaa	gctgaggaaa	gggagtatat	600
gengtacgat	accattttca	agcactatgc	agaggagttt	cggctcggtg	gictiggeat	660
ctactcacat	ccatcgccta	ccacgaatcg	cgcttcatgc	cggtattgta	BRCCBBCCCB	720
at accarage	+++oatoogt	atcateceae	gacaggccga	cgcttcggag	CCgacaagea	720
	gatecogagot	ttcggtacgc	gtctccatcc	gatgcctgtt	ggcgcccaag	
contttcc	costotasce	gatccggaag	aaaagctcaa	gillacgett	geteetaan	840
+ cactca	agteacetee	cggacgcaag	gcgtttggct	gcaagcacgg	666000000	900
	acastaacot	ggaggcatac	accecttaa	gaaagacccc	auctuctucu	960
aacgtatggg	atateactec	gctatctgcg	apptgcggag	acgatcaact	atgtacgcag	1020
acgatectgt	CLECCECTEC	800000000	-60-0-60-0			

cgtaatggcc	gttatcaggc	atacaaacag	aaggattgat	accactactg	catctaaaac	1080
agcatgtttc	aggcacagca	cttgaccaaa	agtttcggcg	atttggtctc	ttcgaagacc	1140
tctctttcag	tatcgaacgg	ggcgaaaagg	ttggactatc	gcacgcaacg	gcaacgggaa	1200
aacgaccctg	atgaatatcc	ttacggaatc	gactcacccg	attccggaga	agtgatctac	1260
caaaacggta	tccgcgtgca	tacctgccac	agcttcccca	agtacttccg	ggcagtaccg	1320
tacggagacc	tgcttcggac	acaacgatga	gatgacctcc	ctgatagcgc	aagggaggag	1380
gcttcggctc	ggggcgacgg	caaacgcatg	ggaggagttg	ccccgaaat	ggatgccctt	1440
ggcgcgtggg	agtacgaaca	gcgcgcgcgg	agattcttac	ccgtctgcat	ctggacgatc	1500
tgcactgcac	cacggacaac	ttctccggtg	ggagcttaag	cgtatcgt		1548

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 646 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...646
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

```
ggacttatgt gttgaacgaa agcttcgata cgcaaacgct tcctaacggt ggacaatgat
                                                                       60
cgatgctgat ggtgatggtc acaattggct atctacaaaa acgtttacaa cactgctact
                                                                    120
catacaggtg acggtgctat gtttagcaat catggacagc tagcagtggt gcaaaaattg
                                                                      180
atttgagtcc tgacaatatt tggtaactcc taagtttacg gttcctgaga atggtaaact
                                                                      240
ttcttttggg tttcatctca agagccttgg actaatgagc attatggagt gttctgtcca
                                                                      300
caaccggaaa cgaggctgca aactttacga taaagctgct ggagaaaccc tcggatccgg
                                                                      360
caaacctgct ccgatgaact tggtgaagag tgaggagtaa aggctccggc accttatcag
                                                                      420
gaaagaacca togatototo tootatgoog gacaacaggt gtacttggca ttoogtoatt
                                                                      480
tcggctgtac ggtatattcc gtctttatct tgatgacgtg gctgtttctg gtgaaggttt
                                                                      540
tccaacgact acacgtacac ggtatatcgt gacaatgttg ttatcgccag aatctcacgg
                                                                      600
caacgacatt caatcaggaa aatgtagctc cggccagaca actact
                                                                      646
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...574
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40

- (2) INFORMATION FOR SEQ ID NO:41
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1057 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1057
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

		conttontat	cotataaaga	gcttcctgcc	60
gactctaccg cgaaactat	a gacttttacc	ceatteatat	accounttop	gatatatcct	120
	~ +~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	CALALLLLL	40055500	0	180
	a ccasattuat	DICERRACECE	CCCC500	- 0	240
					300
	+ catcagratic	CLLEARELEC	CCIIMMMO PT -	O	360
		adaetattu			420
	e casaccasas	Catcagtccc	LLCACCCCG		480
		Taavcaacec	CCEARCECE	00	540
	's ctocaccaaa	PLELLACCAA		0	600
	SO COBBOCACCA	aavalcatte	agacgagg	99	660
	.+ atcagaacac	CHARLEREC	- Caac 6666	0	720
	-a ttcctocaca	ACCEREE	accuuugug	0	780
	ra ttadadtc9C	accadacter	Cagcago	900	840
	s+ +s+t+t+C09	PCALECEARA		00	
	.c accaatagat	CVACAVCCCA	. acaaacca-		900
	ra strototati	CCERCACEC	LCaccguaca	00	960
tctccttgtn ggtaagtg	re tecepation	gatcgatcca	gatgcctttc	ttctctatgg	1020
tctccttgtn ggtaageg	tt tttcgcctac	ppccttg	-		1057
aatgaaccac aattcgat	il lilegiciae		• •		٠.

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1271 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1271
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

```
ctttgggctt caaaaagata cgaggaccta tctgtaggta tatttatcct gtttttcttg
                                                                        60
ttttattgag tggtagtacc tatttttgtg atgagagtgg actctcgtca tgtcgattaa
                                                                       120
aaagaaaaca gaaatgaata agagtataaa ggctcaaaga cagaaaagca tttgctcatg
                                                                       180
gcatttgccg gagaatgcaa gctcggtcgc gctatacttt ctttgcaagt gttgccaaga
                                                                       240
aagaggttat gaacaaattg ccggagtttt catggaaacc gctgagcagg aaaagagcat
                                                                       300
gccaaaaggt ttttctcttt cttggaaggc ggcatgcttg agaaacggct tcttttcctg
                                                                       360
caggaataat cggttccacg gctgagaact tggcgcggcg gntgccggtg aaaatgaaga
                                                                       420
gtggacagat ctctatccgg ctttgctgaa acagccgaag aagagggatt taaggagatt
                                                                       480
gcagccgtat tcgtcagata gcaaaggtgg aagccgagca tgaacgtcgc tatctggctt
                                                                       540
tttggctcat gtggaagatg gatcggtctt cgagcgaacg gaagaaatgc atggcaatgt
                                                                       600
cgcaattgcg gctatgtcat tacttccaag aaagctcgaa gctatgtccc gcttgcgctc
                                                                       660
atccgcaggc ttacttcgag ccaatgaaac gaattactga ggatcacatt catatagaaa
                                                                       720
cgaagtaatt atctgtctca tgtttttgaa ggaggcaccg ctcgggagag tcgtgcctct
                                                                       780
ttttgctctg ttattccctg cgaaaagcgt gtgcgtcatt ttgtttttc gaacaagtat
                                                                       840
agagaccggt cctgtaaagt gggactctca cggtttttcc ggcatacagc cggattgaaa
                                                                       900
agtgctaatc cgatgaaaaa accgtacttt tgccgaaatt acttaataac caaaccagta
                                                                       960
accttagata ccttatggaa tgaaaagatt tttatcactt ggtcttctgc ttgtgggatt
                                                                      1020
cattccgata agctttctgc ccaacaggct cagccactcc ctacagatcc ggctgttctg
                                                                      1080
toggtaagtt ggacaacgga ttgacttatt toatoogtoa caacgagaco cgaaagatog
                                                                      1140
tgcggatttc tttatcgcac aaaaggtagg ttctatcttg aagaagatag ccagtccggt
                                                                      1200
ttggctcact tcttggaaca catggtttca acggtacgaa gaacttcccc ggtaagaact
                                                                      1260
tgatcaacta t
                                                                      1271
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 671 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...671
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

gcaaacctcc		tacatctaca	caatotoaaa	ctggctatgc	aagggtggag	60
gcaaacctcc	gacaaagaac	LgCalcugua	theettenen	acceptorat	oocgagttca	120
cgacatagct	ccattaccct	cagttcgcct	ttttttgagg	agcaccacac	66-6-6-t-c	180
	actaccttca	atgctcgagg	agtggttggC	gcacatette	Cigcactige	
	tcacaacaaa	agtgccgact	gaggatgtcc	gtctgcgttt	ggcgttggac	240
gggccatagg	ccgcagcaag	tacaacttct	tecapttace	tttggccgaa	gcggttctat	300
ggctcttgcc	Caaggaagug	Lgcagcttct	+	gattgracat	trotaccoac	360
caagatcagg	gcagcctatt	ccgaattgct	Cogaageeee	gattgcatat	togtaccgac	420
naactcataa	ctatgaacaa	agagctacgg	gaacggaggt	gaccutgaac	Calcuacus	
255000000	actratrtot	cetcceactt	gtatgtgaat	ggcgatgcca	cgacacgaga	480
gcaaggccga	acceatege	0800000000	agratrogto	cccgactgga	tatgggacag	540
cctcaacctg	aagcattagt	ggcaaacgac	agetteebeg	anactteete	0008008008	600
acaagcgagg	agcgaaaaac	ggatttatat	egetgeteac	aaacccccc	gggacgagga	660
ctcatcgctg	aatactcata	tcggtctcga	tcgctctcgg	cacgcatcgg	cggtatgagt	
		-				671
ggcagatagc	C					

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1000 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1000
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

	agatorgana	tttatgtttt	cggacggtat	ccgatgagtg	ttttatcgga	60
agtectatae	agatttgata	ttatttat	acceacataa	ctttttctac	gcgagttctt	120
tatccggggc	tctcctcttc	ttctttttgt	acceacae	ctttttctac	ttctaacaca	180
gcacatctac	ggctcgtgtt	tttcggagaa	gtggcgcgag	attttttcg	ccccacata	240
+	acttctgcgc	caaaagcaaa	attttcccgc	gccacgcccc	ccgagacas	
224222224	tttccgaacg	caaacaatct	gaacggacag	LLLECCALEC	acceannes	300
aataagaaat	occopact	atasaastca	atttccggct	ctgtcgatct	ccctttccca	360
cgttgacaca	Cagaaaggee	gegaagateg	0000000000	200020222	acgcttgtac	420
ctaatccgac	agatactgat	gcccgcccac	CCBadaaaa	t a cot coat t	acgcttgtac	480
000100000	agatactacc	ttgcatcgca	atcgcggaag	Laguicague	86.060000	540
ancettaces.	gattagggtC	eceeettcea	gtcccgtctt	CCgCCCCaag	aggeageage	
atsossett	tagragicic	ctcatcctga	aaaagggtgt	atctttccag	aaagatcggt	600
algeggeeta	-26-66-66	taacaaaatt	ggtagaccgc	tcgtttcagg	tgcgagtgtt	660
cgataacata	gacgcccggg	Lggcggaact	ggtagacogo	2100200333	арасавасав	720
caaaagacgt	gcaggttcga	ttcctgcccg	ggcaccgact	accgaggaaa	agacaaacaa	780
++++++	coooteteea	attegtagac	acgctacttt	gagggggcag	LECCESCE	840
cataataaat	trasatetea	tctcgcgtac	ttttaatgaa	gaggargree	acceacceee	
BELEE FEE	ttttattta	accasoctor	ccaatggcgt	gaacggtata	aatagatatc	900
catcetett	LLLLELLLA	#66##66#6		• 6008880088	gcatcccaca	∙.960
tttaatcttt	gtataataaa	aaacaggcag	acgaagcagc	"PP"""P"P"	gcatcccaca	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 724 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...724
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

ccgaatccaa	agtctcaagc	tctgcaatga	ttgctttctt	gctcttcagt	tttcgcattc	60
ttcggagcgc	atatctccct	gttcggcttt	tttacgttga	agaatgcatc	gcatgcagtc	120
gtaaaacgct	tccatatctc	atcactaacc	gatgaggaac	ggctccgatg	gttttccatt	180
tcttttggag	ttcggcaagc	gagtagaggt	ttctttccag	tcggaactct	cctgaaggct	240
ctccgttctt	ctaccatggc	cagcttcttc	ttgtagttat	cggtcagctc	ttcagtttgc	300
		ttattgaaat				360
gatcttctca	ttgtcgcttc	tgcgagcata	gctatagtct	tccacttggc	ctgaatctct	420
agtacggcct	tcgtttgctc	gcccatttgg	ccagcgagtt	cagaccggag	gtatctatcg	480
cttccatttc	tcacaaagca	atgttttcgc	agccagattc	tcctgctcgc	gcatctttc	540
ttttcgaagt	gttcctgata	cttcttattg	atagcaagta	gaagcagctt	gaatctcgcc	600
		gcgagctacc				660
ttgcagtacc	ctgaaagaat	ggatgaatcc	gcattctcag	tcagcacttc	ggcctgatgg	720
atca						724

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2863 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2863

attgttttgt gtgtttatgg tatgatcaat gacacaaaat gatggcacgc aaggaaaatc 60 atccaacgag aagaggtoto attcagggac gtcatgtcac gaatcgatac aggaaagccc 120 ggaatgtatt tttgacccaa gtcgatagct tacatgagag gatactatgg tctcctatga 180 gaggatacta tggtctacac gagaggatac tatggtctca tacgagagga tactatggtc 240 tcacaaagag gatactatgg tctcacatga gagaatacta tggtctccta tgagggatac 300 tatggtctta cacgagagga tactatggtc tcatatgaga ggaactatgc tctcacatga 360 gaggatacta tggtcttaca cgagaggata cttggtctca tatgagagga tattatggtc 420 tcacatgaga ggatactatg actattgatg gaagatgcta tctgctctgt gtcggatggc 480 aggttcgggg gtgggaggtt ccgtgcgagc tgttaaaccg atagatgaga ttgtcacacg 540 cattttccgg gagatttcgt tgtcaattga ctgtttttca gtgtctgtta tagacataaa 600 gtatcaaatc aagagtcgtt tgcttggctt gtcgggctat gaatttgtcc tgaataaata 660 gaacagggtg aagagaaggg tgagccattg gggtgtagct cgcaatgagg gaaaagcaaa 720 tgtcgtggtc agccttggca gagcgttcgg cgatggctgt ctcttctatg atacttcgag 780 ccattccaca ccttgtgaga tacgatgtgc catacctatt cccccatgca tatgccaccc 840 aaatgcaagc ccggccagcg catttccatc cgccggatga tgcctgccga agttccgtat 900 cggcgtagta ttgcggtatg gcatggcggt gcgtgagatg tgcagcagat ccggcttaca 960 ggtgtgaggt atgcgcagca atcgcgtagc tcttccattg caatcgtgct gatctcctcg 1020 teggaaagge tatgagegaa geatttegea eeceaceeat gaatatggaa tagagtgeee 1080 cectteaggt getetgeeac ggaaacagte egaagggaac aggatgegag gatgegaega 1140 ttttccctcg aagggatcag gcacccgaaa gccggcggtg tgtggcaaca tttcggcgga 1200 accetacgge aacctetate atggggeata atagagetge tegaacaegg etgatteate 1260 cgcagggaag tggtgaacag tgtggggata tggtgcgctg ccaccgtact caccaagtgg 1320 cggaaggaat ggtgtgctcc tcttccgaag catccgtata ggtaaggccg aagtgtgtgc 1380 1440 tecegggtga tigatgtate ggatttgegt tteegteagg agtgttegeg teegatgtag toggocaaag ottogacoag aagacogagt cocottgtac ggaaaagaco ttgcgcgagg 1500 ctttgcggtc gcgttcgctt gcggctgtcg ggcttttcga acggcaccca gtacgaagct 1560 geogratect getecagate gtatagtttg ggeagggeaa agegagtaae eagttggegg 1620 gatctcctgc ataaatacct ccgaggaaag gatcgactgc gtagtcacaa aacttttgcc 1680 cagccggcga cgagccaagg ctccgaccgt ctcatgggtt gtccgcctct ccggcggaag 1740 1800 ggttcgccga ggatacgcca tttgcccaca gggaaaagag aggagtagcg actgcctcgg cgatgttcct tggaggggat acagtttgtt gcctttccat atcagacggt tagaggccgc 1860 1920 agagtggcta totcaggtto caatoogago agttogaata gotoggcoac tooggagagg agatcgtgcc ggtattcggc cctgtctcga acacgaaccc tcctctctgt aggtgcgtat 1980 2040 ctgtccgccg atatgagcag ctcgctccaa ccagaacagg cctgccggca agctctgagg aaagcggctg tggtcagtcg gtgagcccgg ctcctatgat gacggtcaga tgatccatga 2100 atcaggetee ceacetteaa aggeaagage atagaaacge atetgettga geatgggaeg 2160 aggccgttgg agcgtgtcgg cgagagatga tcttgcaacc ctactcgcga atgaagtaga 2220 gatcggacga aacgatgtct ttcggtttct ggtcttcagt atccgtagta gcagagccac 2280 tatccctttg acgatgaggg catgctatcg gcgcggtagt gcaccttgcc atcttgcagg 2340 gaggetgeta teatacgega etetggeaac ettegataat gtteteegge acettatetg 2400 cgcatccagt tcgggtaggg cactgcccat atcgatcagc agttgataac atccatccaa 2460 tcatcgaaag cggagaattc ctcgatgatc tgatcctgtt ttcgtttata cttggcatgg 2520 gataagctaa tgagtgaata gtcagtgtaa gcggctttca cctgttcgtc caaatatcga 2580 atgacggttt cgcccacgca tcgagtacat ttttgtcgat gatctgcata ttgtccctct 2640 gggtatccag tggtcgccga agccatgttc gttcttggac gagtaattga taatacgatg 2700 caagggatce ctaaattett gatcacaggt acatgatcat ctgtagageg ceteegtegg 2760 cttggatgaa gtagttgcca tatcctaatg cggtgccgtc tgccatacgg cagagatcaa 2820 2863 ccccggggca tagctcttgg agagtactcc caatagaatg tag

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 629 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...629
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

aaagtccaag	gaagagttgt	ctgcttttct	cggctgtgag	catatcgagg	ctgcaaatgc	60
ttcgtcaagc	aggagcaatt	gcgggcgttg	gagaaatatc	gtgccagtgc	cacacgctga	120
cgttgccctc	cgcttagatc	cttcggaacc	gatgcaatat	gtccgacaag	ccgagggtgt	180
gtacaatgct	ctcaaatccg	gcatctctat	ggcttccttt	cgcagggtat	atggaagtac	240
gatatctcat	gcactcgttt	ccatggcaaa	agcccatatt	gctggggaac	tattctatgg	300
aaaaagattt	cggattcaga	ggtttcccat	cgaatagcac	ttcccctcat	actctgtcag	360
tacacctgcc	aaaacgtgca	ggagtgttga	ttgccacagc	ccgaaggtcc	cgttatggca	420
aaaatctctc	ctttgggaat	atcagtgaaa	gaccgtccaa	tgctttcact	tccgtactcc	480
cgtggcgata	gtaacggcca	gattgcgaat	agagatcatt	tgcctaatgg	aggaatctgg	540
tttcgtccgt	ctcttgatta	tgccggactt	tacggatcag	atccttgcgg	ttagtcgctc	600
gggaccaatt	tcttggcatg	tacccagtc				629

- (2) INFORMATION FOR SEQ ID NO:48
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 581 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...581
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

```
tacaaactgg acgttgtagt tattccgaca aacaagccta tcgcccgtag gatatgaatg
                                                                        60
atcgtatcta taagacggca cgtgaaaaat atgcagcatt atcgaagaga ttgtacgtct
                                                                       120
tgtcgaagag ggcagacctg tacttgtggt actacttcgg tggaaatatc cgaattgttg
                                                                       180
agccgtatgt tacgctgcgt ggcatccaac cacaaatgta ctcaatgcca aattgcatca
                                                                       240
gaaggggccg agattgtagc tcaggccggt cagaaaggaa ctgttaccat cgcacgaaca
                                                                       300
tggccggtcg tggtaccnac atcaagctct ctgccgaggt taaaaagccg ggggtatggc
                                                                       360
tatcattggt acggaaaggc acgaatccag acagtggaca gacagcttcg tggtcgttcc
                                                                       420
ggccgtcagg gtgatcccgg tcgtccatat tctatgtttc ccttgaagat catctgatgc
                                                                       480
gcctctttgc acagaaaaga ttgcattatt gatggatcgt ttaggtttca aggaaggaga
                                                                       540
gtgctcgaaa actacatgct nagtaagtcc gtggagcgtg c
                                                                       581
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(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 633 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...633 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49 gtgctgatga cgttagccgt ttactcattt atgcctctga tccggacgaa cagatctcat 60 tgtgacgcga gtgttcgatc gcctttcgga aacactctcg tcgggggaaca acgactgacc 120 atcaatacgg ctacagaact gaatccgtga ttatggattg gctctctgcc ttggacacca 180 atgttgctat cctgctacac tgatgggatt ggtcggaggc ttcacgatga tagcccggtc 240 tgattttttg gtcatggaca aaacgcagtt tatcggcatg ctcaaagctt taggtgtgct 300 gaagggtcgc ttcgccgcat attcctctat ctggctatga tgccgttggt cgtggtatga 360 totggggcaa tgttttggct ottatactot gotootgcag caacatttoo gotggttgcg 420 tctccttcga tcctgatatt tctacatgga ctatgtgcct gttcaagtgg actggctcgt 480 atggattete ttaatttggg tacceteete gttacettet tgatgeteet tgeteeatee 540 atattatttc gagaatttcc cccgtcaaag cccttcgctt cgagtaatgc ttcaccaggg 600 633 aatagggtag gtcatctgtc cattcgagac cat (2) INFORMATION FOR SEQ ID NO:50 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2664 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...2664 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50 ggcaacgtcc tccgcagtgc cgaaaacacc tgcattgccc gatatacctc gaggcatgca 60 gcagcttcgt cgtccacggt accgcggacg atgcttttcg tagaaatttg tcgttctgtg 120 ccggtgcaat gcgcgaaacg gaatattatc gagtggaaga taaccgagcg aaccggctcc 180 gatggggcgg aatatagttc ttcgacaaag acgttcaagc tcttgcccga tacttttcc .240

```
acaattgctg tagcaggata aaccccagat ccgaatactt gtagcgtccg actcattgcg
                                                                       300
aggggtagaa gcgatggtat tgaggacaat ttctttgacc tcttcgatag atacagattg
                                                                       360
gaagaaaaac gaaacggata gtccggccga aatgcccgga aaccaaatcg gagcgaaatc
                                                                       420
cgaagaatgg attgcccac aattggtatc tactcgaacc catcccgaac tccgccgggg
                                                                       480
agagagcaac tgccgtccaa actgctactg tctatcagag attcgtagaa attgatcgag
                                                                       540
gccgaaggcc tgcttcatga agtagaagct gctgtacggt gatgtcttga ggtctgttcg
                                                                       600
ggcaaaacga ggcaatageg tteegageeg gteggagget teaattttee ateetgaace
                                                                       660
aatagcatca cagccggagt agtggcacga ccttggtgac ggatgccaag tcgtagatgg
                                                                       720
tggaagaaga cacctgcctc cacgtgccga tccgtcgaga gtgccgaagc ttttgtcata
                                                                       780
taccccttgt ctcgatggac agcgaggata cgacaaccgg ggaaagcccc ttgcttaggg
                                                                       840
                                                                       900
cttctttcgc tatgcggtct accgccggca tcgggatgag gcggacgaca attcggtcgg
cggcatcatg ttcgctgtcg gatcaagtgt ctcctcttcc tgaacgaccg ggatcccacc
                                                                       960
                                                                      1020
gcccgaggat accacaactc gtcccgaatc ttggaggctg ccattcgagc agcctccttt
acgtttcatt gccacgacta tagcccgagc tttgtccata gccgccggaa tcctatcgct
                                                                      1080
                                                                      1140
acatagggcg atgtgaagaa gacgatggca gtgtggtttt gttccgtagc cggtggagaa
                                                                      1200
acgttcctgc ccagtccggc tgtgtatgtc gaactggacg atcacagcat cgtacccctt
                                                                      1260
gagtttggag agcaactctt gtgtagtgta ctgttgctgc ccttggcata ggaatagcag
tccttgctcg taagcccagc tcttgtgtaa aagtattgga ggctgcacca tctagattga
                                                                      1320
cgctgcaata cggtttccct ccgagagggg gaggaagtgc ttcttgtttt tggaatcgta
                                                                      1380
                                                                      1440
atggatgcct gccaaagatc ttccgacatc cgttccgctt ccggctgttt acctgtcgta
ccacttcctc tgccggtagc tccttggata tcccttacaa atgatgagcg catacttgaa
                                                                      1500
ggccagaatt ttgcgacatt ctcgtccagc aattctttgc ttatcgttct gtcttccact
                                                                      1560
                                                                      1620
gcggccagac ctcggagaaa gtcttgaccg ggtccaccgg accgaggagg atgtcatgcc
ggccaatatg gcacggacgg agatcggttg agaaccggct gtctgtctcc ctgcatggcc
                                                                      1680
                                                                      1740
agtocgtocg taaagatoag cocottgaaa cocattootg cogaagcaga toggtgoaga
tggcatgact gagggaggag ggcgattttt ctttgcttcc aaagccggaa cattgaggtg
                                                                      1800
agoggtcato actogotgag googgotogg aaaaactoot tgaaggggaa caattoagta
                                                                      1860
tttccaattc ctctcgggag gcaaagaccg tgggcaaggt cttgtgcgag tctctgtggt
                                                                      1920
attgccgtgt ccggggaaat gcttggccac ggccatcact ctccgtcctc caatccttgt
                                                                      1980
gcataggcaa tccctcttc tgctactcgc gtgggttgtc gccgaagctg cgcgtgccga
                                                                      2040
                                                                      2100
taacagggtt cttcggatgt tgttcacgtc cagcaccgga gcaaaattga tatgaatccc
                                                                      2160
catcagcggc attggcgcgc tacctcccga ccatagttgt agaggagctg attgtctttt
                                                                      2220
ggtgtcccaa gcccatattg cgagggaagc gtggggcatc tttcaacgca tgtgcaaacc
                                                                      2280
ccactcaccg tccagtgcta tgaggagagg ggtgcggctg cttcctgcaa gcggcgagtc
atogtgtatt gctccgagag tgtccctttt ggaagagtat gcccccgatg tggcaggtgc
                                                                      2340
gcaccagctg ttggcttgct ttactttttc ttcctgtaaa gagggataga cgatcggcat
                                                                      2400
ggcagctggc ctacttttc ctccgtgctc atagccttca tgcggtcgtc acccagcgtt
                                                                      2460
                                                                      2520
tgacatettt getetegaet eeccegaaga ggagaaagga tagtetttgg actgetggge
atgcatggca cccatgttcg tgcgggccgt gccgtagctg tgtacagcac cgagagagag
                                                                      2580
                                                                      2640
agtattgtga tggcggaaaa agaaatcgtt tcatacccta caaatgtaca taaaaatggt
                                                                      2664
ggccgatccg agccttccct tcga
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2706 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...2706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

```
gattettaga aaagttgatt attaacgaca aaaacaaaat ataaagatga categtaetg
actattetea teetgeteat ategetette ettattetgt egtagtggta cagaacteea
                                                                       120
aagggggcgg cttggcagcc ggcttcgatc cagcaatcag atcatgggcg tccgcaagac
                                                                       180
taccgatttc ctcgagaggc cacttggtgg tcggccggta tcattgccgt tctggccatc
                                                                       240
gtttcactca cttcctccac acgggaaagg tcgatgagag ccaaaacgtc ctgaggaaac
                                                                       300
cctggacaag aaggtgaagg aagaaaagaa ctctgcagtg atcacttcgg tggagatgcc
                                                                       360
gctgctacgg aatctgcccg gcccgcgacc gggaggccac tcccgaggag gggcaggcac
                                                                       420
aataaggagg accggccct tcatatccct tgcaggagat acggggatcg acagacgtct
                                                                       480
ttgtctttga ccgaggcttg agggcaaaga cgttttgttt ggcagggtgc cgctcgccga
                                                                       540
cgccccggga caaggctcaa ggggcggaac ggacagagcc tccgaggggt acgacaagcc
                                                                       600
cttgcgaacg gaacggacgg acgtacccga aaaaacgcta gacgttccga caaaaacgtc
                                                                       660
tagacgtttt gactgaaacg tctagagtat cgaagcaaac gtctagacgt ttttcgcgaa
                                                                       720
aggtctagac gttttacaga cccgaccttt tggcagaaga caagagagat gacaaagaga
                                                                       780
ctatcctgcc cgaatgggca ccgcaagagg ccgtacaatt gacctggcct cacaccgaac
                                                                       840
cgactgggct tatatgctcg acgaggtgga aacctgcttc gtcgcatagc caccgccata
                                                                       900
ctccgccacg agcgactgat agtcgtttgc ccgatcgcaa gcgggtgttc ggcctgctgc
                                                                       960
ctcccgagct gcaccaccgg tctactgctt cgagctgccc tcgaacgata catgggcgcg
                                                                      1020
cgaccacggg gcatttccct cctcgccgac ggccgtccga tgatagccga cttcgcctca
                                                                      1080
acggctgggg catgaagttt gccgcccatc acgacaacct catcacggac ggctccacgc
                                                                      1140
cctgggcctg ttcgccgaag gagttaccct ggacaacgcc tcgccttcgt cctcgaagga
                                                                      1200
ggagcactgg agacggatgg cgaagtactt tgctgaccac ggacagctgc ctcttcgagc
                                                                       1260
cgaaccgcaa tgccgcctga gccgcacggc cattatcgac acgctgaaag agagcctcgg
                                                                       1320
                                                                      1380
cgtagccgcg tactctcct ccgccacgga gccttggccg gcgacgacac cgcgggcaca
tegacaegtt ggegeggtte gtegacaece gtaceategt catgteeget eggaagatee
                                                                       1440
ctcggacgag cactactccg acctcacggc atggagcagg agctgaagga gctgcgccgc
                                                                       1500
ceggaeggae ageegtaeeg etegtgeege tgeceatgge ggaagetetg taegaeggag
                                                                       1560
eggacaggtg ecegecacet atgecaactt ecteateate aaeggggeag taetegteee
                                                                       1620
 acctacgatt cgcacctcga tgccgtcgcc ctctcggtga tgcagggctg tttcccgata
                                                                       1680
 gagaggteat eggeategae tgeegteege tegteageag catggeagte tecaetgegt
                                                                       1740
 cacgatgcag tacccccaag gattatacgc taattccaca gcaaagaact atgaaagtag
                                                                       1800
 cactcattca gcagccaaca cggcggacgt ctgctcgaac cgggagcggc tggcagcgaa
                                                                       1860
 gaccgcgaag ccgcccgacg cggtgccgag ctggtcgtac tcccggaact gacaacgggc
                                                                       1920
 tttatttctg ccagacggaa gacgtgcagg tgttcgaccg gcagagacca tcccgggacc
                                                                       1980
 gagtaccgat ttcttcggca ccatcgcccc gaagccggcg tcgtgctggt gctctccctc
                                                                       2040
 ttcgagaagc gcgctcccgg ctttaccaca atacggccgt cgtgctggag cgggacggca
                                                                       2100
 ctatcgcggg aagtatcgca agatgcacat ccccgatgac cctgcctatt acgaaagttc
                                                                       2160
 tatttcacac ccggcgactt gggctttacc cccatcccga cgtcctcgga tgcctcggcg
                                                                       2220
 tactggtttg ctgggatcag tggtatcccg aagcgcgcga ctgatggcca tgcagggtgc
                                                                       2280
 cgatatactc atttacccca cggcatcggt accgagagta cggacctgcc tgccgagcag
                                                                       2340
                                                                       2400
 ctccgccaac gtaggcgtgg cagatcgtac agcgcggaca tgccgtggcc aacggtattc
 cgtggtggcg gtgaacaggg tcggccacga ggcagacct tcaggccgca cggtggcatc
                                                                       2460
 acgttctggg gctccggatt cgtagccgga ccgcagggca actgctggcc gagctgagcg
                                                                       2520
 caacggaaga ggcggtggag gtagtggaat agatccctcc cgaaccgagc aggtgcgccg
                                                                       2580
 ctggtggccg tcttccggat cggcggatcg acgctttctc cggccttacg gancgtttcc
                                                                       2640
 ttcgcgctga ccatcatggc gagagggggg atggcgttcc gtcccttccc cctccacaag
                                                                       2700
                                                                        2706
 gagccg
```

60

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1361
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

```
cgtaagatcg tgaagcctat atcaagcgtc tgaatatctg aagcactcgc atgtcctatc
                                                                        60
cgggcgttat caagacctat gctattcagg ccggccgcaa ctccgtgtga tcgtcggtgc
                                                                       120
cgacaagacg gacgatgcct cggtggaacg ctctcgaacg aaatagccaa aagaatccag
                                                                       180
gacgagatga cctacccgga caagtgaaga tcacagtgat ccgcgaatct cgctccgtca
                                                                       240
gctacccaaa taatcccgca caccggtgga tagtacctgc tcgcatgatg tggcgttatg
                                                                       300
atttatacct cctcctatca gcagcactag aggactacgc cggcaaagca aaagacggat
                                                                       360
ggactaccga ttagacaata cgacgacctc ccgacgaagg atgcctgcaa ggggtgtcat
                                                                       420
agccagccgc tcagcactta tactggctga atgacatccc cgatttgccc gaagatggcg
                                                                       480
gattcgtgga gtacagttca agaatacgcg caaaggatac tacctcaaca gcgagaggaa
                                                                       540
gagctgcaca aaggggatgt agtagccgta gaggccaatc cgggtcacac atcgggacag
                                                                       600
tgacgctgac cggcaagttg gtaaaactcc agatgcgaag catcgataca atacgaacaa
                                                                       660
cggcgagcct ttcaaaatat accgcaagcc aaacagggcg atctggataa gtactgcgaa
                                                                       720
gcaaaggcgc gagagacgat acgatgattc agtcccgtca gatttctgcc gagctgaatc
                                                                       780
tggaatgaag atcggagatg tggagtatca gggcgatggc aataaggcca tttctactat
                                                                       840
atcgccgatg agcgcgtgga ctttcgccaa ctgatccgag tatggcagag accttccata
                                                                       900
tccgcgtgga gatgaagcag atcggtgcaa gcaggaggcc ggccgtatag gcggtatcgg
                                                                       960
tccttgtggc cgccagctgt ctgctcggcc tggaagatga atttcgtatc ggtgaatacg
                                                                      1020
agtgcagccg ctatcaagac ttagctctca atcctcagaa gctcacgggc ctctgcgcaa
                                                                      1080
gctcaaatgc tgcctcaatt atgaggtgga tgcttatgtg gaagctctaa gaagatgccg
                                                                      1140
agtccggaga tcgtcttgga gacgaaagaa agtgcgacca ctatttcaag gcggatgtat
                                                                      1200
tccgtcggga ggtttcgtat tctacgttcc caatgctccg gtcaatctta cgactatatc
                                                                      1260
ggctcgtcgt gcttcgaggt gatcagccag aacaagcagg ggttcaagcc ggtatcgctg
                                                                      1320
gagatgacga caagaagcag tcgtccggac acgaattgtc c
                                                                      1361
```

- (2) INFORMATION FOR SEQ ID NO:53
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 751 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...751
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

```
teetetatgt ettategatt etgatatata acacaaettt tettttgaag tgggtateag
                                                                       120
gcttatgttc tatcctttta tgttcatttc atattgatcc ctaatgctta tgtattgtca
                                                                       180
gataaaatat ggcaaaaggt gigattttgg ctattttggt tgtgtictca tictttatgc
                                                                       240
ttaagatete ageagteeag etgaaceata egetaaetat aagtetatae tetttgaaaa
                                                                       300
atactgttta gagaattatg atcgtgcatt ctcccttggt caggtgctta ttcctccata
                                                                       360
caacgtggag aaatcagaaa tcgagtctga tttgaaatag cctacttgaa tgtagctaaa
                                                                       420
atgttttatg acaaagctcc cgcaatcaat ataagacgat aagggaatac aggccactga
                                                                       480
atccgaagag atcgcctcca tgcaatacca ttcgttaatc cgatttaggt ttgcttgtca
                                                                       540
ttgtcagact cttctgttct gagatattta ggatattttc tgtgtaaaca gaacagaaga
                                                                       600
taaaaagaat gatgagagcc tgactttgtg ttgccacgtc tttttcctac aaagtaattc
                                                                       660
gacataatat gataaccgtt gcccattgat caataacatt ggccaatcag gaccggggat
                                                                       720
                                                                       751
agtcatgcgc gacatattcg acacatggat c
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 911 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...911
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54

```
aggttctccg tctcacacag atcgatgtgc acagtttggg tgagctgcgg tcaatcaagc
                                                                        60
actgcgcaat atcgaagctt tctacgaagc tttcaataac agcctactga taagatgtat
                                                                       120
ttggaacccg aaaagcgtgt agtcgttggt aagctgaccg acactcctat acgggaaaag
                                                                       180
aggctacgtt ccgaggttat tccttggaac gcagcctctt tcgttagaaa aggaacctaa
                                                                       240
teggaaggaa agageataag gaggggttat aaacteggee tategeteat eagataatga
                                                                       300
gaccaattcg agggacgett ggtaacgget gccaccaata cacgatettg gccgcaaagg
                                                                       360
cttctgccaa tggctcggcc gcagcttgta cctagccccg gtagtcagca catcgtccac
                                                                       420
caaaagaaca cggataccgg cacgcgcgta ttcggggaga gggcaaactt ccctttcatg
                                                                       480
gctgactttc ttccgaatag gactgtccgg tctgactgtc cgtatatacc tttctgcgca
                                                                       540
accttcttga acaggtattc ccgttacgcg acttaatcct tgtgcgatag gagtgcctga
                                                                       600
ttgtagccac gcttacgttg tttgcgtggg tgtaaagaac cggcactatc agatcgtaat
                                                                       660
                                                                       720
cettggacag gaaaggatag gateggegge cattegteeg ageatttege egateteact
gtatcctcca tatttagtgc gtgtatcata ggccttacac ccccgtcctc tttgaaaata
                                                                       780
aaaagctgta cagcgcgtcg atataaacat ccccattcag acgatctaat ccaattgcat
                                                                        840
cccttcgata taccgnggca ttctcaccat gcaacgagga caaccccgat ctccgtctcg
                                                                        900
                                                                        911
gcgagcaagc t
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1317
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55

```
aaacgtatcc tcatagcctg cccctccttc gtgtgcgact gtctggagac ctcgaagaag
                                                                        60
tagccgatca cggacaaagc attttcaaaa aagcaggagt gcggatttca cttacatccc
                                                                       120
ctgtctcaat agcggggcga attggatgat gctctccgaa acattttaga ggaataatac
                                                                       180
agcatgctca gttatctacc gatataccga cagacctgcc cctcctgagg caagccgtcg
                                                                       240
aagcctccgc cgggaagaat ccggcggtgc cgtacccgac tccgatcggc cgaggtgata
                                                                       300
tacgaggcgc gcaaccggct ttacgccatc cgtaccgcac aggagagcag gtggtgaaga
                                                                       360
gcttccggat ccctattgcc attcagcgcg tgtctactca ttcttccgcc cctcgaaggc
                                                                       420
tgctcgctct tatcgcaacg catacggctg gggcgatgcg gcatcggcac tccgcgaccg
                                                                       480
tegggetatg categaacge gaaaaaggge ttetgtgeag gagetaetae gtetgegaag
                                                                       540
catgcacgac tgtcgggata ttcgtctctc catgcaggga gtggaagggg cgaggccttg
                                                                       600
ctccgtgcgc tggccggatt catcgcccga atgcaccagc aggcattcat cacattgatt
                                                                       660
tatcgccggg caacgtactg tatcggcaga cgagaaaggc gagtattcgt tctacctcat
                                                                       720
agacctgaac cggataagtt ctacgacaag ccgattgtgg ggcggaaagc ctatgccaac
                                                                       780
tttgacgtct gagcttttgt ccggcagtga gcaagcagct tgccgaatat tatcagaggc
                                                                       840
acagggcttg aatacggacg gagtggtcca aggggtacaa aggaatcgga tcggttcttc
                                                                       900
cgcagcaaag tccgcaagta tgctcgcaag gattggtgcg cgaacaaaag cgaatgagcc
                                                                       960
gctccgcttt ccgtcgggca atatccgcta tcgctcggta cgccttatcc gaaaactcac
                                                                      1020
gggctgcacc gtctcttccg tatcgagaac gatctgtaca catcctatct tgaagtggcg
                                                                      1080
acctgcgcca tacactgaaa agagccgaag gatattcctc gccgaaaacg ttcaataaga
                                                                      1140
aaaaaggaaa ccgaatgaat cgtatagctt ttgatgcaag agaatcacat ccaacgccac
                                                                     1200
cgggctgggc aattacagcc gcttctggtc gaagccttgg ccgcctttca ctccgaacac
                                                                     1260
cgctactacc tetgtetece gggaagggea ateeggetet gtacteegee ttgcage
                                                                     1317
```

- (2) INFORMATION FOR SEQ ID NO:56
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1820 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1820
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56 .

```
aaaaaatctg atcatacgcg ttgcagacaa tggcatagga atagataaac tgatcaggct
                                                                        60
catatottog acatottota togaggacag toogotacga aaagcatgga toaggogtog
                                                                       120
gactetegtt taccaatata etggtegaaa eettegaggt aegateaaag tggaaageea
                                                                       180
gccggggaaa ggaagtcctt caccatcagt attcctacac aaaaccagtc ctcttcggca
                                                                       240
gagatettee ttggetacee teeteegatg acattgteat geetgteeac ateggeecga
                                                                       300
tgactcaccg acatctccga tggtagcagc tctgaatcat cgctcgagga cgaacgtccg
                                                                       360
accatactgc tcgtcgagga caataaggat ataacctgct cgtcaaacta ctcctttgcg
                                                                       420
atcgctacaa tgtgctatcc gcgcaaacgg aaaagagggt atagccctcg ctaccgagca
                                                                       480
tattcccgac ttatcattac ggatattatg atgccgataa tggatgggat agaaatgaca
                                                                       540
teeggatgaa geaategeet etgetetgte acatteeeat tgtegettga eggeeaagag
                                                                       600
taccgaacag gacagattgg aaggaatcaa aagcggttag tctcttatct atgcaagcca
                                                                       660
ttctctccgg aggagctttt gatgcgatcg agcagcttct gaaagaccgt gagttgctca
                                                                       720
agaagttcta tatgcaaaac tcatgctgga tcggaagccg gaggaggagc ctcaaccgat
                                                                       780
agatacagca gtatgcagtt tctccttgct gccaaagatg cagtgtccgg tggatcaaac
                                                                       840
aaaatccgga tttttccgct caagacttgg ccgaaaaaat gtcatgagtc catcccaact
                                                                       900
caacagaaag ctcacgagtg tcgtaggttg cccaccatcg gctacataca gcagatcaag
                                                                       960
ataaaattgg cctgcaagct cttgccgatg agagcaaaaa catctccgac attagcattg
                                                                      1020
aggcaggett teggateegg ettaettete tegeacette aaaegetaca tgaaetgeet
                                                                       1080
ccctcccaat atcggcaaaa actccttgcc atgccgggga gcgacaagag acagtttgat
                                                                       1140
cccaatgaaa taaggagctg tacgcaaggg ggggcctgtc gtacagctcc tttcttcgaa
                                                                       1200
attogatocg aactacatca togaacacga cttttctcac aaaggotocc tgatocgtat
                                                                       1260
tcactttaag caggatgtcc ctttggtcaa agatccgaca cccatttcca ccttatcgcc
                                                                       1320
gctaaggcac aatcacggat aagcttaccc tgcaagtcgt acatgctcag attgtgatgc
                                                                       1380
cgttggccag aatcactaac cggtccgttg acggattgag aagactgcta cctgagcttc
                                                                       1440
tgtcgaaggt gttgccattg aggtaagagc ttgtacgtat agatatagtc gaatatagga
                                                                       1500
gtagccacat ctccttcgtg gaggaataag tctctttcag tcgctttgcg ttgaatccgt
                                                                       1560
acatattago caggiotigti coggoattga oggaatgica atgacattig oggagatgac
                                                                       1620
ttatcgctct cgatgtctcg cttgtacacc tttgtgtcgg taccgtaata gccaaatatt
                                                                       1680
gtatgcagat attgtcctca taggtgtatt cctctttttg agtacttgcc atgcctttcc
                                                                       1740
ttgctggacg acgaagtact cggcttcacc atattatctg catcgtcata gctgtattcc
                                                                       1800
                                                                       1820
 gttttgcccg gtgcttgaat
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...513
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

```
tgggctgtcg tattccaacg tgccgaaggc gaagtctggg ctgccaccgc catcgctctt 60 ctcagagact ctatttccgt cttgcggcgg acggactcgt atggcagaaa acggttactc 120 actgttcacc gagcgagata gctgggaggt gacgctgttc tcttttctt gcgttggggt tatacacctg ctgatacaca ttgatccgcg aaatacggaa acttcccccc ggccatgccc 240 tacgcataga gtcggagag gtattacgac cactgcctat gacacagtag accgtatgcc 300
```

ccgttngaca	gccattttt	tatcttatga	aggaggntta	aagagtnnct	gaacccccgc	360
cttattcttg	ccggcaagag	actcgttcgc	tactgaatgg	cagatcggcc	atacttcccc	420
tttccggagg	atttcgactc	gggatgatag	cctacatgct	gcatcgtctg	aagtacccac	480
atgtctattt	tatctcctat	ggcaaagagg	aaa			513

- (2) INFORMATION FOR SEQ ID NO:58
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...711
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

ntccccggcc	cacatcgtcc	aaacgggcag	cagcccttcg	ttttgctcac	gaaagcgacg	60
			ggaaaaagat			120
ctcggtaggt	gtcccagagc	gagaaggact	gtagtgtttg	cgtgccgtct	ttagcgtatg	180
			tctgcatcgc			240
agacttgata	gagcgcggta	tagaaaatag	tgtccactcg	gggcgatatt	ccttttccgc	300
cactatacgc	gacaaggcac	gttgccacag	cagcgatgct	tcccacggta	gcggtcgaaa	360
tcgtggtggg	gagcttcttt	cgccagattg	ttgccgctcc	cttttcgtcc	acgcccgata	420
gggcggtgga	gatcgtcagc	ggctgtcgga	cttggctatt	aaaaacgaaa	ggtgggctac	480
aaggccgtaa	caatgaattg	cgtcgtatcg	ttattggcat	attggggtac	actgtctatg	540
			tgcggaagaa			600
accgtccgag	aagcgataac	cgcttatcgt	gtggctgcga	tcagctgcag	acggcttgtc	660
tgtcgtcctg	tcccaattca	tcgtgcattg	agatcgaggc	gacttcagta	c	711

- (2) INFORMATION FOR SEQ ID NO:59
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 796 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

ccgcagtatt	gccgaattgg ctgcccaaat	ctcgctcccg gaactcctat atccgcatga gagcgaaaac	attgggtgaa gactaccgaa	tggttcattg caaatcattg	acttataatg ggaacacgat	120 180 240 300
ctgctttcct aaaagcagcc acgcacactt atccgctgaa gagatcaatg taggcgaaag	caagagaata cagccattga ttgcgtccaa acaaaaatca taacggtaac gatggtatac ttgcatctgc gtgtttggca	gaagtgagag aggacaagaa tcccccgagg gccttgatga	ccgttgctcc tgtccgctct tacaatcgtc cagaacggct tgctcaaagc	ccgattccac cggtccggat attttaaata ccactcctca atcaacctta aagctgcagg	atcctgtaaa ggtaacactg ggcaagatgt atgacagcaa ttcggtgcga actaccggca cggacaaggc ggagaagatt	360 420 480 540 600 660 720 780 796

(2) INFORMATION FOR SEQ ID NO:60

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...766
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60

(2) INFORMATION FOR SEQ ID NO:61

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1914 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{9}14$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

```
ccctggctaa tgtctatccg atcaatagct tcgacggtat ggctaccgaa gtctcggacg
                                                                         60
 ctttcgtttt acgacgagca gcactttccc gatgcgtccg tggtttcgca tatcaattat
                                                                        120
 cacteegata egettaceat teggaaggag ateegatgga gaacateege ateegeetge
                                                                        180
 gcgagaccga tgactaaagc tctccgaagt cgtcgtcagt gtctccgctt tcggggtggg
                                                                        240
 aggcagcaga acaagacggt gctcaatcct atggatgtct acacgaatcc aagtgtaacg
                                                                        300
 gagatetete gatggegetg egteagaeae eeggeetgea ggagtgggag ategtgaggg
                                                                        360
 ctttttcgtt cgcggaggag cctcttggga aaggccgtga cgatagaagg cattagagtg
                                                                        420
 aagcgttttt toggcaagaa cgattogacg otootgotog ttoacgttto gagacaggaa
                                                                        480
tgttcagcgg ctttcgctct ccaccggagg ctatggggcc acggaaggcg gtgcgctgac
                                                                        540
ggactactcc ggttgcgatt ggcgggtaag tctccctcgt ccgtcgggta ggaatatccc
                                                                        600
cgctttttgt aaacggtggg ggtgggcatc tttccagtcg aatcgtttct atatagagca
                                                                        660
aaatgootca gtgagogatg cogoottato ogtotgotgo toaagoogga gtacaaactg
                                                                       720
cccggtacca accgccctat gcctacaatg cacggacgat atggaacccg acttcgcaag
                                                                       780
atgagtgaag gggctttttc tcttcgtaca cgacctttcc tcttcggctt tgccataccc
                                                                       840
totootgoaa otgoatatat gototatgog ggaogaaaca coatggatto gggatggotg
                                                                       900
tttggaggca tgacttcgaa ggaggcaaaa cacctccacc ctgtccgccg gctatagcga
                                                                       960
agaccacaac cggctgcacc ccagcttgaa atcgagccgg acatagagag cactttccgc
                                                                      1020
accgtagagg cgatgccaat atccgccttc gcttcgattc tcggattaag gcttggaact
                                                                      1080
ctcctacgga tccgattata catatagcga agccaagtct tctgttcgga ggataaatca
                                                                      1140
tcagccttac ccacactgcg agaacacctt gtggcaccta tgccgaagcc ctcttccctc
                                                                      1200
tgtcgaatcg gatctccgct acagcggatt gcgcgccgaa tattccggac ttaccgagtc
                                                                      1260
ggctattatc ctacccgttt gtcagccact tacaagctct ctccttcgag ccggatcacc
                                                                      1320
ttgatgcagg aggctatgcc gccccggcg actactacct ctcccatggc atgtgccgca
                                                                      1380
aaagcgcgaa cactcgcagc agtacaacct gacctatgaa tgcgaccctc gcgtacacaa
                                                                      1440
gtgctacgcc tccaagccta tgacaaagaa attcccgact gaccacgttg gctcccgatg
                                                                      1500
gcacagcete caacetegga agggatatge acgggggetg gaettettet ggaaagcate
                                                                      1560
cggactgaca gatctttcga gcattggttc tcctattcct ataccgatgc tcgcaggagt
                                                                      1620
atctcttttc gcccgatcag gaacgaccgg atttcgtagc caagcaactc tttccaccgt
                                                                      1680
gctgaagtat tggtgtgctc ctatcagctc actatcaacg tgtcgatgtc ctggcgttcc
                                                                      1740
ggcatgacct accacgatcc caactagcct ccccggctta titgaacgca tcgctaccgg
                                                                      1800
ccaatttcag catagigcct cgtacaatta cccattcaag tacaagaaag ccggcggtgt
                                                                      1860
actgtcttca gcgtgcacaa tctgttcaat tcggatccca cctacggcta tggg
                                                                      1914
```

- (2) INFORMATION FOR SEQ ID NO:62
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...355
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

cggaacgatc	cgatcgaaac	cccttttttg	cgatagagac	aaataagacc	aggtatgaaa	60
cgattgatta	tcgcaggcgt	tttggcatgc	gccttgtgcc	ggtatatgga	cagagagtac	120
tgagcgtgaa	cgaatgccgg	cgccttgcct	cgaacacaac	agagacttgg	ccataagccg	180
cgaaaagata	aatgcgccac	cagtactcgc	aaagccgctt	tcaccagcta	cctgcccgag	240
ctctcgccac	cggtacttac	ctgcacaacc	agaaggaagc	tatcgctatt	gagcacgagc	300
agaagcacaa	gctccagaat	ctcggtaccg	accttgtcac	agcatagggc	agaat	355

- (2) INFORMATION FOR SEQ ID NO:63
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 642 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{42}$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

cggctcgtgc aggacaa	tac atgcttgtct	gtacgggcga	tatggaatcc	ttatggaaga	60
tgcctcatgg atagagt	tgg cttccataga	agtagcaggc	atacgagcac	ccattcatcg	120
ttactggtgg cctccaa	ccc acagatcatc	ttctcacagt	tcatcgggcc	aatcccgaga	180
cattgccgac tttcaga	tta caaatgaagg	tggtgctact	ttctccggga	aaatcgaaat	240
agtggtataa aggcttt	ctc ggaaactttc	ttccaagcga	aagaagaaca	catggtctcg	300
cccaagggga aaccaaa	gta ttgtctccgg	agctgactgc	gaatcttctc	tctatacaaa	360
tgccgaactc tttcccg	atg gcacctatta	catgtcatca	gagagcaggg	attttgggat	420
ccgatcgatt tgtttgg	gga cattactatc	gtatccgtct	cattacggat	ctatcctctt	480
cggacatcgc ggtaagg	atg tttctactat	agtactttat	cccaatcctg	ctcacgactt	540
gtccatgtag ccattcc	tcc cacatatgcg	ggcagcacac	ttcgtttgtc	gatattcaag	600
ggcgaatgca gctctcc	acg aagatcgaat	ctgccgaatg	cg		642

- (2) INFORMATION FOR SEQ ID NO:64
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...307
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

ctttgaaggt cccct	ctaga ggatccccgg .	gctgttcgct	ttcttttggt	cgggccgatt	60
tgaggactga atagg	aaata aatgtttat	aagacaaaca	ataagatgca	gatgagaaca	120
tttcgtgtcg ttgcg	atcgt ttcgctgtct	tttcttcttg	gatgacgctt	acggcgcaaa	180
agaatagttg gtggg	tggtg cccatgccgg	acgcgagtac	ttcaacaaca	caagtgagga	240
tatgagaaag gatgg	aatac cggagtagtc	ctgcgctact	atttctccga	tcgatatatt	300
ctttggc					307

- (2) INFORMATION FOR SEQ ID NO:65
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 654 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...654
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

cggcagaaat	aggaaaaaag	gaacggatgc	atgtcagact	ccggttggag	agcttaagct	60
			tctttttccg			120
			ccgctaacgg			180
tgaaaactcg	tgtggaacgg	atgccggagc	tttgaccata	cagggcagca	tcggcctcga	240
ttctcctggc	gacttgccga	tgtagatgct	catgcgacta	ccgaaagact	ggaatcaagc	300
tcatggcaga	ccggcacgat	tggcctgaac	atgtggcgtt	cgactgaaga	tgaaggcccg	360
actggctgcc	ggcaatctcc	tctcgggaag	tgggagggac	gcgtgtcgca	cctgactttc	420
cgaggctata	cctatgagga	ctgacgatcg	acttacaggc	cgacaagggg	cagtggtcag	480
gcatcctgaa	atgaacgacc	ccaatggcca	tatccggcta	tcctctgccg	gagaggggcg	540
cctttctctt	cgagttcttc	ccggttcgaa	tggaatctga	cagcgcacaa	cttcgtcccg	600
atcgactttt	gcccgcttcg	gactgccatc	ggccgatctc	ttctgatttc	ttcc	654

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 654 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...654
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

catattcaga	ocgatatoct	gctttctact	gcccaaaagt	ccaagaacac	tggttcggca	60
actoctatat	catogotata	atcaagaaca	attatctgag	tttggtgccc	gtttcgagga	120
tctctataag	cccctrcccr	gacatgaccc	gagatggggc	gtggcgttcc	tcacatgtat	180
ctcacacaa	gctatcttgg	gcggagctga	ctatgggaga	cttctacgat	cagttcggta	240
ocoottoota	ttccgcacct	atgaagagcg	caacctcggt	atagacaacg	cggtcgcggc	300
ggacgtatag	tactcactcc	ttttgatgga	gtgcgtgtca	aggtattgca	ggacagcagc	360
gtaactactt	cgaccgcacg	ggcaaggtat	tcattccggc	cgaggctacc	tactgggttc	420
tgatctggag	ctgaatgtag	acgttggagc	agtgccatgc	gcgacaatga	ctatcatttg	480
gctatcgggg	atcgttcgtt	tccaaacacg	aagcagacga	agatatattt	gtgggtgtag	540
cgaagatcgc	aagcgactca	acctgccgct	caatgtcccg	attatgggct	gcgcaccaac	600
tttcaaaaag	gaggtctcgc	cctctacgca	gagtatgata	caaatacaac	gatc	654

- (2) INFORMATION FOR SEQ ID NO:67
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1812 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1812
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

```
tcgcaccgga ctttgattac agtgtaatat gaaaagaata gtattgattc gccacggcga
                                                                       180
aagettgtgg aacaagaaaa tegetttaeg ggatggaeag atgtggattt gteegaaaaa
                                                                       240
ggtatgaaga agccaagaaa gccggcgagc tcatgaagaa agaaggcttt cagttaccaa
                                                                       300
agcctatact tectatetea aacgtgeegt caagaceetg aacgtgteet egatgtaatg
                                                                       360
gacttggatt ggataccggt ggagaagacc tgcgtctgaa cgagaagcac tacggcatgc
                                                                       420
tgcaaggcct caacaaggcc ggactgccga gaagtacgga gacgaacagg tactcatctg
                                                                       480
gcgtcgcagc acgacgtccc ccccacgcct atggagaaag aggatccgcg ctctccgtta
                                                                       540
tggatccgcg ctacaaaggt gtgtgcgaga aagacctgcc actgacagag ctctntgcga
                                                                       600
cacggtaaat cgtatcctcc cctattggaa cgagacctat tcccccacgc tcaaggagca
                                                                       660
tgacgaggta ttggtagcag ctcacgcaac agtctgcgtg gtatcatcaa ggtgctgaaa
                                                                       720
aacatttcgg acgaaacatc atcagcctga acctcccgac agccgtgcct tacgttttg
                                                                       780
aattgacgac aatctccgtc tggtgaagga ctatttcctc ggcgatccag aaggatcaaa
                                                                       840
aagctgatgg aggcagtagc caatcagggc aagaagaaat aacccccatc gccggccctt
                                                                       900
tcctattctg cttttcgaca gaaggcaagg aaaaaaacaa gaagagagcg ttgcacgacc
                                                                       960
gttagcggtg caacgctctc tttcatttca tctttttttg ctcggttgcc gcagatgtta
                                                                      1020
tttgctccga ggtctttctc ctacaagacc ttgtcgtaca catgcatcag ggatcgggta
                                                                      1080
cggcttcggg tgagaaacgc tctatatagg tacgcccgtc ggctatctct tctcgcggag
                                                                      1140
agagetgteg gagaggatge tgteeageat ggatgeatea ttteegeate gteggggteg
                                                                      1200
gtgtacaggg acgaagggcc tccggttctt ccagacacga acccgtggcc gcaacgaccg
                                                                      1260
gcacgcccga agccaggctt cgacaatcgg gataccgaat ccctcgaagc gcgaaggata
                                                                      1320
gacaatacct ctgctccgcg atagatgccc ggcaggaaag caaatgggac atgtgcagca
                                                                      1380
tgacgagccg gtctgccaca cctgatcgct ctgcacactg cgcacctccg cacagtatgg
                                                                      1440
cgtacgette cetacggega cgageegaat tgteggteae ggeaatgtge caaageetee
                                                                      1500
acggccagtc ggaggttctc ctcgtctcga tgcttcccac atagagcagg taacgctcag
                                                                      1560
gcaaagcaat cgctccctcg ctctcgactc atcctcctcg gtagcctgtc cgaaggcggc
                                                                      1620
gaacaaccet gatagacgae ategateega teggeaggea egtggaaaae teeateacat
                                                                      1680
cgcgcttggt ctgctcgctt atcgctatca ccctgcggca caacgggcag catggccgta
                                                                      1740
tttgagccga tacagcagcc tgtcacaggc ttataatagt gcggatagcg aatgaagatc
                                                                      1800
aagtcgtgga tc
                                                                      1812
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 672 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...672
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

```
cgatttctgg agggctatca tccgatccag acgggatagc tttacctctc gggcacatcg
                                                                        60
tccgcgaggt ggcgagcagc ataagtaccc ggccgttcga atacttgaac atgaaggcag
                                                                       120
agtcgtaacg cacctcttcc atcaggcgag agtggcttcg aagtcttcct ccgtctccga
                                                                       180
atggaagcca cagaagggtc gctgctgatg gcgcagtccg gtatggcccg gcggatagct
                                                                       240
gctacctgtc gagataccac cggcgcgtat agccgcgctt catgacgcgg agcacttgtc
                                                                       300
gcttccgctc tgtgccggca ggtgtatatg attgcagata ttgggtatcg tgccatgacg
                                                                       360
gcgatggcct cgtcatccat atccttgggg tgggagaggt gaagcgtatg cgcatgtcgg
                                                                       420
gcacagette ggccactget ggageagate ggggaagegg #tgateegee egttttgtte
                                                                       .480
```

gtatcggtag agtttacatt gatcccgcac ttcgttgagg gggtacgatg cagtagctgo atatgtacgc ca	, afoctiticta	tttcgcgggct	CCLLLCLCBC	CCCBCBCBCC	540 600 660 672
--	---------------	-------------	------------	------------	--------------------------

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1412
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

```
tttcgtagcc atgcacttag tgcggacgaa tgagagagag atcttcttgt ccgtgtaata
                                                                        60
gatacccgtt ctatactgag agccgacatc gttccccttc tattgaggat tgtaggatct
                                                                       120
atggtottga agaaaagato gagcagogag agagogatag otcactogga toatattoga
                                                                       180
ctcttaccgt ctcggcaatc ctgtggtttg ggaacagacc tcttcatacg aaggatcctc
                                                                       240
gacatgccgt tggcataccc gacttcggta gccacgacac cacgcacttg tttgagaaat
                                                                       300
gctcggtacc ccagaagcac ccaccggcaa agtatattgt cttgtctcgg gaatactgtc
                                                                       360
attatgettt geegaagaag ageaactace ggaetaagag aaaaactaaa agaageeata
                                                                       420
ctgataagaa taagagaaag aacttcataa caaatcggat tctcttttca tgagaatggg
                                                                       480
gaagagacag ctcgaagtag tggcaggtcc tattcatgat gatagggctc atggttgaga
                                                                       540
tagtcatggc acgatacacc tgttcggtga agaagaggcg gatcatctat gagagaaagt
                                                                       600
catteggetg agegatatte tateggttae ageeteegea etgeaggget aaateeatat
                                                                       660
gggcctccta tgacaaagac cattcgcggg tgccgatcag cattttcttc tgcaaaaagg
                                                                       720
ctgaaaactc catgcggaat actctctgcc tcgctcatcg agcaatacgg tgctgtccga
                                                                       780
cggcgaagac gagcgagtat ctcccgacct tcggcatcct titgctgttc ggagaaagct
                                                                       840
tgctacccag acggacatcg ggtattacct ccacttcgaa agaacataat ggctcaaccg
                                                                        900
acgaatgtat toctcogttg cotgaaccat tgtttgctgt oggtottgco tacaacgago
                                                                        960
agtacgatct tcatcagaaa gcagatcatc ccccgcatcg gcgttggaag cccaacccgt
                                                                       1020
tgccggctgg acggcatgct cggttgttgc gttggaaaag tcggagcacc ggcggcagca
                                                                       1080
tttcctgtgg caactgctgc tgaccttgct ggcccgatat atccgcgtcc atgcgccaag
                                                                       1140
cetteacate ggtgtaceaa eggeegttga acteaegett teaatatega eeeagaeegt
                                                                       1200
aacctgatcg cctacttgat aggaagatca atacgatctc cccacacgct gaagtgtatt
                                                                       1260
ttgcgagggt attgtcgagc gtttccagta tgtactcttg ttttttccat tcctttccgg
                                                                       1320
aagcttgccg actcccgaat tgagtggcag tatctgaata agctgccctt gatctgaata
                                                                       1380
                                                                       1412
 tccatatttg ttttgttcta acatagttat cg
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 612 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...612
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

cccggtggag	aaaatagaga	gaaagctgcc	atcagctgga	cggacgaaag	atgaagttag	60
tcaccgaagg	agaagaacag	atcttcaagc	tcatcaggaa	aagtaatccc	accaccccc	120
actatctctt	ccgttcggaa	tggaagcgat	aggaaaagag	gatatgctcc	atgcaccgag	180
tgccggcata	tcctctttct	ttttcagcta	ttgctgctga	tgaaacagcg	tcccccgtca	240
gtctacctgc	gagagccatc	gctgataacg	acattgtaca	ccttgggttc	gcggcgaatt	300
ggttccttgg	aatctctnct	nggcattctc	gacaaagaga	tcgacagttc	tttcttgacg	360
aggttgatcg	tacaaccgcc	aaatccgcca	ccatgacgcg	cgaaccggtc	acgccacaat	420
cccgtgctat	gccgttgagg	agtcgagctc	ttcgcagctc	acctcataga	gacgactcat	480
accatcgtgc	tttcgtatat	tttctgtcct	acggtttcgt	agtcgtcgcg	ctccagtgct	540
cgcacacatc	gagcactcgc	tgcacttctt	cgacgacata	ctcggcacca	tataatcctc	600
ggcagagact	tc					612

- (2) INFORMATION FOR SEQ ID NO:71
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{498}$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

cgtgatacgt gaagcgatg	c cttctttgtt	tccggctccg	ttaacgatat	agtattgtcc	60
ttatcaaccg ttactttc					120
gaccggtctc ttcgctgat					180
cttgcgacga tcgccgato	c gggagccttc	actgcacaga	tcttgaggct	gccgcgcaga	240
cggttacaac caaggtgg	g agtgcttcgc	tgtcgatgtc	ttctgcaatg	atgagagggg	300
cttgcccgtc tgaaccgtt	t gttcgaggat	cgggagcatc	tcttcaggac	ggatattttc	360
ttgtcgtaga tgaggatga	a aggattttcc	attgcacctc	catcttatcc	gtgttcgtta	420
cgaagtaggg agagatgta	ig cgcggtcgaa	ctgcatacct	tccaccactt	ctaccgtagt	480
gtcggttccc tggcttctt	c taccgtgata	acgccttctt	tcttcacctt	gcgcatggct	540
cggcaatgag gctaccgat	g ttttcgtctc	cgttggcaga	gatcttggta	cgtgctcgat	00a

```
cttctggaag tcgtcgccca cttccttagc catacctcaa tgtgagttac cacagccttt
                                                                       660
acagcettgt cgataceaeg etteaateea teggattgge teetgeegta aegttettea
                                                                       720
gacccacgcc gataagctct gggcgaggat cgtagccgta gtcgtaccgt caccggcatc
                                                                       780
gtcatggtct tggaggctac ttctttcacc aactgggcac ccatgttctc gaagggcact
                                                                       840
ccaattctat ctctttcgct acgctcacac cgtccttggt aagtgcggag ctccgtacgt
                                                                       900
cttgctaagg ataacattac gacctttcgg ccgagggtaa ctttaacggc atttgccagt
                                                                       960
gcatctacgc ccttcttcag aggtcgcgag attccatatc gaatttgatt tcttttgcca
                                                                      1020
tagtotttat atttattatt tattttttt cttttttgga ggattattgt ctcttcctta
                                                                      1080
ccactggggt ttcctgtttt tgaaggccaa cctgcagtgt taacttgtct gatttttttg
                                                                      1140
ttttgcccat tagatgattg ccaagacatc gttttgcgca tgatgatata tttttcaccc
                                                                      1200
tocagotota tttcagtgcc ggcattttgc cgtagagtac ggtgtctcct gctttgagca
                                                                      1260
ccatctcttc gtcttcgtgc cgttcccgac agcgattact tcacccttga gaggtttctc
                                                                      1320
tttgccgaat ccggaataat gatcccgctc actgtttttt cttctgctgc agcggcttta
                                                                      1380
caagtacgcg gtctgccaat ggtttgatgt tcattgttgc tggtttgtta ttgttagttg
                                                                      1440
attgtttgcc tgtacaaatg ggaagcctct atgtagctcc gcaattttta tgtcaata
                                                                      1498
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 733 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...733
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72

		tcgaaagcgc	gcaattcttc	cgcggcagcg	tacgtcccaa	60
agtcgatcag	accetegega	togaaagege	ttgaggaggt	atooccatce	agatggcgca	120
gcccngtaag	tctgcaataa	teggeceace	Ligagiage	25665555	cataccatas	180
	cageractet	togogagoaa	attgggccga	C88880C888	6666666	240
********	2102200020	tacgageete	gagaatcaat	gccligicgg	ggcggaaacc	
gacactccta	trotracect	ggcggcatta	cggcgtgtgt	CECCCCEEC	00000000	300
gacaccccta	ctgccaaaata	80.00	agaaagagcc	gattcctcta	tcttcaccgt	360
ctacgccttt	gracaaggra	agegaagega	-66-6	ccotaaccaa	ccctttgact	420
atatcccgaa	gccacgccgc	gggctattgt	teagecaagg	tatetestee	agccccatcg	480
tcacccgggg	agaatgtcga	tgggaggaaa	ttagattggt	caccegeee	agccccatcg	540
tacctcaact	atcattttcg	gatacatcgt	ccgcttgccc	gigicitigea	545566	600
+ + + + + + + + + + + + + + + + + + + +	casacttooc	catttcttct	gtacagctat	accegnice	care googg -	
cccccccc	cttccaaacc	oogaaaattt	ttcccgaaac	cgacaaaaat	aaattttccg	660
cgattgttt	CLCCGGGCC	anacttagat	atataaatna	aatctttgga	tatatgttcc	720
		anceceggae	a ca cada ca		•	733
aaaactttgt	tta					

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 733 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...733
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73

			tcttactatg			60
tgcattttgc	tgaggccata	cgctaaaaac	atttcaaagt	atgtatttgt	ttggataagc	120
ttttccctat	catatattat	cgctgctgtc	taacctctat	cattgagtat	cgtatcatcc	180
gccagcaatt	cggttaaagt	tcccgacggt	attctggtgg	tagaaacttc	ttgtcaggcg	240
gatagtgggg	taagcctgaa	cgtacaagaa	aattatcatt	tgtgggacca	aaaacgtggc	300
gcggcaattt	tttgcttttg	gttcgggaaa	aaataatttc	tcgaccaaaa	cgaaaaaaaa	360
ctcgcgcgta	aattttcaaa	aatacgaacc	atatctcgac	actttgggtt	cgtaaaatct	420
ttttggccaa	aatctttcgg	aaaaacaagg	taagcctcat	catctttctt	gttgtggaaa	480
tccgtgtcgg	atggagtttt	acaccggttt	tcctgtcggc	ctcttccatc	aataccgatg	540
aagcaattcg	cagggtctgc	aagtttgaac	cggatacttt	atttttgtct	cattacgaaa	600
ctattttcgg	acagcgatat	gagccaaaag	cctacaacga	tcggaaaatc	atcctcatta	660
ccggcgggca	cgttcgggca	aaagtcctat	gctgagcaga	tggcactagc	gcttgccgtc	720
atcctatcta						733

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...3401
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

ttcataggta	taaacgaaga	cagcacgacc	tcctttcgtg	cccatcgtag	gtacacgata	60
tgttgcgctc	catgcttccg	cctcataagt	cctttatgta	caatactcca	aggattttac	120
cgattggctc	ccttattact	ggcaaggtac	tctcagacta	cgcgatatac	gtacaggata	180
gatctaagcc	ctggaacgat	gtcgtacgga	tggctnattc	gncccgacgc	catgaagaag	240
atacgaaggc	tgaaagagac	ggactccgct	gtacgtcggc	cacggtggac	gaccgctgcg	300
cctctgccgt	atatccatgt	tccgacagga	agcatangga	tttgcagcgg	agacattgca	360
gcggctggcg	gaagtcgcca	tcgaaaggca	tgaggtgaaa	tagtcggttg	cgaagatagc	420
gaagggcgtc	tactggctgc	ctcttcctcg	cccacgatca	taacacggcc	tacacgattg	.480

cttccggcca attcgtgaag gacaggggcg caatgccgga gcttttgtcc tgtatgaggc 540 atttggaggg cttgtgagat ggaaggcatt catacatttg acttcgaagt tccatgttgg 600 aggggataga gggattette egetegtteg gaggtateaa acacettatt teegaetgte 660 caaaggtogg attggottat atggocacta agacgtaaat ggogagcott toatgataco 720 ggtcagcaaa aacagtatga atactgaagt aatccactac atcattcgct ttctgatcgg 780 agataaagcg gaaacgatca gctcctcagt cgcatcggtt atacctcgaa gcaagcgaga 840 tgtcccgata cagcattgtc atccgtgctt caaacttctt cgttcggata tttacgtacc 900 gataaggett tteeettgtt acegetgaaa gatgggaggg egtaeetete etttttggag 960 agccgaccga agagctgttg aagagagcga cacactggtg ctgaatgccg acattgtcgc 1020 ctctacatat tctgatctcc cgctacgaag aggatgtacc ggcgtaaact tcgagataac 1080 acggacgatt tccgggaaga gagtccttgc ctttcaaagc aggattttac agcgtcctgt 1140 agtagatgaa tacggggcca ttctgcgcac caaaatcgtc agatgggctg gccggtaaaa 1200 gacccagtcc cccatttctc catgggaatc tgacgcatga cgtagacgaa ccgttcgagt 1260 acagaggatg gagagttttg cccgagcatt gatcaaagga acgcaaatct cccttcaagg 1320 cttccgtctg gcttatgcca atccggcaag tgatcgtttc ttcacttttc ccgttttgtg 1380 gattgggata aaatattgcg cagcaaaatg ccggattgct gcggattatc ttcttcttca 1440 aagcacccgg aaaggcccca caggatgcac gaactattcg ctgagaaaac cgctctatca 1500 atcgctccga tctttggtta aaacaatgga atagtgatag ggcttcacag caactactct 1560 gccggtctaa cccagaactg atcggaaagc agcgcaagcg acttatgagc gataccgtat 1620 ggcagtcgac tgcaacaggc atcactacct tgcagctcgt gagccgagga catgcaagcc 1680 ctgatctcgg caggtatcag acacgattat accatgggta tgccgatgtt gcaggtttcc 1740 geettggtac atcccgtece gtteetteat tatgcettee acaagaegge tgaccgaget 1800 1860 gatectgeae ceattacact gatggattgt acgetgeaca ggeaagagta tatgggeetg gacgaagcta cggccataga agttggtgca aggaaactgc tgatgcatac ttcatccacg 1920 1980 gaggagaagc cacactcctt tggcacaacg aatatctctc cgcnacattc atccctggca 2040 tgcccgtttg tatcgagaag tactgaggcg atagaaacca tggaggaaaa acaagaggag gaatettteg actacgaacg gecategace aatgaaacgg gtacteatet tegeogatat 2100 cttccctcgg cttttgctcc gagagctgcc tatctgacca aatatctgcc tcgattggtt 2160 gggaaccttt tgtaataacg gaaaaaatgc cgactccggc atcccgtcgc acggcgatgt 2220 gtttggtgga ttttgcagtg atattccggt aacgctatcg atctctcttc ggcttcgttt 2280 2340 ctgtctcaag cgattcgttc agccgtctgt tcggcgaatt gttttgggag cagaaagaag 2400 agcgattcta caagaagcgg cgaaagcttt tcccagtgtc aaattcgatg ctgtactttg tttacctatc gcaagtttcc ccttgctacg gcttgccgct atgcacaggc catcgattgc 2460 cctgggtggc ggattgccgc gatgtgatcg aacagtacac aactacgatt ttcttcctcg 2520 2580 tggcaagcga ctgccaagtc tgctgatgag tggcttcgac accgctatat ttctctccga 2640 aaccattatc tccacaagct gatcgtgtag tttcggtatc accctggcac tgcaatctgc 2700 tegeagagtt aateetegta cagaattgat etacaatgga tatgateeeg agetttteet 2760 cgaggatcgc ttccttgtgg caaattcatc ctctcctata caggcgattg ctgactccgg aaatgcacga tcctaccctt ttgttcgaag cttggcttct gaagctcttc aggaggtgcg 2820 caaagagaga cgaatagagc tgactggtat gtggacgaat actcccgctc catcctgcaa 2880 2940 ccattcattc gcagtatgct ctgaaggata tgtgccgctt tttcccgatg gttccggctg 3000 tcaggtaccc gaaattctcc gccatagcag tgtcctgctc caactgggca cacagagaag 3060 cccggaggcc cccatggtat agtatcgacc aagctattga gtcactggcc atggaaaaac ccatcctgat ggtaaggagc gatgaagtat cgtggcagat attatatcgg aggccgaggc 3120 aggattggct gcacagcgac agaagaggta gccacattcc tgagtgatca atacactcgc 3180 tggaagcaga aggggatact tctcttcgga acccgaacag gaattttatc tccatttttc 3240 gcgtgaagag gaagccaaac aatatgctcg tctactggaa tcgtcgtcgc taactaaatt 3300 cagcatcgta tcatgaagta ctgtgatttt acccgttgcc tctcccttcg gagcctaata 3360 3401 cgacagtcat tgccggtcct tcagtgcaga aagtgaggag c

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 784 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...784
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

ctgcgccaaa	agctttacgg	ccaataagcg	tcttttcggc	cgcgacgagc	gtataagcaa	60
		gagaagcata				120
		ctatcgcgtt				180
aactccctgt	acatccctta	tacatcggca	gatccacacg	aagagcctcg	gcctcacgca	240
cgacaagccg	gtcagcgtct	ccacttccgt	ggatccgccc	tgcaagaaat	cgcttgcata	300
gaagaagtac	tttcgggagg	catcttccgc	tgtttgtcca	gtactgttgg	actacatcat	360
cggggacttg	cccgtatttg	gcgcggaaaa	gccggccacc	tcttccaata	aagacagcag	420
ctcgggttcg	tgttcggtca	aatcgagccg	atgggtttgt	cgaagtaggc	cgtagcggta	480
gccgttacgg	gatcatcatg	aatttcttca	taatgtacca	atcgatatcg	gtcggattaa	540
		taagcagttc				600
		gaaaagttcg				660
		tagacaatcc				720
acgcatgcgt	tccgcatgtc	tgcaccgttg	agcaagggca	ggatcttcgt	gttctgcccg	780
atca						784

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1584 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{5}84$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76

gtccataccg	ctaataggtc	tcaaagcgat	gtcacataga	tgtcaattaa	ccttcatatt	60
		caaggtttta				120
		ttgacagcat				180
tataactgca	gaccagtctc	aaaagtgtag	tagtgaccgg	atgatgactc	cctgtttaaa	240
agcatgattc	ccctctattt	caatatatca	tgtagatttt	cggcatattg	ctacgaaaag	300
aacgagtaat	gcccctttgt	agatccccca	agagaatccc	ccccgaatct	cgcccaagct	360
ctatcgcaaa	atgactcccc	gccagagggc	ggtttagcgg	ctgtcaaccg	aaagtcgtct	420
taaagagtaa	ggtgtgtaaa	ccataatgga	ctttagagaa	atctctgtaa	ttttaatctc	480
gaaattaaca	tctccgagtg	tcaactcttt	tcagtacacg	tcactccaaa	attttcctat	540
gtacgctccg	aaaaacgtgg	ttcgagaaaa	ttttcatttt	ggttcgggag	taaaaaattc	600
		tccggttcca				<u>,</u> 660

anattacaat	tcotaaaata	cgatccgcaa	atgagatgaa	acagtaaaac	atgtctttt	720
gaarracggr	ccgcaaaaca	gacaaatgga	gacaagataa	aaagaaacca	tccggagagc	780
atctgcttt	ggaacgaaac	agccccccta	ctccattttt	aatatatact	accttaggga	840
ttttcccggc	Ctctcggcat	teceteceta	agatatagto	actaccatat	tatatactat	900
ttgaccctac	aggatttttc	tcgctcgaga	adacacagec	atancarac	accustocco	960
ttttgcggag	aaattggggt	gttttggcct	ccgggaaaca	atgacaggee	acceaccec	1020
tgaaacggat	ccgtcgatga	caaaaccacc	gccggccgga	agagggtgtc	agtctcccat	1080
tctttctcta	gatatagcaa	taagaatgtc	acaaaagaac	aagaagcggt	cttctgcctt	
ttccattcaa	ggtttttggc	cattatgagt	attgccgttg	tcctcttctt	ctggggacta	1140
trograticat	tgagtttgtc	ggcagaggaa	taggcattcc	gtgagagaag	acctctcctt	1200
caatctgctc	ttatcctccg	acatgatgaa	acgcaggcac	aagagctaca	gcgacagata	1260
acaaccacac	ccttgtcaaa	gatgtcagct	atatctctgc	cgatcaagcc	ctcgaagaga	1320
t casasacas	ttooocoaao	acgatccggc	caagatgctc	ggctataatc	cctgcaagcg	1380
cgaaaaagaa	ttcacctcaa	agrecaatae	acccatccgg	aagtctgaaa	accatagact	1440
gaaatgtgcg	cocceaa	agectaasca	tctggaatac	agggcggata	tgttcgacat	1500
ctgccatccg	Cacacggaac	tataggtata	attetactea	-666-66	cttectcctt	1560
agtacaccgc	aatacacgcg		greeteg	ccccaccago	cttgctcctt	1584
ctgatcaact	acatacagat	caac				230 .

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...627
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

						60
tegattccgg	cagatttctc	cgtccaactt	tagaagaatg	agttggatat	ttggggtaag	60
nactataast	agattattaa	aaacataatt	totapppaat	taattgctcc	ttgtataacc	120
aggiglagai	88accecce6	undentalet		atataanata	attacatttt	180
aaatcaatgg	gatcattcgc	atttccattt	tgccaatgaa	gicigcagia	gttacatttt	_
taacaggata	ctgcttcgtc	gcttaacccg	tcagacatca	atatgatatg	cttatccaca	240
	aaccataata	tttctcgcca	ttttaagccc	cccctgggta	tgtgtcccca	300
gcagtgaagt	ggccataatg	ttttttt	cccaagooo		0000100001	360
aataggagtc	aaagcccgga	ttttttgaca	gagaaaagca	gtgctttggt	aaaatcagat	7.2.2
aagroatoao	gctcatggtc	ataactcaca	aggcgatncg	caccccttct	gtagccgtcc	420
aagegaegag	6000000000	nnnnnaata	toccuatura	atoocaoact	ttaatctggc	480
ccttaggcaa	cattttttt	aaaaacgccg	CCCCgacgca	acggcagacc	ttaatctggc	540
aatgttttgc	ctcccattga	cgaagactgg	tcgataacca	tcaccacatc	gacaggtacg	7
++accacttt	aotaotoatt	tttagcgtca	catcccaage	attgggattt	caggatccat	600
				000		627
tggattggca	accggtaccg	catactt				• • • • • • • • • • • • • • • • • • • •

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 611 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...611
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78

ctgctctaat	aaagaaggtg	atataatagc	tcttgttact	tcatatacag	atttatgagt	60
ggaacccttg	cgatcagaaa	agcagatgaa	ggcaaatgca	acttgttggc	ggagatatac	120
agaatgcgat	cgttcaaaat	atatgcagat	ggacgacaac	aagattgctt	gtgaagtctt	180
cgggactcct	aacggataga	tggtcggaca	agggtttgtg	tttctgacgc	atctgtcttt	240
gatttgagtg	gtatgaagat	gaaatatacg	gaggcctgat	atttgacact	ttctctatag	300
cccttgggac	aaacttcttt	atgcgaaatt	tggtgggatt	atgtcaggag	taaagagtct	360
tttataacct	ctttcatttc	tccgacagtt	gtcaaggagt	ggatgtctat	actttggccc	420
gggaagataa	ggatcgaaag	taaactccgg	tgtctgaggt	gttgcttttc	gacctggctg	480
		ccattgataa				540
ctaaagcgaa	agcggtattt	acgtagtctc	ggtgcggtct	cttccggaag	gtatcagtcc	600
taaggtgcag	g					611

- (2) INFORMATION FOR SEQ ID NO:79
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...648
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

cgatggtttg	ttattcatag	aagagttgcc	taagatctta	caatatccgt	agtggtgttc	60
tttttcctca	tggtaatcaa	tagtataaat	ctaattgagg	aatcgatgga	ttggctacaa	120
gtctggtgct	tctggggatg	ttatttttat	accattcttt	atctatgtca	atatgtattt	180
atatgtaata	atctgttgtc	tgttattggt	tgcttgggag	cttttcttcg	gatgaatctt	240
tatggacaac	tgagaagcga	acaaagattt	tcatgggaga	tacgggatct	ttaatttagg	300
ccttcttttg	agctttatgg	ccttacgctt	gcttaccccc	attcaaatac	tgctttacct	360
cttccatatg	tagtagctcc	gctacttatt	cctggttcga	tttattccat	gtttttgtat	420
tgagaatttt	atcaaagaaa	atccttttaa	acctgataag	agtcatattc	atcatagact	480
tatggctttg	ggttgacgca	gagacaaaca	ctgttgtcat	attactatac	tctatcgcgt	540
ctctttgtta	atatctttgg	gtacccattt	tttaatatca	atgtgctgtc	tgctggatat	600
cgtcatatgg	atcacatcca	atatgcttat	agccaatttt	egcgcaaa	- -	,648

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1764 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1764
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

```
60
cagcatcata ccgggacagt atgacatcga aagcctcatc gcatccttcg tataaaggct
gaccaattca tcatcagtca gcttgtggaa actgctcaag gagaatcctc tttatttatt
                                                                       120
gttcagaagg tagatatgcg tcgatagcga ttcttttaaa tgagacttat tgcaaagaaa
                                                                       180
aacattttt ttcgacaaac aaacagaagc aactgcttat caacccgact aatgcagcgg
                                                                       240
                                                                       300
aagagcagcg atcgttcttt tccaagcgga gtgtcatcgt ggggctatcg cataatgttc
ggggccgaag aactgtatcg ggccggggta aacgtactcg gtgtcaacgc ccattcgcga
                                                                       360
cgcatctcgc gcaatgctcg gtacggttca cctccatatc caccaatgct tttcgaatca
                                                                       420
cgggcttcat ttttccgctc cacgctccat attcatcatc atcgtcatgg gcacgccgcc
                                                                       480
ggetteccat eggatacagg atetgeegta ttettgateg cagecatgta geeegtette
                                                                       540
ccgctgcgat caggatagaa gctgcacgtc cgagacagta gcagtagtgg catcgaagtt
                                                                       600
ggagggcatg gcacagcgtc cttcgtagcc gaagaagggg taagcgtact gaaccgcccc
                                                                       660
tgaaatcgtc cttcttccgc ccattcgcca gcttctgagc cgtcatgtct gccaagagct
                                                                       720
tctcggtggc aatgacgaaa cctgcacatt gccgtgaggg tcgcgatcgg caatcaactg
                                                                       780
tegaccacat ccaceggeaa getgtegtae aggegegaat tetegggaet gagttgttet
                                                                       840
tgatatactg tototgtgcc gaacgtttga tgagcttgaa ttggcatcat tttgggagag
                                                                       900
aaactcgttc agctccttga tcaacctctt ctggccggca ggaattcgat caacccttc
                                                                       960
ggaatcagta ccgtcccgaa ttcattcctg cctccgaccg acgcaccacg gtctcggcga
                                                                      1020
                                                                      1080
tataggtcac acatcgtcca gatagtaatt gttggcctcc acctcttcgg atacgataag
atattggggt gggtctggag ggcgcactcc agtgtaatat gagatgcgaa cgccccatca
                                                                      1140
gcttgatgaa gtgccagtac ttccgggccg aattgcatcg cgctggatat taccgatcag
                                                                      1200
                                                                      1260
ttcgctatag actttggcgg ccgtgcgaag ccgaaggagg tttctatctg tttgttttc
aagtcgccgt cgatgtcttc ggacagccga tcacttgtat tccggcatcg atcgaggcat
                                                                      1320
agtctcggcc aggatgcagg cgttggtgtt ggagtcgtcg ccaccgatga tgccaatgcc
                                                                      1380
                                                                      1440
ttgatgtcca actctcgcaa tatctccagt ccggcttcga atgttcgggc ttgtccagct
                                                                       1500
tggtacgtcc ggatccgatc atgtcgaagc ccccgtattg cggtattcat ctattacctc
agcagtcagt togogatact atgetcgate aggecatecg gtcccataag aaatccgaag
                                                                       1560
agccggcttc ggggttgagc agcttcatct catcgaacag accggctatc acattgttcc
                                                                       1620
                                                                       1680
acceggagee tgteegeeg aaaggataac ecceacatte gtaggagata eteegteege
                                                                       1740
tctcctccag gtgcgaaaga aataagcggc aagcctatgt gcggggaaaa atagcagcaa
                                                                       1764
 tctcttcttt gtccgaaacc gggg
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 670 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...670
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

cgctggaaac	ctgaaggagg	tgtgcccgag	gtactggaga	ttccggccgg	gagcaagaca	60
aagcgaaaga	aatgcatcag	gctttggtgg	aggctgcgcc	gaaaacgatg	agagcctgat	120
ggaaaaattc	ttcgatcagg	gaagtcttct	gaagaggaga	tgcgcgatgg	tatccgtgcc	180
ggtctgatct	cgcaggtatg	taccccgtgt	tctgtgtcag	tgcggagaag	gatatgtgtg	240
tgcgcgtaca	ctggagttcc	tcggcaacgt	ggttcccggc	gtgaacaaac	tgccgcacct	300
gtggctgtga	gcggagagga	agtgaaaccc	gatgcttcgg	ctccctttgc	atccatttct	360
tcaagactac	gatagaaccg	catattggtg	aatatcatat	ttcaaagtaa	tgagcggtac	420
cctcaccgag	ggagtagatc	tctcaatgct	gaccgaggct	ccaaggagcg	catcagtcag	480
atattcgtgc	ggccggacag	caacgcatca	aggtggacca	gatgtgtgcc	cggcgatatg	540
gagctactgt	gaagctcaaa	gaggtacgcc	gtggcaatac	gctgaacgaa	aaggcgtgga	600
gcatcgtttc	gacttggtca	aattcccgag	cccaagtccg	tcgtgccatc	agggctgcca	660
acgaatccga						670

- (2) INFORMATION FOR SEQ ID NO:82
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION $1...3\overline{43}$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

tgatcgccat	attgtcccaa	gagcataagg	atatggagga	gaaagtccga	agaaacttca	60
ggaaatgata	gcggatacgg	atcatcgtct	ggatatgcgg	atcggcagac	cgaccgaaag	120
atcaggatcg	gcagaaagaa	tgccggctgc	cgaagtcggg	tgtcatagcc	gactggctgg	180
tacgggatat	gatgcgtttc	agcccgtggc	gaaagacacg	agtggcaagc	ctctgaacaa	240
tagcaggcca	acagcaccga	ataccggatg	ctacagcgcg	ccctcgccct	tttcgcggag	300
agaaagagcg	tctgacaccg	tatttccgcc	agatgaatct	gac		343

- (2) INFORMATION FOR SEQ ID NO:83
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 656 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...656
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

ccgaaccaat	ggcttggcta	tatgccggag	gcgatcgtag	aatcaacaag	tggtggggga	60
ataccggcaa	tgctgagaat	aagccgatca	acttcttcgc	ctgacaactc	gcggtggact	120
tgtatatgac	gtgccgatta	ttacgcagaa	ggtgctattc	cgggagggca	gtacttacct	180
tttgccaaag	gcttatggcg	gataagccga	gttatacggt	ttataggaat	cgtcattaca	240
tatatgtatc	aagacgctgc	cggataagat	agaagtgaag	tattctattt	gcgatggaat	300
tttagtaccc	aacgatactt	atatgggcta	tggctacaac	gtggagtcga	tgagcaaggc	360
aatgtcacca	ttactaatac	gatgcagaat	tggatcccca	tgttgtgaga	ctcgttgcta	420
aaaatggtgc	ttactttggc	tccagcctac	cgatacttcg	gttgagtttg	ctgagttagc	480
caacggtgct	cgcaaacatt	caaagtaaat	aaagatgctg	tggcggtcgg	ttctgcttac	540
tggaggttta	ttacaacccg	gatccgaatg	caacagggtc	gttccggaaa	agttttatca	600
agaaatagac	agacttatga	aaaagtattg	gtatatgctc	gttgctaacg	agtgtt	656

- (2) INFORMATION FOR SEQ ID NO:84
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1128
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

```
ttaaggagaa ggataaatga aaaaacctta aaaacatgaa agtaggagat aagtgtgaga
                                                                       180
atgagtgcgc ctgatcttgt gatcggcgca ctcttttcgt tgtttggtcc tatggacagt
                                                                       240
ctattgtatc cggatcgtat tcgggttaga gccctcctcc tcctgatccc tgatgccacc
                                                                       300
accggtttga gaattgctat cgcctgcatt ggcagaagca cctccggaag cggcttgccg
                                                                       360
tactoggoga acttoagato oggagogato aggtacaato cogttogoga gtgacogtat
                                                                       420
                                                                       480
tgtaacgaca ctctgccctg aattgacccg aacggagttg aactgggagg ctttcacatc
                                                                       540
ctctttcttc ccactcccga tcctttggcc tgtgcaatga gacggaaaca accgatgcct
                                                                       600
cgagcttgat cttcttgccc gaagccaatt ccctgcgcat gacgatgcca aatcgcgcag
gataccgaat acatcgcccg ggctggctcc cgaaagtctg agatttgttc tgcgatgtgc
                                                                       660
agggtggagg caatgctgcc gttgatactg tctgcggata ccacagcttc ttgcctgttg
                                                                       720
ccttgtgggc aatacggatt gtcttctttt gaagaataac ataataattg aaagaattaa
                                                                       780
tgattaataa tgcggacttt ttctgtccat taatttaata atagcaatcg agaatcgatt
                                                                       840
                                                                       900
cggcgccatc ctcttctctc tgtttgcact gcaaagataa ggtaaagaaa ctgatcgtcc
aaatgttttg cagaaaaaag ttttcaacaa caagggcgct ttacgcttta tatataaaac
                                                                       960
ggcttccgta tttcttatac aaggcttcga agcactcttc cggctttcgt aaggggagct
                                                                      1020
gaaatccggt attcggcgtt gtccgaatga tttatatata aagtattttc gattaataat
                                                                      1080
aaatcgattt ttatttatat attaatcgtt ttcattttgg gggatccc
                                                                      1128
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1094 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1094
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

caaaccttta	ctgttttctt	cecteagtac	ggcacatgcc	gatatgccgt	ttggtcttcc	60
at cat coat a	ttctttaggg	tatettacet	ctggtggtgt	tcctctattg	ectectteea	120
gicalicata	caccaggg	caracactac	ccaacttcta	cacattccc	aaatggcttt	180
tcattcgttt	Cacgageeee	Cggacactgc	ccggcttctg		tatastass	240
ttggctatgg	gttacccgct	ggctatcatc	atggccaaaa	cgacaggcta	tgtgatggca	
caaggtccga	cagcatccgt	ttggagctgc	tgttggcgtt	gggtggtctg	cttacttgtt	300
gccttgcaat	tcgggttggg	cangtggcta	agcaaacgat	attgaaagag	agcattacgg	360
ccggtcaggc	tttgggacag	aaaaacacgt	cgttgccatt	tggatgtcgc	ttacctattt	420
gaatccgata	gcttctatcg	ccctgcaagc	tatgtggtat	ggcaaaattc	gctcaattcc	480
atccaaatct	gctatacgat	aaacgaaaga	ataaaaccga	cagacaatga	aactaacagc	540
cgatggttta	cttccatcag	tgaggatgag	aagggcaaca	tagtattctc	aatggacgct	600
tggagcttga	cgaattccga	ctgagtggca	agctgaaatc	cgaatcgaaa	tacgctggcc	660
ctacgaagcc	gacgaacaag	gtctgctaca	gaatcggcag	gcaaacggat	cgaagagatc	720
gagctgctca	tccgtaggct	atggaaaagg	acaagttggc	catcatgaca	ggcaactata	780
CCEEEECEE	acaaagtatt	gggtctatta	tgcccgtact	gaacgagtat	tcgcgaacgg	840
ctcaatgagg	tetteeccc	ttacgaaaca	ttaccgctgg	agtagaatgc	gaagtcgata	900
ccgactggga	agagtacctc	gatatgctct	catgaaagac	gaaaattcga	tatagccatt	960
ateccatete	tctgtggcga	gggagctatt	ttttattggt	caagetteng	aaccggatcg	1020
acgetacet	catterere	atootagoto	tcgatttcat	gccggagtgt	ttctctgtga	1080
		~~66~466		000-0-0-	0 0	1094
tatgggtata	gatc			4		

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 652 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...652
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86

gctcaacaag	agaagcaggt	gtttcatttt	ctgaaccttc	cggctactga	caggctttgg	60
staccaaga	casagctato	accatogtag	acgacaatcc	ggactggctt	ttgagaatcc	120
totage	caatataaat	ccaatagcac	gcctttcttt	cctatttata	ttatatgagt	180
ggctctgctc	ggatatgaat	tattatacat	catccatcaa	agagcgtggc	atetegeete	240
ggttcgcata	tgggcatgct	Lgitalgici	cgccgccgg	astcagasta	coatoccacc	300
ttggctgcgt	ttcctgaact	acgggtctat	gcaaggacac	gatcagaatg	charactacc	360
ggctctttta	gtgcttcgga	tatagctgta	caaggatttt	acaccatgaa	cigagiaaci	420
acttccgcgg	tggagtcagc	ctaaaagcat	tgattcttct	atcgagacgt	atagttcctt	
teecctteet	gtggatgtcg	gatcagttat	tacgacgatg	acaaaggata	ttccgtttcc	480
getetgttea	gaacgtaggg	gcgcaactga	aaggctataa	tgaagaacgg	gaaccgctca	540
ttgggatttc	cagetegget	tttcccgcag	ttttatcaat	gctccgttcg	cttgcacatc	600
acattattca	atctgaatcc	gcactatttc	aagcgtctgt	accacgcgat	ct	652
acereere		6				

- (2) INFORMATION FOR SEQ ID NO:87
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1402
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

cgacatttta tatatcgctg atagaacaag aaaactcaaa cctatgaatc agttcctgct tctgaaaaca aaggtcaatc ccgtacagtg gaagacgacc gcagtacttc ggactttatc

```
tcaacctcgc acgagagaat ttgatagagt cgaaagtcat gttcgcatta agttcgggaa
                                                                       180
gaagaaattg aatgaaagtc gctcaagcaa tctcttcttt gtgatcacct gctctccgtc
                                                                       240
gatcgtggac caaagtctat ggccatagca gacgctatct gcctttcctc catttttcga
                                                                       300
tccggatagt cagatcgaaa aagaccatga tagcaagacc ggttggatcc cgattcggcc
                                                                       360
caaaggctga tcagagagct ttattcttta ctgatttcct gcgcaatgac ttctcgcaca
                                                                       420
atcggcttga tggcactaca tcgagcatct cgaagtcagc cctgacatca gctcctttat
                                                                       480
taccgggaca actccttggc atgcgggaga gcacaatcgc ggtttgcaga tttcttcaac
                                                                       540
ccgacgactt tgtcctggca aagaacagga aggaacaatt gataagcgag cggacggaaa
                                                                       600
agaatgeetg accettagtg geettgeett ttteattgee tetteetega tagggageag
                                                                       660
gcttccggta tgctgagcag gattcgggat tcaaacgaac cgatgagaat tgggcacgag
                                                                       720
cegtgeacga gacetetgeg atetetgeat cegteateet caegacagge tegaaagcag
                                                                       780
caatcgaaag aagctctctt gctcgatatg ctcaacgaac tgaaccgttg ccccgcatcc
                                                                       840
tttacgatat gctccccgaa gaggagcggg cgcaagttcc tcctgcgctg gacgaaaata
                                                                       900
gcatgaacaa cctctcggaa aacagcctga agaagagagt cgattgcttt gggacggctc
                                                                       960
ttcggattgg gcagaggcac gaccaagagg atccgccatc aggatcgctt cccctatctg
                                                                      1020
atgcttcgtt tatcgaggag atggatctgc tcaagggtat acgctttcgt gtcgatttgg
                                                                      1080
tgaaatcgag ctggattctt actccaaaaa ggtaggccgg aatggtggta cgatcgcacg
                                                                      1140
ataacggatc atgccttggc attcggcaag ctgtcaactt ccagaatgaa gaagaggtaa
                                                                      1200
gtaggatgat cagtggagag gcgtctatcc cgtacgcttc tctctctttg ctccccgcta
                                                                      1260
tgccatatac gacataagat aggctattgc catacatccg accctgtata tcctaagagt
                                                                      1320
aagcagggag taagagggcc ttgagcaatc ctcagtcgat gggattatca gttgcacaac
                                                                      1380
cttcgtaagc ttctcttgat gg
                                                                      1402
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1336
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

aacaaggatg	ctccatctgt	catttttcca	ttcgttctga	ccgaataggt	gtagttgttg	60
atattctgat	ccaattcggg	atagagggga	atggtattcc	attggcatcc	tcgccggtct	120
gccatgaaag	gatgggcatc	acgtcatgag	ttcatcacgc	gtatattcgg	ctccgaacaa	180
aagttgcgaa	ggcatgggag	gaatttgtcc	aagtcgtagc	tgtactggat	accgcccata	240
tatgtttgcc	tttggtcacg	ccataattat	tgccgtattg	atcttgaggg	ataggtagcc	300
ttccgtacca	ccggggtggc	cattgacgtc	aatctctccg	atactccgta	atagctcttg	360
cgatttacga	tctgtccgga	agtataagcc	tgaagtggtg	tttatagttg	gaagagaaga	420
gatcgtattt	caagtttccg	caaatacgct	atggtcagtt	tgttcagcta	cacccactac	480
gtgaggaggc	aatcgatacg	atcgccacca	cggcggaatt	cactgatcgt	gtgaaactcc	540
ccgtcaattt	gctgtagtcg	ctcaagcgca	aataagaatg	cgctcccacg	agcgggcatc	600
tattttaccc	aattcggaat	aaccgtcatt	gttagcaccc	aatggttgcg	gtaacgagcc	660
tgcccgaata	ccatggcacc	ggcacgttgt	catcgctgac	gatggaggca	ttgaagttcg	720
tgttgttatc	cagctgctga	aaccggtaaa	gctcagagat	tcattgaatg	tgaaagaatt	780
gtgaaaggtt	ccttggtgat	gatattcacc	actccggcaa	tagcagaaga	acctacaagg	840
ccgatcctcc	accacgtact	acctccacac	gttcgatcat	atggcaggga	tctgctccag	:900

			agacaactat	coatoaooat	ctgtgcataa	960
accgtaaaca	ccggcaaggg	cactcatgat	ggacggccgc	CBacbabbac	ctgtgcataa	1020
	a+ccattgat	coaacttgat	tgaaaccaca	gilligatag	CCBCCCCC.	
cgaccaccca	Buccaragas		anccapotta	gaagcattga	cttgcgagag	1080
cacgaactcc	ggctggaatg	acaagcereg	agccaggcca	644644	cttgcgagag	1140
	+castacatt	taccagagta	ggagcaagac	RACHARBECC	46,556,66	
accerees		tecamattma	togcatetet	tctgcttcga	aattcacctc	1200
tggccgaaat	cacgacticg	CCCagaccga	0660000	tattatagcc	catoccacoc	1260
	+00++++0+4	rorogetace	CECECCIARC	LLLLatagec	cacpcoacpc	1320
644644	teatteacce	спрасосаво	ttacgaagat	agtagtgccc	ggttgcatct	
ataatcaaag	Lgattcaccc	CEBROSONA		0 0 -		1336
gtaatgtacc	aaaggt					

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...501
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89

```
ttatgcctca aaaattttat attcaaaagt ttttctccca tttcaataag cttttgacat
                                                                        60
tttcttctgt tgcaggctgt attttatgca ctccaaattt ttagcgatat caggagatag
                                                                       120
ttttagcaat tctcttcctg tctgattatt ccaatgatta caagcttggg atatttggga
                                                                       180
ttggcaacat tgtctgtgca agctttgcaa tattagacaa acgcaaactt caaatgggtc
                                                                       240
aacaatctat ggaaatcatc tataacaaaa tttcctccct cttcaaaatt actataatga
                                                                       300
gttgatttat tntcgtcgtt tcatctatat ttcttgctga caatattcaa aatgtatttc
                                                                       360
ttcttttatg tcagataata tcttcaaaat agagaagtct tccctgttcc agtttgtccc
                                                                       420
tctatgataa ctggcttctt ttacttgtta catcaattag aattttcgta gtagtttagn
                                                                       480
                                                                       501
ggttcgacat tgttaagtgc g
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

```
tccccgggaa tttacaacta cggctattca ccagggaaag cctgacagta ttttaagaag
                                                                        60
gcacgttttg gaggagctat cgacctcaaa taccatatac acctacgata ggaatacgcg
                                                                       120
gggcctatcg gatcatctac gatactgccc tattgtacct gtgcggaaag attacaacac
                                                                       180
cgttgatgtt ggtatcatat ttcgttttaa gcgagtagta tatgacagat atgatgattc
                                                                       240
aaacgcacag ggagagatgg agatgcgcct gcaagaacaa gaagccgtat ttgtaagaag
                                                                       300
cgcaccggag aagaaccagg catagctcca ggatcattac ctagtggatg tgcctaagcg
                                                                       360
taagttcatc ggctttctta gtgatgactt agatcagact agcgggaggt cattgaaatc
                                                                       420
tategeaaae gttggeteat aagegaetet teaageagat taageagaae ttteeeetga
                                                                       480
aatacttett gagategttg cacaatataa eeetetaeee etteatattg atcaagacaa
                                                                       540
tacaagcatt gatttgacga agaaaggagc gcttcatgca gtatctgcaa cctcaagtat
                                                                       600
acacctctga tggaagcttg gggaaatttc tgtttaccgg tgcccatata cttgagattt
                                                                       660
gacctttcct gaaaacacaa ggaatcgccc tgcagcaaaa gaattcaatg aaaatcccgt
                                                                       720
gcaacagtct caaaaagaga agctgcctct ttcggaactg ttccgggagg cagcctcttg
                                                                       780
tggatcattt caatttcaat agcaaatggt tctctggttt ttcagaagat cttagctttc
                                                                       840
cgtccacaaa agtcgtgcaa atcgaataaa ccgccaaagg aaaaatatgt tgttcagcaa
                                                                       900
gttcacccgt atccacatgt cgaaagcggt acagaaaggt taagaggact cttccgttat
                                                                       960
agcctgaaac taacccctac atgacaaagg gagtagccca gccggctgat acttctgaga
                                                                      1020
acaatgcaaa tcgcgctgaa caaagaagcg cgctccaaga tgaataccgt agacaaagcg
                                                                      1080
gtatcattgc cgaaatagcc tcccagagtc tgacctaaat agccatcaca gcagaagcca
                                                                      1140
gctgatagtg aaagtctaat ttagtggcta aaatgaggca gagaaattgt gttccgtgcc
                                                                      1200
gtaatagcca aggcgacctc ctacataatg gcgcctttgc ctctggcaag accgctgatg
                                                                      1260
ataccggttt cgagtctacg gtgggcataa atgcagccga tccgtgatga gaaccgatac
                                                                      1320
ccaaccgacg ttgagcgaaa cgtcaccctt gcggatagca ctctgagcat tcttgagaat
                                                                      1380
atgccggcca agatgatagc cagactaaaa attacttttt tatgttgttt tcgtttttg
                                                                     1440
acgtttgatt gtctcttcta attttttgat tgtttatcct gattctgatt gtagtcagca
                                                                     1500
aggettteag ttetteattt etategt
                                                                     1527
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...3\overline{8}6$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

```
aaaagagatc ggaagacagc gaaaagagat tgggaaacga tttatatacg aacgaattcg 60 atttatatat ttatcatttt cgatttatat ataaatcgtt tcatttaata tatagattgt 120 aaagtgtttt atataaaa cgagaggaga aaaggcctct tcgaccgatg aaataaaaag 180 aggcacccac ccaagtcgcg accgaactcg ggcgagtgcc ttagtatctg acagaaatgt 240 cgggacttat tcgcgcttgt acatcacaaa ttcggcacaa gcgtcctcgc tcgacgatta 300 cttcatgtta gtcttcccag cgtacattgc gcatgtcgcc $ctttggcca attcctgatg 360
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...588
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...473
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

ggagactaca	gcaagaccac	cagtctgaat	atccgatgac	acacagtcag	gatccgaagg	120
ccaatccttt	gcaaacette	toggocatgt	caattttgcc	accggnagct	atttccagaa	180
ttcgctgaat	accaccatga	tgtcaatgcc	cgtactgcta	cgacacgaag	ttcggccgtg	240
actatogo	caagtttccg	ggtactcctt	tttcgattac	gggtagcatg	gatacagcca	300
dacatacac	gatacgacgg	tgagccttac	cttgccgaat	cttcgattaa	tatgtccacg	360
cattateett	tcaagcggaa	gacccgtgta	ggccggagcg	atggtacgag	aagttgagtg	420
tagactattc	cggtcagctt	ccaatagtat	cttgacaaan	gagaaagatt	tgc	473

- (2) INFORMATION FOR SEQ ID NO:94
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...516
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

cgggctgtaa	ctacaatctt	tctcattgtt	ctttacttat	tgtttttaag	ttttgagtca	60
			gtttggcacc			120
			tgtcgagaag			180
			atgcttcgcc			. 240
			cgatcctatg			300
ttcagtccga	gttcgcggaa	gaattcctcc	gtccgagcaa	tagtgcatct	atacgctcct	360
			gtcggcatat			420
			ggtagcacta			480
		tctcatgacc				516
gtgagtccgg	cagtgccgta	teteatgace	gattat			210

- (2) INFORMATION FOR SEQ ID NO:95
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 889 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

```
60
cggcaactcc atccttatca aggtaaacca gattggtacg ctcacagagc cctgaatgcc
atcgagatgg cacaccgtca cggctttacc agcgttactc gcaccgctcc ggagagacag
                                                                       120
aagacaccac tatcgcagac attgctgagc aaccaactcg ggacagatca agacgggatc
                                                                       180
gctcagtcgt accgacgtat ggctaagtac aaccaactgc tccgcatcga agaggagtta
                                                                       240
ggccctgcgc tgtatacggc tacaagaaag tgtaagcgac aaagtacaca caggtacatc
                                                                       300
tttctgccga atacggaaaa ggggaaaaga tagtaccact gccaaaaaaa gaatgccccc
                                                                       360
aaagttggaa acacaacttt gggggcattt atttgccgac ttatttagaa gcgaacaccg
                                                                       420
agacccacaa agaagtcatg atacgcaaag aagtcttatc cggagcatcc ttcaacatat
                                                                       480
taagcaatcc tgctcatatc caatttgtac gtaataacgg tcgtagctca aggcagcagc
                                                                       540
                                                                       600
aagcccaagc ccaagtcgaa acggttatat ccgttatcac caaaggcact acagaagccg
taacgcctgc aactttagtc ttaatcgttc cggcgaccca tatgcgaaat agggacctgc
                                                                       660
ttccaatgaa atagccatgt tgtcagaaag ctaaatctca taccggcatt caccggtatt
                                                                       720
tgcagataat gcaaggagtt gtcgtttcac ttagtgattc catcttagca cctctcatcg
                                                                       780
tatagccaat ccgggggcga gatagaatcc atcattgcta agagcgaact cagagcagca
                                                                       840
                                                                       889
ccaacacgta agcctacgat catcttattg ttcacgctcg tgttgcgac
```

(2) INFORMATION FOR SEQ ID NO:96

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 640 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...640
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

gactgccaag	ggtccgctca	gtaccgtgat	acccataata	tagaatcggc	tcgagcagag	60
gtggtaggag	gtctgcataa	tcgtattgag	catattggca	gacccatgac	atgccctaca	120
tagccgaata	tggcgaagaa	gagaatgtga	agccgagggc	ttcgaagaga	tgacgcctga	180
acgtcagttt	cttgtgtgag	atcttgtctc	catttataat	gatgtatgcg	gtggtttttg	240
gtgggaaaag	acaaggccgg	agcggagctt	cgttcggtgc	tccgctccgg	tcttgccgtg	300
aggattatga	gttggtgtag	acgaccctgc	ctcctttgac	ggttgctcca	cgaggttcat	360 420
accgaagtga	taggagagga	atttgtacga	tggtattgga	gtacgacgag	gtcgcccttc	480
ttgcccggct	cgatgctgcc	gtcgtatcgg	ctcttcctat	ggctgcagcc	ccgccgaccg	540
tgagggctgt	atggcttctt	cgacggtcat	gcccatgtag	agggtggcaa	gggcaaacag	600
		cgggccggag		cgctccccgt	600006000	640
APECPPEPLE	gallallica	CEEECCEEGG	CECUECCEC			

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 838 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...838
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

acgctcgcta	tgcagatcaa	ccccatgctc	tgcggttctt	cgttcaagac	aagggcgtac	60
agacactgct	cgatgccgta	tgtaagttcc	tgcccagccg	gcagatactc	ccacagtgga	120
aggtacggat	ccttctgact	cgagtaagtg	atagagcgca	agacctctcc	caacgageet	180
ctctgtgctt	tggcgttaag	attgctaccg	acccttacgt	agggcgtctt	tecttettee	240
gcgtaattcg	ggcgaattgc	ctgccggttc	atacgtttac	aatgctcgtt	ctgaaagaag	300
gagcgtatct	ctcgtctctt	ccagatgcac	tctaacaagc	agaccccaaa	gaggtgatcg	360
gttgcggtga	catcggtgcc	ggtgtaggct	tcaggatatt	cgtacgggcg	atacgctttg	420
cgatgagagt	catcctatcg	tctcgaatct	atggacttcc	ccgatccggt	patcoptatt	480
gccgtggagc	gaagacgcag	aaggacctcg	atcgtctggg	tgtaggtttg	pccaapctoc	540
tgaagaagac	cccacgttcc	gcgttcagac	gaacgaagat	tccggccaac	gottatcage	600
ggtatgggtg	agcttcacct	cgatattatc	atagacetet	protrotoso	tttaanntnn	660
aatgcaacca	gggacgtcct	caggttctta	Caaggagget	atcaacoatc	ctataggegg	720
tcgcgaagtg	tacaaaagca	gaccggtggt	rorootaact	ttaccaacat	tatotatoat	
gtgggcctgc	cgatgccgac	ttcgaaaggc	gaattgcagt	tostosatta	-acciging	780
0 000 -8-	. 0		Buncegeage	LLELEBALLE	agggaagg	838

- (2) INFORMATION FOR SEQ ID NO:98
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1088 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1088
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

gacteteteg ttttggacgt	cgctctcgaa	agaataccgc	cgcggacatt	tcccgggcgc	60
agagagitte coccigitte	cggatgcgga	acgagccggg	taggtacgct	ctatgtcaga	120
catagicge aggoggoogt	agagcgagat	tggagttcgt	tgggccgcgt	atggccgaga	180
rggrgcgaga agctcgtccc	ttgctgccgg	cagagacatc	atcctctact	gctggagagg	240
aggtagcgaa gcgagagtgt	cgcttggctg	ctatccgtag	taggacttcg	catcgtcgtc	.300

tccgtggcgg a	tacaaaaca	taccgccggc	atttccccga	tatctgaagc	tttacccgtg	360
gcgtttcatc g	tattaagea	ottatacooo	ataggaaaaa	cgcccatcct	gaacgaactc	420
gcgtttcatc g	cccaggeg	gtcatacass	aaggattggc	ссассасава	postctscct	480
acccaaatgg g	ggaacaggc	gicgatetgg	caccanacat	ttcatgaatc	tettacacat	540
tcggtgcctt g	ggcaagagc	agcagccgac	caccgaacac	ccacgaacc	coccecace	600
gctctctccg c	ttgtgatcc	gaatcgtccg	atatgggtgg	aaagcgaggc	aagactateg	660
ggcgcgtatt t	cttccggac.	gatttctaca	aagtcatcgt	caageteett	tgatcgagct	
gtctgtcccc C	gtcccgtac	gcatcgccat	attgccaaag	agtacggcgt	gtacgatgca	720
gaggcactgg c	aaacctttc	gagcatatcg	ctcgccggat	gggaggagcc	gctacgacac	780
aagcataact g	ccctcaagg	aaggacgtct	ggaggaggcc	gtatccttgg	ctccgattac	840
tatgacaagg c	ctatocaca	ctcgctggct	gaattcaggg	aagctcctct	gctcgactgg	900
cagtagaaac g	ratacacct	Cacdagacad	catcaaacta	ctggaactat	ctcatataaa	960
agggttacaa t	gatacacct	caegaaacag	gggggaaact	ctecccctc	cctcttattt	1020
agggttacaa t	catgaaagt	guggatactt	88888	atctccataa	toactoacat	1080
tgctcaagaa g	ccgttgacg	gcactcccgt	Cggagaagaa	acceceguaa	cgaccgacac	1088
gaaacggc						1000

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 958 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...9\overline{58}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

			tacastascs	ctagtaacaa	60
ataaaattca	aacagcctaa	acattettaa	Lgcgacgaca	teageaacaa	120
agctnnggaa	aaaattacag	cgtaatcaaa	tacatctcat	tctgaaaaaa	
acggctgacc	aaaataagaa	aggctcaagt	ggtaatacgg	agaaaaccta	180
ttaagcgtag	attgatagat	aaaacagcaa	caacaaaaca	agaccaataa	240
gcaagagcgt	tcacaaactg	attgtgtgag	aaaactcgca	tgccgtcttc	300
gctcaacaac	ttgagtatac	ccctgtccca	acaaaattca	taaatattac	360
teettetate	ccattcaccc	aaaagaagta	cgtccagatc	cttttaaatc	420
gcagaggat	totatorara	ttgcgcccag	ttatccttgc	ctgaaactgc	480
gtagaagtat	recarecas	caccaactaa	occtatcaaa	aatgaaaatt	540
acagaaacaa	acaagagcaa	Caccaaccaa	5000000000	220222300	600
tgaatagtaa	ttttacgagg	aagcattaga	ataaccaggc	aacaagaagc	
ctgtacggac	ataggcctga	aaaacagaat	taatcctact	acaatcagag	660
accettetga	aatgactcct	aaatttattc	agtctaaatc	cgtttgttag	720
gatgcgcgaa	gtangangaa	tcccgcatga	ggagctccaa	aaattccaga	780
cocctcast	tccapaagca	tragragata	aaaagtette	cacegagata	840
CCCCCCaac	CCCaaaagca	ccagoagaca		+ 0 0 0	900
aagtactaaa	agtgatgcaa	gaagtacaaa	ttggctaagg	Lacaaaggaa	
cgatcaactc	gattagagaa	ttaaccaacc	aaaaacgaaa	aaagagag	958
	agctnnggaa acggctgacc ttaagcgtag gcaagagcgt gctcaacaac tccttctatc gcagaagcat atagaaataa tgaatagtaa ctgtacggac acccttctga gatgcgcgaa cccctcaat aagtactaaa	agctnnggaa aaaattacag acggctgacc aaaataagaa ttaagcgtag attgatagat gcaagagcgt tcacaaactg gctcaacaac ttgagtatac tccttctatc ccattcaccc gcagaagcat tgtatgcaca atagaaataa acaagagcaa ttatacggac attgacggac atagcctga acccttctga gatgaccct gatgcgcaa cccctcaat tccaaaagca agtactaaa agtgatgcaa	agctnnggaa aaaattacag cgtaatcaaa acggctgacc aaaataagaa aggctcaagt ttaagcgtag attgatagat aaaacagcaa gcaagagcgt tcacaaactg attgtgtgag gctcaacaac ttgagtatac ccctgtccca tccttctatc ccattcacc aaaagaagta gcagaagcat tgtatgcaca ttgcgcccag atagaaataa acaagagcaa caccaactaa tgaatagtaa tttacgagg aagcattaga ctgtacggac ataggcctga aaaacagaat acccttctga gatagangaa tcccgcatga cccctcaat tccaaaagca tcagcagata aggtactaaa agtactaaa gaagtacaaa	agctnnggaa aaaattacag cgtaatcaaa tacatctcat acggctgacc aaaataagaa aggctcaagt ggtaatacgg ttaagcgtag attgatagat aaaacagcaa caacaaaaca gcaagagcgt tcacaaactg attgtgtgag aaaactcgca gctcaacaac ttgagtatac ccctgtccca acaaaattca tccttctatc ccattcaccc aaaagaagta cgtccagatc gcagaagcat tgtatgcaca ttgcgcccag ttatccttgc atagaaataa acaagagcaa caccaactaa gcctatcaga attgatagaa ttttacgagg aagcattaga ataaccaggc ctgtacggac ataggcctga aaaacagaat taatcctact acccttctga aatgactcct aaaattattc agtctaaatc gatgcgcaa gtangangaa tcccgcatga ggagctccaa cccctcaat tccaaaagca tcagcagata aaaagtcttc aagtactaaa agtgatgcaa gaagtacaaa ttggctaaag	ataaaattca aacagcctaa acattcttaa tgcgatgaca ctagtaacaa agctnnggaa aaaattacag cgtaatcaaa tacatctcat tctgaaaaaa acggctgacc aaaataagaa aggctcaagt ggtaatacgg agaaaaccta ttaagcgtag attgatagat aaaacagcaa caacaaaaca agaccaataa gcaagagcgt tcacaaactg attgtgtgag aaaactcgca tgccgtcttc gctcaacaac ttgagtatac ccctgtccca acaaaattca taaatattac tccttctatc ccattcaccc aaaagaagta cgtccagatc cttttaaatc gcagaagcat tgtatgcaca ttgcgcccag ttatccttgc ctgaaactgc atagaaataa acaagagcaa caccaactaa gcctatcaaa aatgaaaatt tgaatagtaa ttttacgagg aagcattaga ataaccaggc aacaagaagc ctgtacggac ataggcctga aaaacagaat taatcctact acaatcagag acccttctga aatgactcc aaaatttatc aggtctaaaatc cgtttgtag gatgcgcaa gtangangaa tcccgcatga ggagctccaa aaattccaga ccccctcaat tccaaaagca tcagcagata aaaagtcttc cacggagata aggtactaaac gattagagaa ttaaccaacc aaaaccgaaa tataaacgaaa cacgaaca agtgatgcaa gaagtacaaa ttggctaaagc tataaaggaa cgatcaaacc gattagagaa ttaaccaacc aaaaccgaaa aaagagag

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 885 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...885
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

ggtccgctga	cattcggcta	ttctaccacc	tatatatatg	attttgcacg	gatagtaagc	60
gtgctctgat	cggtacgctc	tccacggact	ggacgcgcgt	cctttccgct	ttgccactat	120
catggagtac	aatatggaga	cgggcaagcg	gatacgctta	tcactcgcga	tccttccatc	180
gacgcaatcc	agtataaccc	gacggcaaac	atctgatcgt	aatgggttcg	gcagatgctt	240
tcggcatata	ggactgaacc	tgaaatcggg	agtcactccc	aattcttacg	acaacaattc	300
ttcctgttcg	atctctccac	acggaaagca	acagccttga	ccagaatttc	aaccccagtg	360
tatcggcagg	gagattcgac	agaaaaaaca	acactattac	ttcagggctg	aaaacggatc	420
gcgcaagcag	ctctatcggt	tggatctgaa	aacccttgag	atcagtcaga	ttcagaccgg	480
agagggatgg	agtacaatgg	ttcggtgtgg	cagctgataa	tggtgctgtc	tggtacagcg	540
ccagagtgcc	aacaatgctg	acagactcta	tcggctcgat	gggaccaagg	aaaactcgta	600
tgggatctgt	ccgccgagaa	gttggccaat	atcgattcac	accggcacgc	gactggaact	660
atacggctcc	ggatggcaca	gtcgtaaggg	ttggtactac	ctgcctccgc	aattcgatcc	720
ttccaagaaa	tatccatgct	ggtctattac	tatggaggaa	ccagcccgat	caataggaca	780
ctggaggaca	ctactcgctg	gcgatgtatg	ctgctcaggg	ctacgtagtc	tatroctraa	840
tcccagcggt	actaccggct	ategacagga	gtatgcagct	Cacac	Lacebottaa	885
3 00		- 66	9 9 cape c	CECUC		000

- (2) INFORMATION FOR SEQ ID NO:101
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 838 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...838
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101

gcataatgat gagcagc	aac gagaggctcg	ctggccgaac	gataggttcg	atcttcggat	60
gaatctgaaa gaggacc	tcg caaatcctct	tcaaagcgat	tcaggtgatc	cgcaacgate	120
aataataaag aatagaa	aat caaatacata	gataaatgaa	gaagacaatc	ttccaacaac	180
tatttctgtc tgtttgg	ccc ttacagtggc	cttgccttgt	t*cggctcagt	ctcctgaaac	240

nantataana	agtttactct	teaecaacte	atgcccggag	gaaaagagtt	ttatactttt	300
gaguguaagg	ageceaecee	ttaaaataaa	+00020202	ttagtcttta	troappotga	360
accccgaata	cgtggtcggt	Ligitatigga	cgggagacaa		**********	420
tgatttagtt	tttaataagg	cgaatggcaa	atggctcaga	cgaccagatt	Licigity	
gateteaatg	cactcatgcc	gagggatgca	aatttcagac	gactgatgct	ttcccttcat	480
tecacacact	gatgccggac	poppactggt	cgttctattt	acccaaggag	gattagtcga	540
Licgiacacc	Bacgeeggae	agt and that	cttttcgata	ccaatoaoao	acggettett	600
ttcgatatgc	ttgctcgaaa	ggigacitat	CCCCCgaca	ccaatgagag	106600000	660
tggattttc	tcctgtggga	gaccgtgttg	cctatgtaga	aaccataacc	tttacattgc	
trotogaggt	aaattgggag	aaggtagtca	cgagctatcg	ctgtgactat	cgatggaact	720
	tatatoccao	accatacacc	agcgtgaatt	cggtatcgaa	aaaggtacat	780
gagacteteg	Latatgecag	50050acaca	-6-6-6-6-6	antongagta	tannaann	838
tctgtctcca	aaagggagct	gccttgcttt	ctategaatg	gatcagagta	CEEEaaec	030

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1046 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1046
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

```
60
gcttcggttt gctcggtctg tgcagagata agagagccgg ttcctgtatg cagaataggc
                                                                       120
gcaatccgat attaaccgac atttcctgcc ttttgagaga aaacttctgc cacgatcatg
                                                                       180
ttacgttttc acaaaagtgg cgatgaaggt gacaaaatag catgccgaac agcattcgaa
                                                                       240
tgacttttgg tctaattctg ccccatcggc acggtggcac tgtatttgta gcctcttaca
                                                                       300
agcaagattt acagcccgta aaaacggatt cggacgatgc ccaaaggagt attcggcgga
cccttcatac tttatactat aaacccttcc gactttatac ttaaaccctc caccctttat
                                                                       360
                                                                       420
actataaacc cataccactt tatactataa accataccac tttatactat aaacccatac
cactttatac tataaagcct catactttat agtataaagc ctgcgagctt tatagtcgga
                                                                       480
                                                                       540
agtattaaag gatgattgtc gtgctacact tgtgcaagaa aaaggatcag aacggatagc
                                                                       600
tactgcaatg tgccaagcga aattggaaga aaggtttggg cgtgtgatgc ccatttgtaa
                                                                       660
cgccctgtct gctgaggatc gtaggctttc agtccggatc cagccgcaca aggaaataat
                                                                       720
cgaagtcgag acgaagcccc agaccgaggc caaagctatt tccttgtaga agcgatcgaa
                                                                       780
acgaaagaga cogtotootg attotoatac tootttatog tooagacatt googgoatog
                                                                       840
acaaagctgc tgcgcgaaac ttccagaaca gctttgtcct gtattcgaca ttcgatccag
                                                                       900
acgaatatca cccatctgat cgaagaaggt cttgtccgga gtatcttcat actccccggg
                                                                       960
ccgagggtac ggacactcca gccgcgaacg cgttcgatcc tccggcaaag taacgtaact
                                                                      1020
aaagggtata tggcgagcat gccataaggg aaagccagtc cgaaacccag attgcagtgc
                                                                      1046
caaagtattg ccttttcgag agaacg
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1026 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1026
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

g	ggcctcaac	aatcgaataa	aacggcattt	gagaatgatc	ttttctcttt	tcttccgtgc	60
C	ggagcaaga	gttgcataca	aggactaaag	ataattgcgc	atacagagtc	catcgggcag	120
a.	ttggagccg	gaaatcaaga	tcgttcaatg	cctgcgaagc	agatcgagag	aattacggtg	180
t	tctatacgg	atggcactat	caagagtttc	gctcaaacaa	agagtaagcc	tctcttttt	240
C	gtaatttgc	actcgaatac	tgcaactcga	tttctcgatg	aaatacaacc	ataactgcgt	300
g1	cgcgacca	atacgaagct	aaacgacagc	tatttccttc	ttaacttgta	ccggagcata	360
at	gaagtacg	attatctctg	ccggaaataa	agccggacag	tttgttcagg	tactgactgg	420
a١	gtccaagg	ggcttttttg	ctcggcctat	ctctgtttgt	gatgtcgatt	acgaacggca	480
gg	gaactattc	ttctggttca	aaaagtaggc	aagggtacac	gtgctttagc	ttcattacag	540
Ca	itccgattc	attggatctt	ctatatccgc	ttggacaggg	gtttacgcta	acgatctgcc	600
gg	gatggagag	tatcgtcctc	ttctcgtggg	tggcggttag	gcactgctcc	tatgctctat	660
	ggcgcgtt	gtatcagaga	gaggggatcg	tgccggatgt	tctgctcgga	gcgcgttcgg	720
Ca	igatetgat	cgttagcagg	acagattctc	tcgttttgcc	aatctgcatt	gcaccacaga	780
gg	gatgttcgt	tgggggtgaa	gggctttgtc	acgagccacc	cgacccttcg	ggaggcgatt	840
tt	tctcatat	atatgtgtgt	ggcccaaaag	caatgatgat	ggtgtagcat	ccctggcacg	900
tc	aacgaaat	atcccgtgtg	aaggtctctc	tgagaatacc	atggcttgtg	gtatcgggca	960
tg	tttgtgtt	gtgtggaaaa	tcnaaagaag	gcaatctttg	cgtctgtacc	ggaagaccgg	1020
ct	tcaa						1026

- (2) INFORMATION FOR SEQ ID NO:104
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 962 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 (B) LOCATION 1...962
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

gggccatgag	tttgtccgta	aaagaggcga	agtagtcatc	cggcacagat	agtgtcgaat	60
actgtcctct	ttcggacgga	tattcacatc	ggggtcgact	gtttcatgtg	agctttgtta	120
gttacgatta	tagaggcttg	ttcttaggca	agtttaatca	€cgggcgaca	aaaaacgctc	180

	ncaccagata	ggaccaatgc	cttgagagca	ccttccgagg	taccggtgat	240
Caacttette	acagcaggeg	catatage	tantaccasa	oottoaacac	caacgctgtt	300
ttcggcattt	tttcgtaagg	Cattleaceg	teta	ggttgaacac	catcgaaata	360
tatcaggcaa	ttccagtata	gccttttgga	aggtaatete	ggctcatctc	tatagtagta	420
aacatccccc	gtgaggttgt	cgagcagata	gggttttcgt	ccgtgatcga	Latacicata	
trotritroa	tctttttctt	ctcaggaaat	tgagtgattc	gtacatggct	atccgataga	480
accadataga	agtttggcct	ccccacgaaa	accgtccaat	gcactccatg	ccttcataag	540
gccaggcgga	acasatcatc	cotatootca	teacteagca	ccattcgggg	atttgccagt	600
gtattttgga	gcaagcegee	catactacct	tttcaaagcc	atacgccgcc	ttgccggatc	660
agagtttacg	gttgtacagg	cgtactacce	stantaget	tatcagccat	aatoatocoo	720
tctcagctct	tccagcaact	cttcttcgaa	accaacagee	tatcagccat	atataataat	780
taaagatagc	aaaaggtgct	ttatctatgt	caataaagtc	gaagattcag	ctctgatcct	· -
gtaggagaga	ccgaaacatg	agagagttat	gctcctgtgc	tttccattct	atgeegaete	840
tateettteg	gctcatgcgg	caatccaaat	tcaaatcctt	tgagttgcgc	tactcagaca	900
actettees	aatacctctc	ggctattacc	caaatacgtg	cgaaaaaagt	tttcaacaac	960
aggtattgca	aacgcccccc	550000000		0		962
ta						

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 599 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...599
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

206666000	atattraaar	gracgotoca	gtcctgagct	ttgccgtccg	aacgtaatcg	60
ggcgaagagc	tatageaatt	Cacaaacota	tropopaapa	tctttcgatc	cggctgatga	120
aagagatagt	LgLagCaact	tagaaacgca	ttotogttog	2207202000	cattotacca	180
tttcgccgat	ctccggtttt	teeceatgag	Licitegetteg	aagcagaggg	atteauttu	240
gagagcattc	aattcgcgag	atagccctca	cgggggatga	cggctttgcc	atteagere	300
gcatcatcca	acttaacggg	aagcctgtgc	ctaagacgta	gagaagccca	ttttacgaat	
tteteccetc	gggtgctggg	cggacagata	ataagatacc	actcgctgac	gaaggagccg	360
aatctcttgg	ctgcttccag	accettecee	cggcatactg	ctggatggcc	caaatagccc	420
aaccccc266	atccaattca	tragrecete	tatggtgtcg	tcatcttcat	gcagtcgcat	480
adattttaat	torogranat	gacggtattg	acoatoccot	togaatogot	tccggtgctc	540
gtagcgttcc	ccgccggaat	gatggtattg	acgacgacga	cacaaactaa	acotcoaac	599
tacacaccag	agtacagccc	ggtaagtgcc	acgaacagac	cgcgagctga	ace ce eace	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 655 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...655
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

```
cagtattgcc caatgggttg atgagcgtta cccctttcaa tgtcagcggt cgacagagaa
                                                                        60
togottogac aaagattogo gttggtggag tgogootttt oggoogacaa tagttactgo
                                                                       120
atcggtttca gccatgtgaa tctgagtgag taggctgtcc cgaactgagt ggaatactgc
                                                                       180
tgatggccac ttccggacat tcgatcctga ttactgctgc tatggctctt cgctcagtcg
                                                                       240
agaattgcgc gcccgggaga atacaaggct gtattggaca aatacggtat agatcagccg
                                                                       300
tgaccgtaac cgagcggact gctttgaccg aatttgcttt tccgaaggag aaggccatat
                                                                       360
cctgctgaac ctgggacagg ccctaagcaa tgatcgggag cctctgttcg attcttaaac
                                                                       420
gactccacag tcgtcggcag cggctgatgg ggacgttctg ctacaatccg caagcagttt
                                                                       480
ttcgtcagta ttcgtacttc aggtgagtcg gcgaccgatc tctgccggct attggaagag
                                                                       540
cagcctccta tgacagtgga agcccaatgg gattcgactg cagggaaaat agcagtacga
                                                                       600
cggctacagc gtgagatgag cgtgatgaca tcgtgtcgat ctcgtcaact ggatc
                                                                       655
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 891 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...8\overline{9}1$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107

ggggctgatg	gaatatettt	ttcccgaact	Cttaggggtg			
999998	Baarargee	ccccgaact	Cttagecete	aaaggagcaa	aacgcgtgat	60
ggcatcgggc	ataaggacaa	tctcactcat	acttataagt	agtggacaac	ttggctcggc	120
acagcgatag	tctttggctc	aggtgggagc	attgctacac	gacataggca	aaccacgcac	180
taaaaagttt	gttggcgaca	gtggacattt	cataatcaca	actttgtcgg	agccaagatg	240
ctacctctct	cttcaaacga	ctccgacttc	cgctggatgc	caaactcaaa	tacgacaaaa	300
actcgtagat	ctgcacatgc	gtccggcagc	tctggtggac	gaagagttac	ggattctgcc	360
gttcgccgtc	tgctcttcga	agccggtgat	gaatagatga	tctgatgatg	ctatocoaso	420
ctgacattac	99009999	CCCCCCC			Cracecane	
ougueuccuc	aagcaagaat	ccgacaaggt	gcgcaagtat	atagacaact	atgctttggt	480
acgicataag	ttaaagaaat	agaggagaaa	gaccacgttc	gcaacttcca	accaccgatt	540
ccggcgaaga	gattatgcag	accttcggtc	taaaaccatc	gcgccacgtg	gcaccatcaa	600
ggaggcgatc	aaagaggcca	tactcgacgg	ggctatccca	atgactacga	agctgcccga	660
gttttcatga	tcgaagcagc	tgcttcctcg	gtcttcaccc	caaaaaccaa	acatcatecc	720
acagogtata	gacctcgagt	00000000				
B-Bcaca	Buccegage	gegeeegaa	gaggctactg	acgaacaaat	actgcgcaaa	780
catgagcgag	acagacaaaa	acagatccga	ccgacataca	tactataata	atcgacgtcg	840

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2496
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

```
60
accatatatc gctatgaaat taatccaagt tcaaattcat tcttccggag gaactgattg
cattagagcc gaccaagttc cgcgacgaat cgcgaatgtg gtcgtacatc gtcgtacagg
                                                                       120
agaaatcgaa catcgcgttt tcaaggaatt ctggagtatt tcgacaaggg tgataccttc
                                                                       180
gtcttcaaca ataccctgtt tttcctgccc gtctctatgg taataaagag aaaaccggtg
                                                                       240
                                                                       300
ctcagtcgaa gttttcctcc tgcgtgaact gaatgaacga ctgaagctgt gggagtcctc
gtggatccgg cccgcaaaat acgcataggc aataagctct attcggcaat gatgaagagc
                                                                       360
                                                                       420
tggtggcaga ggtgatagac aatactacct ccgagggcgt acgctgcgct tcctgtacga
                                                                       480
tggctctcat gacgaattca agaactgctt ttccaattgg gacagactcc tctgccgaag
tacatcgatc ggacgtgaac aaagaggatc cggagaggta tcaaagcata tttgccaaat
                                                                       540
                                                                       600
ggaaggcgcc gtggtggcac ctgctgccag tcttcatttc agccgcgact gatgaaacga
                                                                       660
ctggagatca aggactgcca tttctcttac ataacggaca ccacgctttg ggagcttatc
gcgacatcga tgtagaagat ctgacaagca caaaatggat agcgaggaga tgtatatcac
                                                                       720
ggaggagtcg tgcataacat caaccgttca tgggacgaag aaaagaagat ctgcgccgta
                                                                       780
                                                                       840
ggaattcgat tcttcgtgct ttggaaacag ctgtgagcac agacggtcat ctcagccgtt
                                                                       900
cgaaggttgg accaatcgct tcatctttcc tccatacgag ttcatctgcc ttctgctttg
gttacgaact tecatatgee getetetace caetgatgat gaeggeeget tteggaggae
                                                                       960
                                                                      1020
atgaactgat tatgagtgca acgacctcgc tgtaaaagaa aagtatcgtt tcggtgctta
tggtgatgca tgctcatcat cgattgagta tggccatagt gtatctttct ttgggcagaa
                                                                      1080
                                                                      1140
cttaggcgat cgacacagtt tgttgtctgc agcattggag atgctacaac gagggtgggc
                                                                      1200
agactgctca ccctttctcg gttctatgaa accgagcgtg gggattcgaa tcgccccatc
ctttcctcaa tgcggtggtg gctttcgatc ggaactcaaa ccacaggaca ttctgcacat
                                                                      1260
                                                                      1320
cacacaagcc atcgaaggga attgggtcgt acacaaaaaa gcaatggagg ggtctatcac
gatgtccgat agatatagac attctattgc attccgtata cccgaaagta catcacctga
                                                                      1380
gctggaactg ccccacccac aaatgtggca acgggatttt ggcgtatgcc gctatcggac
                                                                      1440
gtagctcctt ggctgcatcc ggaggctccg ctccgaacct ctgactaatg aaagaaatga
                                                                      1500
atgtaaacga cttcgagata tggctccagt cggttcgtac gaatcgctta tggcagccat
                                                                      1560
caaggcagag cagattcagt tracttcggg attgaaggac tgaatatgcg tgcgcgactg
                                                                       1620
ccaacaactt caccacagaa gatctgtaca aaatagccga gatttgagag ataaaggcgt
                                                                       1680
                                                                       1740
aaagagctat ttaacggtga ataccgtcat atacgtgagg acatagcact catgcgctcc
                                                                       1800
gtcatcgatg cggcacaaaa ggcaaaatat ctgccattat agcttccgac gtagctgcga
                                                                       1860
agatgtatgc caacagatcg gagtagaagt gcatctgtcc actcagctca atatcagcaa
                                                                       1920
cgggaggccc tacgctttta ttcgcgcttt gccgatgtgg tcgtattggc agagagctga
                                                                       1980
atatggatca ggtgcgtaca atccacgaga ccatcgtcag gataatatct gtgggcctaa
                                                                       2040
aggccatccc gtacgtatag agatgtttgt cacggcgctc tgtgtatggc cgtttcgggc
                                                                       2100
aagtgctatc taagcctgac gaacacaaca gctccgccaa cagaggagcc tgtgcgcaga
tctgcagagg ggctacaccg tcaaggacaa ggatagcggt ttggaactgg acattggaac
                                                                       2160
```

caatacatca	tgtcgccgaa	agatctgaag	actattcatt	tcatcataag	atgatggatg	2220
ccggcgtacg	agtattcaag	atagaaggaa	gggccgtggc	cccgaatacc	gtctatacgg	2280
tctgccgctg	ctataaagaa	gcgtcgaagc	ctactgcaac	ggcacctatg	atgaagaggc	2340
cataggccgg	tggacgaaca	attggctacg	gtattcaacc	cgaggctttt	gggatggcta	2400
cacctcggac	aacggctcgg	cgaatggaca	catcgttacn	gctcaggagc	acgcgacaga	2460
		atcaaatact				2496

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 656 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...656
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109

cgcaattgat	cgggatggct	attctgattc	ttctcgttct	ctatgccaag	gcaatgactt	60
gctcagggct	tttcgctgac	agaccgctat	gattcggagg	agacttaccc	ccacaacttc	120
gaggagaaag	tgggtttcga	tgagattgtc	gccttctcat	cggccattgc	catagtccga	180
		agatgcatgc				240
		gcanattatc				300
		gcactaaacc				360
		ctactgctct				420
		ggtaaggata				480
		atctggagaa				540
		gcccgaactg				600
		ctccaaggca				656

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1055 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110

```
60
cgggggattt tcctcctctt tttgggcttc tgccagcaat gagggattta ggctatgccc
                                                                       120
aatcccacac tgccgtaccc ggtcacactc gctgacgagg ttatcagggt cgttgcgtgc
ggatgcttac ccgacccggg atcaaggata cggcatgggt agttatctgg tggcggcatc
                                                                       180
gcttttttcc ggtaagtcga tgtatcgaaa ctgatctctg ccccattgga agccacttac
                                                                       240
                                                                       300
ttcggcacag agtacgccag cgtccgattc ggctgcgagg ttactatcga tacaggccgg
aagcaaatat atcgatggca gcatagggcc ggatgccgtg ctgaaggcaa agaccaatgc
                                                                       360
                                                                       420
acgatcgccg gcgtattcta tgaagtaact gagatacgcc ctacttgaat ggcaagaacc
                                                                       480
tctatactgc accgtccatc gatctattgc caaagtgata gcaaatgata cggatgggtg
                                                                       540
gcagccgttc atctcacgtt ccgatccgtt ggcaataaag tcgtggactt ggccaacaac
agtaccgctt ggctctggtc ttttcgtctt catcgcgtgg agacgagtta tcggctccgt
                                                                       600
ggatagogaa ctgottgtog atgaagtaac cottacgtga ctactttaco ogaataaacg
                                                                       660
                                                                       720
ttatgaaccg gcgatatttt cttttgatgc ttgcttttgg agcctctgct tcatcctgtc
ggctcaggag tcgaagcttc tgtccggccg tcgctttggg agttttccag cagagtgggt
                                                                       780
                                                                       840
atgctgtggg agcatccaca ccggtacccg taccccaagc catggagcac gtcacgcgtg
                                                                       900
gtatccgcga ctgaatccga tggtgcaact gagtgcttcg cgcgtttgct tgccggcagt
ccgtgggctg tgaacgtggg tatagccgta ggaaaaaagg catggaagct actacacgag
                                                                       960
tgaaagatat gaaagtagct togtgtogga otogoottat goooggcaac cotgatgaag
                                                                      1020
                                                                      1055
aatatccgga ctattcaccg gcgacaacaa tacgg
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 578 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...578
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

tecceatag	aaatctcaaa	caaccgcaaa	gtctttctga	ccaatcaata	ggggttgtaa	60
acatcactga	coppatopaa	cctccgatta	ttgccggatc	tctgcttcct	atggatcttc	120
catccaaata	tatootrato	tctcacacgg	toppacatca	taggccattg	ctatttggat	180
et et eccess	ccaattctat	ccactcaaca	cgagacccgt	tecappagac	gatgaggttt	240
ttatanaan	Caarragg	aaatagagat	cgatagcaac	agccccatag	tccagtggtc	300
tigicaacaa	ttaaggcaggc	aaacagagac	Cacabadaa	tgacgaaaac	gcttataccc	360
gtatacgatc	LLgaggggaa	aaguguttta	taccatcata	chacharacac	aaaattcoat	420
tatcctttag	agcacccatg	teeggettta	tacaccaca	acceatacac	aaaattcgat	480
tatcaataaa	aaacttaatg	tacacagcia	cgaaacgaac	aattelatta	ctcagtactc	540
				ggtttagatg	cttattatca	578
caaatgtttg	aactaatccg	ttccgacttt	cgaacgga			370

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1352
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

```
actictagagg atccccggaa tgataaagcc gacgggatta cgaggctttc cgctttttct
                                                                        60
ttttgctcca acagctccgt cagggccgtg tacaactcct gaactgcaca ttacagctta
                                                                       120
cttcaaggtc ttcgatacgc tttttgattc ttcataaccg gcaatcatcc gacgcatggc
                                                                       180
aacgaaagtc cgcatgtggc aatgttcact tctattgctg tcggactgcg cagcaccgat
                                                                       240
gatagatggc tactccctgc tcggtaaaag ccatcggagc aacggaactg tgttgagggt
                                                                       300
ttcgggtaac cggtcacaaa ttgtgaccag ttccgtccat tcgtttcggt aagttcgaac
                                                                       360
ataaaatctt ccgggaagcg ctgcaaattt ctctgacggc ctgtttgagc acttttgtct
                                                                       420
gcacaccgta gagttcggcc aatgataatc caatatcact ctgttgccac gaatctcaag
                                                                       480
aattttattc ggatgacgct tacatctgct gttattgtat tcatatcatt gatttataga
                                                                       540
tttgtattca atttcaagtc attgttttgc ttgtgacacc ggagatctaa tatatccagc
                                                                       600
ttatccgata gcttaagcat gtcctgttct atcttttatt ggtgatacgg gcgtaaatct
                                                                       660
gcgtcgtttt gatattggtg tgtcccgcat cttcgacacg gattcgatgg gaacgccttt
                                                                       720
gctcaaagac atcgtgcaaa tgtgtgccgg gccatgtggt aaatacaagc ctaagcaagc
                                                                       780
gtaaaggaac ataggtggaa atatggtaac tggttgtgaa ttagttgttt ttcatgttct
                                                                       840
gcgacagata gggataggca aaacagtatg ggatattgag actttcagtt accaaaccgt
                                                                       900
tatcctgttg tttcccgaac aaactgaggt atgattattg gaagaatttt tctcatacgg
                                                                       960
tttcttttta tctgtttatc atattttgcg tatcagagaa cgctttgata acgggtaatt
                                                                      1020
ttgcccataa gttaaagcgt atgaagatag agaaattcaa ggtgttgctc tacctgaaaa
                                                                      1080
gagcagaccc gacaagtcgg gcaaagcccc gatcatggga cgcattacgt caatcgttcg
                                                                      1140
atggtgcagt tcagttgcaa actctcctgt actcctactt atggaatccc cgtgagagtc
                                                                      1200
gattgaacgg taaaagcaat gaagcgtaga ggtcaatgcc aaattagaca agttgttgct
                                                                      1260
ttccattcat gctgattcga caccttggtg gaacgcaagg cagactttga tgccgaagcg
                                                                      1320
gtcagaatct gtttcaggga agtctcgaaa ca
                                                                      1352
```

- (2) INFORMATION FOR SEQ ID NO:113
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...633
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

gaatacagcg tcagcaaatc cactgacgac gactagcaaa tgatgataga aacattataa attatagcgt	aacaggataa ttttgtttat gagaaaagag ccaagctcgt ctgagcagga aagaacttga agccgatgct	gatgaatatg aaagatgatt gagggtaaag aatgcagttt aagcctgtcg tcagtaccaa ttcgtgatgc gagataatga	aacttcttct aaatttagga ctattcttag gtggtgagcc ttactatacc gtaaatattt gatgaattac cttttgcaga	agcettegag	ttaaacatat aataatgaat ttgacgtttt ggagcaggca gatgcttcag caacacttgt tgcaaggaaa	60 120 180 240 300 360 420 480 540
agaacctcaa	gagaaaaaat	ctaaaaaaagg caataaagaa	gaaagacaag	gccacttcgc	tcagaatctc	600 633

- (2) INFORMATION FOR SEQ ID NO:114
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 868 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...868
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114

ttttttctta acatcgacaa gagagaaaag caaaacataa ctgtcgaaag tatggaaatc atataaatcg agctaaagaa tttagaatca gtttgccata cctatcctac	catttgtgga acagtaaggc aacgctatac ggcacgcacc ggctttcttc gatttatata aaaatggttg ttcgttttac ttcaaaactc agctccggag ccccaaaaat ggcagagccg	ctcaacaact cgatttcta ctatgacgaa cgattcgagg atctacgatc taaattgaaa aatacaaatc caccttttgg atcttcgttg agcagagaaa accgcttagc aaaaagggaa	aaatgcccat tcccacatac caagcaggaa ctgaatcagg tatatataaa acattaatat gtttttccat ggttcaaaag ttgaaaactt aaggcctcca tacttatcga tcgtgcttca	tagtatgattg tagtatgagt ttatttatta	acticatata atcgcgaaag aatagccgga tctttatcgc tctatataga aatgatttat cccgaatccg tcaggtgcta attttcagt tcttcctccc gcggctccgc cttttgcgcg	60 120 180 240 300 360 420 480 540 600 660 720 780
cctatcctac tcttgatgcc ataagttctc	ccccaaaaat	accgcttagc aaaaagggaa ggccgatgac	tacttatcga	tagtatgagt	gcggctccgc cttttgcgcg caaaacattc	720

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 751 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...751
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115

cgatcttctt	ccagtatgta	ggccggagat	gctatgtcgt	ggtattttgc	atctcttagg	60
attagttctc	attcggtatc	agttccaaga	acagctctgg	agctgtgcct	catcaatgac	120
agagggggcg	tcgatcatga	catcccgccg	gcattgttct	tcgggaaggc	gatgcagtcg	180
cggatgctgt	ccaaacggcg	aagagcgata	cccagcggtc	taagcccgta	agccaatccg	240
ccgtgggagg	tgctccgtac	ttgaaggcgt	tcatcaggaa	gccgaactgc	tccttgcttt	300
	aagccgagca					360
atggaaccac	ctccgacttc	gacaccgttg	ataccatatc	gtaggcattg	gcacgcacgg	420
cacctggatc	ggtatcgagc	aagggatgtc	ctccggcttc	ggactggtga	aggggtggtg	480
catggcgtag	atcgcttcgt	ttcctcgtcc	cattcgaaga	gggggaagtc	cacgacccaa	540
ggcaggagaa	tttaattctt	gtcgcgcaga	ccgagctgag	agcccactcg	aggcgaagtt	600
cgcacagttg	cttgcgcgtc	ttcatgaggt	cgtctccctg	aggatcagaa	tcaggtcgcc	660
cggttctgcc	tccatcgtcc	gncgaactct	tggagcgtct	cttgtgtgta	gaatttgtcc	720
	tgacgtgccg					751

- (2) INFORMATION FOR SEQ ID NO:116
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...885
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

					gctgaagatc	
gataacgtat	acgactcaag	cggctatccc	aagcccgcgt	cttcattagc	gtagaaggtg	120
acgaatggga	agagggcatc	gatcgctacc	agccatcgtc	daagaatgca	atctggatgc	180

```
aaaagaaatc gtagccaaat ttctgcagcc cggtattgtg ggtcttggcg gtgctacctt
                                                                       240
ccctaccatg tgaagctgtc ccctcctccg ggcaacaaag ctgagatcct gatctcaacg
                                                                       300
ccgtagagtg cgagccttat ctgacgagcg accatgtcct tatctggagc acggcgaaga
                                                                       360
gatcatgatc ggcgtgagta tcctgatgaa agcattcagg taaacaaggc cgtcatcgga
                                                                       420
gttgagaata ataagaaaga totattgoto acctoaccaa actggcoact gcatatcogg
                                                                       480
gcatagaggt atgccgttga aggtgcaata tcctcaaggc ggtgagaagc agctgatcgt
                                                                       540
gcagtgatcc gcaagcaggt aaaaagcggt gccttgccta tcagcacagt gccgtagtac
                                                                       600
aaaacgtggg tacggtattc gccgtgtacg aagcagtcag aagaacaagc ctctggtcga
                                                                       660
gcgcatcgtg acggttacag gaaaaaactg tctcgtccgt ctaacctcct cgttcgtata
                                                                       720
ggtactccta ttgcgctttg atcgaagcag caggtggctt gccggagaat acgggcaaga
                                                                       780
tcatggcgga ggtccgatga tgggaccgcg ctctgctgtc accggatgtg ccttgaccaa
                                                                       840
                                                                       885
aggcagctcc ggagtattga ttcttcgata gagaagaggc agtcg
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2231
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

```
60
cgtggttgat ctgcaaatcc accgattcta cctttctact aagaagaatc ggatttagaa
aaagtgtttt tototatoga toatgcaaaa gggacaatgt taataagaaa tatatgoott
                                                                       120
                                                                       180
atggcacggt tttagattct gtcctaagaa tctcgttacg gatctctctg caaaaaagtt
                                                                       240
gcaagtagcg gttaatatgg ggagtataaa gattggcata ataaagattc gttgtggttg
cgcgatgtca taccttgcat ttaatggttt tcgacgaaag tggcgagaaa acgaaaagta
                                                                       300
tactgttacc ctcaatcgtt atgattatca accgactacg ttttttggca tatgctcgat
                                                                       360
                                                                       420
ggagtagett taceggatat caatgettet ttgtegatgt tgtaacacat getgacaggg
                                                                       480
tttatttggt agcagccaca gtaataagac gctgttgtat tcatctgaca ggaaaaatcc
tgttcattgg ctttactatc gtcttccggc ttgtccggtg catgtaggca gatagccgca
                                                                       540
ctgaagatgg acgcgcttgg attctaacag attccggtat ttatcaaacg atgacttcac
                                                                       600
aaactggagt ttgctccct ctgaagtccc tgtgaccccc tgctgggtgc catggtttgg
                                                                       660
ccacagggaa gtcatacact ggcattcttg ctgaaaaaga tggctctctg ttctttgcca
                                                                       720
ccaatatcga tggagccatt cttggcagga gcaagctccc gaaactttcc ctgttcgcaa
                                                                       780
tttcgtactc aactatataa agcaaacaat catccaatgc tccgtttagt cggggtgtaa
                                                                       840
                                                                       900
cgcgtacggg tgctcctgcc acttccgttt ggatcacgag catggaaacg attggtttgg
acttgacttg gctgccggag ccattcccgc acaatggaaa aaggggcttt ggtgcaaact
                                                                       960
ccatcggatg gtaacttgta tattatgcca cagaacaagc cgaaggtata aagcgagtag
                                                                      1020
                                                                      1080
ctgtggcatt tcgactgata agggcatcac atggaaacgt ggagccgccg atattatgtg
ccggccgatc ctttctacac agccggctat ccgttgtcgt tcgtctggct tttgatgatg
                                                                      1140
gggcttacaa tatatatcag ttgggaggcg ttagctttca ggaacattct tttcctcaat
                                                                      1200
                                                                      1260
atggaagggt atcctgaaac tgaataaaac aattagtaag aaccatgcgg cacggatctg
tgccgccatt gcttgtttgc agtgtgtaac ggccggatag ctgctcagga ttttctctat
                                                                      1320
gaataggagg aggttttggt gctgctcagt attttggcga tgcaaacaga ggttgttcgg
                                                                      1380
ttcatccgga gtaggtttgg agttggtcgg acgttacaat ttaattttcg ctgggctttc
                                                                      1440
agtaccatgt tggattggcg tacattgaga gcgataccga taagtccggg aatgtcttcc
                                                                       1.500
```

ccgattttgc	tcaagcggat	ttaaggtcgg	cttgactcag	ctccacgtta	gaagcgaatt	1560
taactttccc	cttatagcga	tggctataag	tatcttggta	cagctcggct	gtctcctatg.	1620
tagcggccgg	gttgtctttg	ggttttgctt	cgggtgctaa	aggttcgctt	ttgctcccgg	1680
gattactgcg	ggaatgggag	tgaagtataa	gcttaaccgc	ggatcaatgt	cggtatcgag	1740
tattctttca	cgggggttac	ttacgatgct	ttggatgcgc	tgacggataa	aagtgtttgg	1800
ctcgaggatc	cattaagatc	aatgactcct	gggtcaaaaa	caaggatgct	acaggggcct	1860
tatgcttagg	attacgtatg	acttcggcct	gcgtaagact	ttttgtaata	acaatagggc	1920
ctcgaaacat	tctaagggaa	tagacctctc	ttggattggt	gttaggtgaa	atatcttgat	1980
agaaaagaga	tagatggaag	gtgatggagc	aagctccagt	cagcagttat	agtgccgagg	2040
catatcgctt	tggtcatgat	ggtaatggcc	gttgggcaaa	gatacgaggg	aaagagcgat	2100
gcgaaagaca	tgcggccggt	gtggatgctc	tgcgcgtagc	tttgcgtgca	gcagccggtt	2160
gcggtgtgga	atatctcaca	gcctacacct	tcagtaccgg	agaatggaat	cgtccggaag	2220
aggaagtcag	g				-	2231

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1121
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

```
ggttaccggc tctctgaaag tattgcagac cttttaagat cagtaaggtg gtacgatcgc
                                                                        60
cggttgtatg gtcaaaggaa ggtaaggtca agcgaacagc aaggttcgtc tcatacgcga
                                                                       120
cggtatagtg atccacaccg gagagctggc tctctgaaac gattcaagga cgatgccaag
                                                                       180
gaagtggtgg ccggaccgaa tgcggtctta atctggctca ctcgaacgac atccaagatg
                                                                       240
gtgattaatc gaagctttcg acgagatcga aatcaaaaag actctctaaa gatcaaccga
                                                                       300
gacgggttac cacccatgaa cgcgatcgat ttagccatac tgaaattttg gcgataggat
                                                                       360
tactgaaagg cctgtttgat ggtatcatca aaaggcagtt tcacttatag ccatagtcgt
                                                                       420
tgccacgtat ggttgtgcct tcttgccgtt cccatagaga cgtggatcgg acctttttc
                                                                       480
ggcctttcac aggcgtggct catacttttg ctttgatcgt tgggttcttg gctattttgt
                                                                       540
tatcatcccg atggtcggca ataaggtctc gaaaatcgtt ggcaagaccc tatcggcatt
                                                                       600
ctcaatcact tggccggcgg aatagtcggg atagggttag cagctattct gatgagctat
                                                                       660
cttttcctga ttgccgacaa tgtttttcaa gagacgaagc ggacagtgac aatccgtccc
                                                                       720
ttcgcaatac ttcgagctgt atgaccatgt aaaaaacata gtcccaactt ttagccccca
                                                                       780
toggtgttta tgaattgaaa ttogtaaaga gottactoag agaottoaaa tatoaagaga
                                                                       840
acaataatat attggatgag gttacaggca gtgaatataa atcggcttcg taaccgacat
                                                                       900
cgaaacagaa actataggac gcggactttc caagatacag ttcgtctcat atctgcgaag
                                                                       960
aaggaagagc cggaatggct ctcgaattcc gcctgaatgc ctataggcac tggctctcta
                                                                      1020
tgaaagagcc gactgggcac acctcaatat tccaccgata gactaccaag atattatcat
                                                                      1080
tatgcagctc cgaaaaagaa aaaggggccc aagagtttgg a
                                                                      1121
```

(2) INFORMATION FOR SEQ ID NO:119

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1335
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

```
atccccgcaa gctcgaaaca cccgaagccg taacggcttt cgagggactt ccatacctga
                                                                        60
geegggeett gaacegeget tetgegtaeg egaaggegge aggaagteee egttaegaeg
                                                                       120
agatatacgg acgaggettt ctggcagtgt tcgatttttc tttcgtcgcc ggcaagcatt
                                                                       180
ataccgaggc ggatgccgat cgaacatcgc cgtggcagtc attaccgaca ggttggcgcg
                                                                       240
ceggtetteg getettegag egaggeegte ggeeggeaag etetgateaa tggggeaaat
                                                                       300
acaccette cggagtggtg cgccatgtga cccctttctg cgattcgctt acggagatgt
                                                                       360
gtggatgcct gtgttcaggc tgtacgaaga aaagtgaaga acaacctatt ctccagattc
                                                                       420
aatgtaatct gtctggccaa agcccgaagg acttcgatgc catcaaggaa gaagtcgggg
                                                                       480
ccttgactgc aagtgcaata gtgtgcagga gaagttcaat atcagttttc ccggccagct
                                                                       540
geogateagt teacgaegat geacegeaaa ttteacegtg aegataceaa eetetggagt
                                                                       600
atcgccgtcg cttcattctc ctcctggcag tgtttcttgc atcccggcca tcaatctttc
                                                                       660
                                                                       720
gggtatgacc cttagccgta tgcgtcccgt ttggccgaat tgggcgtacg acgctctttc
ggagccgtcc gatccatata gtccgccaag tgctggcaga gaatatgctg atcagtctga
                                                                       780
taggggggct ttcggattgc ttttgagtta tctggtcatg gccctctttc cctgtggctc
                                                                       840
ctcagcgtgg ggagccgggg aatgatgcag ggcgacatca acgagccatg ttcaatcccg
                                                                       900
teatttteet gatagetete gtettetgtg tetgateaat etgeteagtg cetttatece
                                                                       960
tgcctggcgc atatccaaga acccatcgta gaatccctct cccactaacc tcatcataca
                                                                      1020
                                                                      1080
gatattatct gctacatcat attatcaaga tcatccgcgc cgaacgtcgt gccaaccttg
gatatggctg gagatgctcg tcgtatgtgg cctgctttgg ttcgtcagga ctatgccgtg
                                                                      1140
acagctctgc gtgcttggac acgcccattg aactacatat agaacacgtg taccgcatca
                                                                       1200
cgctggcaac cgtacaaaaa gataagatgg aaaatggaaa gagaggtctg cggatcaggg
                                                                       1260
aaaaaccatg atgcaaccct cgatctgatc gctgcatatc cggagtggaa gcgcttgtct
                                                                       1320
                                                                       1335
ccaagtgggg cggca
```

- (2) INFORMATION FOR SEQ ID NO:120
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 530 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...530
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120

cctgaaagta	atatccggat	caaggggtgt	gcagaggagc	atgtcatcct	gtcgcacaag	60
ccatcgaaca	tatctaccag	atcaccgaaa	cgatcgcttt	gaggcatacg	gcaagggcgt	120
tgatggtgaa	gtcgcgacga	cgcaaatatc	ttccagcgta	ccatcttcga	ctatcggctt	180
acgactatcg	tgtcggaact	ttccttacgg	gcacccacaa	attctatctc	cagatcacca	240
tgcttacttg	agcggtaccg	aaattggcga	aaacggatag	gtgagccttc	cgtccagctt	300
cttggctaca	gctttcgcca	ggtcgatacc	gcgccctacg	gctctatatc	gatatctttg	360
gaaggacgat	tcaagaatat	atctcgcaca	taccacccac	gacataaggt	ttccagtccc	420
aactgatctg	ccactttctg	cataagacgg	aatatcggga	tgtcgattta	ctaagaatta	480
actctttgtc	ggcattctaa	aaaatcaagg	aatggattgg	ccgacaaggt		530

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...457
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121

cagcttggag	gctccgagtc	cgcgctgaat	ctgaatggta	ctggcttgat	catcagacca	60
ctccaattgc	tccaatatac	tttcccgtct	tccatacctt	gacaggaact	ccgttgatga	120
gtacaccgaa	gttgtaagtg	tcgaatcacg	cacattggta	cgaccatcac	cgaaacctcc	180
gcttcctttt	gtcgtaaggt	agagggagtg	gatttaacca	gttcgggaaa	ttcgacattc	240
aacgagctgc	ctgaatatca	gccacacgga	tattggaaac	gggtaccggc	gtcaacggtc	300
tttgggcacc	acagaggcta	ttacctgaat	ctcatccaag	ccgtggcctg	gggatcgagg	360
agaatcgtac	cgaggtcttc	ttgagaacct	ctcctataga	gcgagttacg	gtagcataac	420
ctacgcaacg	gaaagttaag	aagatttggc	cggtact			457

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...495
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

catatcgtag gccgctacgg cattcgcccg	ccggcaagac tgtggaagtc aatacgagct	gctctacggc accctcggga cgtctatctg	tgcaccttgc tacccgccat gagactccgg	gtatgcgtga cttcctcacc ccggaagagg ccaaccccaa	cacggactga tggaggccgc tatgtacctg	60 120 180 240
				aggcgtacgc		300
				ctggtgccga		360
				cgccggattc		420
aagaggacta	catcaaggag	ggaagctcgt	cggcgtcaag	gacctnacgg	nggccaatat	480
gagtccgtcg	tgctt					495

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 603 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...603
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

gtagacgccg tgtcgtgtac gatgtcgtcc accacgagca gcagaaagac gacgcggatc cgaccagcac cgacgcacg gtcgtcagca gttcggatat tcgcttttgg ctatgggttt gttgtagtat cccgagaggg cgaagagaga gaccagaaaa gcagatagag gatccccacc cacaggctct tggcgttgaa ggatattcgg acagagtgga gtatatgcgc tcttgctctt ccgtgaggta cgcagcgtat tgtagctcaa ataggaagcc acaattaccc gaagacatcg ccagcagata gcgccaggcg gtgtagcttg catacgtgtc aattggcgat caacctccac 600							
ccgtgaggta cgcagcgtat tgtagctcaa ataggaagcc acaattaccc gaagacatcg 540 ccagcagata gcgccaggcg gtgtagcttg catacgtgtc aattggcgat caacctccac 600	atgtcgttta gcagcacccg tagacggggg gtagacgccg cgaccagcac gttgtagtat	cggacttcag atgataacct aaatatccca tgtcgtgtac cgacgccacg cccgagaggg	ccacgaagcc tttgtctttt agggcaacac gatgtcgtcc gtcgtcagca cgaagagaga	gtctcttcgc tcgctctttg agtcgccacc accacgagca gttcggatat gaccagaaaa	tatcgtgccg atgccgaagg atcataaaga gcagaaagac tcgcttttgg gcagatagag	ctcccgatga tcgtcaccca agagccgcag gacgcggatc ctatgggttt gatccccacc	120 180 240 300 360
ccagcagata gcgccaggcg gtgtagcttg catacgtgtc aattggcgat caacctccac 600	gttgtagtat cacaggctct	cccgagaggg tggcgttgaa	cgaagagaga ggatattcgg	gaccagaaaa acagagtgga	gcagatagag gtatatgcgc	gatccccacc tcttgctctt	
	ccagcagata						600 603

- (2) INFORMATION FOR SEQ ID NO:124
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 858 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...858
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124

- (2) INFORMATION FOR SEQ ID NO:125
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1879
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125

agatgctgaa	atcggcattg	caagtcgacg	agttggaatg	cgtgttctga	attgtgcgat	60
					agctccctgt	120
					ttcatggcga	180

```
tottgaagoo accgccacgo gaccgagaag attototttg gggacgatac agttttcaaa
                                                                       240
aataattege atgtageega accaeggata cecatettaa getetteett teegtagaga
                                                                       300
accegggagt teettttea acgatgaaag eggtgatace aeggtgeeet ggetettate
                                                                       360
tgtcatggca aataccacgt atacgtgagc atttcggcat tggtgataaa aatcttgtta
                                                                       420
ccgttaagta cgaaatgatc tccttttctt cagcaaaagt ttgctgagca gcagcatccg
                                                                       480
tacctgcatt ggttcggtaa gtccaaatgc accgatccat tcgccagaac agagtttcgc
                                                                       540
aaatacttca tottttgtto ttotgttoca ttttcgtaga tgggagotog cacaaagatg
                                                                       600
tgtgtgcaga gagaaccacg cctgtggtag cacataccgg cttagttcct ccactgccat
                                                                       660
tgaatacatt acgtttgtac cgccggacca ccgtattcaa cggggaaagg gatgcccatc
                                                                       720
agtccgattt cgccctcttc tttactgttt cgatggggaa acgttcctgc tcgtcaattt
                                                                       780
ctgcgccaga ggttttactt ctttctcggc gaaactgcgg atcatctcaa gaacaattgt
                                                                       840
tcttggggtg tctgagaaaa gttcataatt cttgaagttt attggtttgt agtgatacta
                                                                       900
aaaactettt tattgttgea tegggatgat eeagaageaa aagteaatga agetteagtt
                                                                       960
gcagcttgta cttgttctgc gtaaaatccg gatgtatttc tgttacgaca aggccttttt
                                                                      1020
cegggeacat tegateacae acatttetgt gataateaag tttaettgte ettttgeeta
                                                                      1080
agtggcaaag agcattttt catgatttg gggttaccct tggcagttgc tccatagcta
                                                                      1140
aaattacctt gogggttoot atcagcaaat coatggtoot cocatacogg gtgctttott
                                                                      1200
geegggaate ageeagttgg ceaageteea ttttegteta ettgeagtge teegagtaca
                                                                      1260
                                                                      1320
ctaacatcca catgccacca cgaatgatgg caaatgaggt agcactatca aatgaagcag
ccccggaata gccgtaatgg agcctccccc tgcattgatc agataaggat ctctttgcct
                                                                      1380
gtttccggag cagggcccat cccaatcatg ccattttcag atgcaaatat acttgcactc
                                                                      1440
cgggttttag gtaattgggc accatcgtcg cagacctata ccgaggttga ccacatcacc
                                                                      1500
atctttcaat tcgagggcac acgcttggcg atcacttctc tgatttgatc tttttccatg
                                                                      1560
atgaaaaaat tttatcgatt tctatttgtt attcattctc ttatgaaact cctgagcatg
                                                                      1620
aatgaagcaa catcatcagc atatgtattg gcaccgaatc ctgcatatag ccaagctctt
                                                                      1680
                                                                      1740
tggccaattc ataggtgata cgaggccctc cacagccaag atcatcttat ctctcagacc
ttctgcctcc atgagttcga ccagtctatc agattcttga tatgcacatc tttttgtgtt
                                                                      1800
actgtntgag atacaaaaga ncatcggcat tcagttcgat tcctttggna ataaattctt
                                                                      1860
                                                                      1879
catcggaacc tgactgcca
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 662 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...662
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126

```
60
cgggggattt ctttgtggag tcgccgatca tcttgctggc ggctattatt ggttcctgaa
                                                                       120
gatatatgag aacggcaggt attgcacctt tccgcatgca tcgagtttct gaacagacct
tatgcgcaga tctttccgat tctgactctt acgatgagct ggccaactat ctttcaccct
                                                                       180
                                                                       240
ttatggacgc atgggaggcg gcgcacagga tcaacttcag ggacagatcg cttcggccaa
                                                                       300
agaatccgct ttcgaggatg atttctccgg cactttactg ggtaatgacg ggcgtgactt
                                                                       360
ctcgctcgac atcaataacc cgaaagaacc gaaaatcctg gtgtgggcaa caatcccgac
cgacaaaata totattoggo ggoactoggt tttacaacag coggatogtg aaactgatoa
                                                                       420
ataaaaagaa gcagctcaaa actcggtgat tatcgatgag ttgcccacca tctacttccg
                                                                       .480
```

agggctggat	acctgattgc	tacggctcgt	tccaataaag	tggcaagtct	gtctgggctt	540
					attcagaaca	600
					tatcggaacg	660
ct						662

- (2) INFORMATION FOR SEQ ID NO:127
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...395
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

catcggccat c	cacacgagtg	atgagcaaag	gagcggtacc	gctgttgcga	acttgaagct	60
atgccctacc g	gatccttttt	cttccggaat	caggccaagt	taaaggactg	ctcctcgacc	120
tgtatttccg g	gactctcctg	agctgtcgca	acagaggagt	caataggaaa	aggaagaaga	180
gcagccctcg a	aatgtctga	cgatcatacg	ccttgtacta	cttgcagagc	tatgctattt	240
attctcaacc c	ctttgatgc	gtagcgtaaa	ggtaccatcc	ttaccattgc	tgtaacggct	300
atggtcttta c	gaactgacc	cggacggccg	gcaggattat	atggacgtct	attttgcttg	360
tctgacccgg a	ecgatgggc	tctttgctaa	acggg			395

- (2) INFORMATION FOR SEQ ID NO:128
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1939 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1939
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128

```
120
agattttcca gcagaagccg aatccagctg aatcagttgt cgtcgatgaa gagcaattcc
tcgataatcg tgaaatcctc ctgtgtcgag ccaccgagaa ggggcgtaca aattggtctt
                                                                       180
                                                                       240
tgtcgaagaa tcgggcgcat gcagcctttt gactgcagca cgaagctcct gcctcattgc
ggacgaatct ccgttcgtcc ctcttggatc caatcgtata tgaccacacg atgagttctt
                                                                       300
cgtctttgtc gttgaatagc tgtacttccc ccgcagccgg atcatttgga cgaaaagatc
                                                                       360
actgatggct atcggtgccg ttttggagct gtggggtgtt cgatcggtgt gcggaacagg
                                                                       420
cgttcgagct gaatctgtac tcgttgggtt tcattgttgg ctaaagagat tgtgtatggg
                                                                       480
                                                                       540
gtttatttgg cgattgcaac tgattcagac tgtctcgaag tgtggcgatt cgcgcttcgc
atcgcttttc ttcttttgct ccagttctat gacagcttgc ggagccttgc cacaaagctt
                                                                       600
tegttgeega gettetteat gacegaageg aggaattete etgataggee agttegtegg
                                                                       660
acaacttctt gatctcctct cccacgcgat caatgcgccc atcgggatgg cgtattccag
                                                                       720
tgtaccgatc aggaagaggt agagccgctt gtctttctt ccactcggtt gatggcttca
                                                                       780
aggtgcccat titgatgatg acggcatcga aagaggcatc gtgttcgttt cctcttcgag
                                                                       840
cgtcagcttt tccttgaaag gaatgttctt gccggtgcgg atttgcgaat ggcggctatg
                                                                       900
atctcccgtg tacggtcgaa ggcttgcagg agtccctgtc cgtctcatgc gcatcgggca
                                                                       960
ggaggcagag catgatggtc cgccatcgtg acgcggttcg agtgcatgcc atagctcttc
                                                                      1020
                                                                      1080
tgtgataaag gcatgaaggg atggagcaaa cgcagcagct gatcgaagaa tccgatcgac
tgccgtaggt cttcgcatcc atcggctgac cgtatgccgg cttcacctct ccagatacca
                                                                      1140
                                                                      1200
ggaggagaag togtoccaga acagottgta aaccaggtoa gtgcotogot cagaoggtac
ttggagaaga gatcgtccaa ctccgcttca cctcatcgag acgatacccg aaccatttca
                                                                      1260
cggccagagc cgagcttcgg gctgcgtgga cgtttctgcc tgctgccatc cttttacgag
                                                                      1320
                                                                      1380
gcgaaggcat tocatatott attgcagaag ttacgtccct gctccgagag cgttcgtcga
agagcacate gttgccggcc ggagcggcca teateagtee etgcgtacte egteggcace
                                                                      1440
gtatttctcc atcagcatga tcggatccgg gagttgccga ggctcttgga catcttcta
                                                                      1500
ccctgaccat cgcgcacgaa ccggtcagat atacgttgtc gaagggtttc ttgccacggt
                                                                      1560
                                                                      1620
attcataget gecatgatea taegggetae ceagaagaag agaatgteeg gageegtaeg
aggtcgctcg tgggatagta gtagtccagc tnttcgttct ccggatcatc acatcnccga
                                                                      1680
                                                                      1740
atacgcttat cggccatagc catgaggaga accactatcc agcgagtcgc tgtcctgtcg
cagatectet actgtgageg agtegatece gtttgettae gtgccagtte caeggetttt
                                                                      1800
                                                                      1860
toggoogtot cogoactacg atacttoogt coggoaggta gtaggoaggg atacgatgoo
ccaccagagt tgtcggctga tgcaccagtc cttcacgttc tccatccagt gcggtaggtg
                                                                      1920
                                                                      1939
ttcttgaatt tggccggat
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1073 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1073
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129

```
cccgtgcttg tctcctctt gctgctatcc aaatagagga tggccgaatg acgaagccga 60
acagactctt tcgcgactga agaatcgcc gcaatttggg atgaagccga tgcttatatc 120
gcggaaatcc aactgttgcg aggcgacacc gcgaagcggc cgaaatagcc gacagactct
tgtcgcgcaa ttcgccatga gacagcgacc tcaactcctg cgtgtggcag gcaatgctta 240
ctacctttgg gcgattcgaa caaaaccatc gactatcttt ccgactacag cgaaaggtgg 300
```

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223

aaggccgacg	tgtgctgaaa	anggccggaa	gtcgganagg	ttaatccgac	cttgtggtat	60
agaaagagtc	ggtattgtac	cggactcttt	ccggtttatc	ttgccttaat	tctatcgttg	120
tatgaccaat	ccggggttaa	agagccataa	tcaccaaact	attcgacgag	gatttcggga	180
tgccacgatg	atgaagcagg	ataataaagc	aatcggggca	acatcggaga	gagagaaaac	240
ctctcccatg	ctgccccgat	ctgtttgtta	gtactcgcgc	gtcgttattg	aacgtcactc	300
tttctgtaat	atcaccgatc	tgcaagagga	aaacgccctt	gagtggctga	tatctatcte	360
ctggaagatg	ttattaagcg	taactctgta	aaaatctgtc	cgttcatatc	tataagagat	420
gccactttgc	ctaccatttc	tccggtatct	ctatcgtcaa	atcttttgat	gtgggtatgg	480
gatagacatg	aagcctttgg	tgtcgacttc	tcctacggca	ttgctcttct	tcatcagggt	540
gtcacttctg	tatctttctc	aagaaggaat	tcatacggag	cttcgatatc	tctccgttca	600
ccattacctt	gtccacttcg	taaccttcgg	cagggatgga	tgtattttaa	tacgacggcc	660
tgccactaat	gtggaaccgc	tgttcagggc	tgcccatcgg	ccgttagctt	tatctctcca	720
ttttcgggct	ggatgccact	acggaatata	cagagatagg	ttcataaatc	gcttccactt	780
cattgtagat	tctttgacta	ctacatgagt	ataactgttt	ttgaagggta	gtctgaaaaa	840
tccacataat	ctttaagtcc	gaaatatact	aaatctgcta	tgaaggcttt	gggaagaatg	900
tctctgaagc	gagcatttct	ttgtcgtact	ctagtagtac	cagaaatcgt	Cacecceec	960
tttgacaata	tccattcctt	actgtcgtat	tcgtatatca	attcaaattc	gttcaaacct	1020
gtactggccg	ggatc				•	1035

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...588
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224

gatccatacg	gaataataag	cggagggcgt	attccaaaag	gagggggtgc	ggggttggcg	60
ciciccaatg	ccagactttg	caagacgatg	agcaaaacca	aacgagggta	tagataagaa	120
ccacaagcga	cttgttcata	ttctaatgag	gcttaaccgg	taaaagaaag	ctatctttgt	180
acgicacaaa	gatatattat	tgtacggcta	tccgtatata	aataacgaca	gaaccgaatg	240
gaaataaaaa	ggcggcattt	gtaatcagta	ataccgatgt	gcgcaaatgt	cctetaceae	300
cttaccagaa	tatgetttea	teggeegtte	gaatgtgggc	aaacctctct	gatcaatatg	360
accattttat	aaaagggact	ggccatgacc	tccaaaagcc	gggcaaaacg	cagctgatca	420
tttgggtgcg	categaegat	atcettagg	ggtcgatttg	cccggctacg	gatatgcccg	480
agcagettte	castctctts	tectgatega	aggatcatcg ttgcaggcat	agacgtacat	cctctgtcgg	540
	Cagcottet	cccgaccga	ccgcaggcat	gąacccgc		588

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2199 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2199
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225

```
gagaaaggcc tcgcgctttg atttcgatcc gtcgaacttt cttaagtagt cgcttgtctg
                                                                        60
cacttatete tgattaaggg acttetaett tgtteaggte teattgaega eageateegg
                                                                       120
                                                                       180
agtcaaacta ttagcctctg cctcatactg agtccgatac ggtgacgcat cacgtcatga
catacggcac gtacatctca ggaatcacat aacctctatg cttgatgaag gcgtatgcac
                                                                       240
gtgcaccaat gctaaattga tagaagctcg gggcgaagct ccgaaactga tcattctttc
                                                                       300
agagcattca agccgaattg ttcgggatag cgcgtggcaa aaaaatatca actatatatt
                                                                       360
gctcgatctt ctcatccaga tacacctgcc tttcacttgg cgcgcttcca gtatttcctc
                                                                       420
cgtagtgatt atcggacgaa ttctgccgac cggccaccga tattctgacg aatgatctgc
                                                                       480
atctcctcct cttttgggga tagtctatca gcaccttcat catgaatcgg tctacctgtc
                                                                       540
ctctggcaac tgataagtac cctcttgctc gataggattc tgggtagcat tacgaggaaa
                                                                       600
ggctcaggga gcttgaaagt cgtttcccca atggtaactg tctctcctgc atcgcttcga
                                                                       660
gcagagcact ctgcactttg gcaggacacg gttgatctca tcagccaaaa taaagtttgc
                                                                       720
gaaaataggg ccttgtttac ttgaaattcc tcccgtttct ggctgtacat catggtacct
                                                                       780
accagtcagc tggcaagagg tccggtgtaa attgtatgcg gttgtacttg gcataatcag
                                                                       840
teeggeeaga gttttgatag ecaaagtett ggetaateee ggaeteette gageaggata
                                                                       900
tgtccatcgg ccaacagtcc gatcagaagc gctccaccaa atggttctgt ccgacgatat
                                                                       960
tetgegecat accetegete teagatteac aaatgagett ttetgeteaa taagetetet
                                                                      1020
gagagoctta tgtcaatggg tttcactcat tttttctat atctttctt gctaaatata
                                                                      1080
atgaagatta tgcacaccat ctcatgttga gatagacata tagcatctgc agggtttaag
                                                                      1140
                                                                      1200
cgcgaagttc agccaacggc cagcattcgc tcgatcagag caaagccttc tccctgattt
cagcaggcac ctttacttca taacgttgtg gcggagagct tccaagacct cccacaaacc
                                                                       1260
tgtttgtttc atataaaaca gcggttgtcg ggttgaatgg caataaacgt tttacccgga
                                                                       1320
tttctttccg caacacgtgt agcgtctccg gctctgtcgc aataacaaac atttttgtc
                                                                       1380
ggactecega geatgattaa gaatacegge egtggaatae aaaageageg ategetaete
                                                                       1440
 agcactogtg gogaatgaga gocotogoto coggatgaat gagaatatoa goatogggat
                                                                       1500
 acagetecat ageetetaaa tggattette egtaattege teatgtaega aacaegaage
                                                                       1560
 attccaaatt ccatctcccg tcctgtcttt cgcgagatat aagctccaag gtttctaccg
                                                                       1620
 ggccaaagag aatttttctg tctcgaggca agctctccac taccttagtg cattgctgct
                                                                       1680
 tgtcaagcaa gtagtccgtc caagccttta cctcgcaggt cgtattgaca tagctaacga
                                                                       1740
                                                                       1800
 tgagtccatc ccgggttctg ctcctccacc gacgcaagcc ttcagcagag gcaccttcgg
 ccaaagaaca accgcgtatt tcgtgggagt gaggatagtc ttctgcggcg aaataatcga
                                                                       1860
 agcgtttcgg ccatgaagtg gactccgcaa aagagtatcg tatccgcctc ctatcggcag
                                                                       1920
                                                                       1980
 cctgacggga cagaccaaga gaatcgccga tataatcggc atgtcctgca cctcagggcg
 tgcatagtag tgcgccaaaa taatggcatc cgttctttct tgagaagttc tatctcctta
                                                                       2040
 agaatateet tigittgeta caaaaaccaa ettaaagett aattgagtaa ggaggaaatt
                                                                       2100
 catgctgtgt ccatggccgt aacgctatga gtcaaagcgc ctatgctgat gtaatcacac
                                                                       2160
                                                                       2199
 ccgtttctgc cacactttgc agccgttcga gtgtcatat
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1796 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1796
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226

```
gggggagcga gccggtcagc aaaggactgc cgagcgattc ggcaagaagc gggtcagtgg
                                                                        60
atgaagagcc aggcggatac ctacctgctt tcgattctga aaaccttagg cagcgaactt
                                                                       120
ccggccggta ggacgaaggt atatttcgca tgtggttgtc cttcatatag cggaatgcct
                                                                       180
cgttgtctat acggcatatt cggctgccat gctcatgtcc gaacacatga tcgagaggct
                                                                       240
tttgcccgag gatccacacc tttcagctcg catatccgct ccacgctccg attcgaaggg
                                                                       300
categeatee gtaggeatae ccaacttegg tgggatagat gataetttge egtegegaag
                                                                       360
ageogatacg geaegtteea attetegtet gtgggattgt eggggtaaat ettgatgate
                                                                       420
atatcatttc agtgtatatc gaatagggtg aaagtcttat actgtcttct tttgtgaagg
                                                                       480
toggtagett agtagttgta cocagetace etgecattgg etgetgegta geageegttg
                                                                       540
atctcggccc gttgtttata gttaatataa ggatgccgaa ggatactact cctacgactc
                                                                       600
cttttagatc gatacgatcc ggcttgattc ctattttaac catggtctca gagcgcaaaa
                                                                       660
gcgttcgtag tccatgccgt aaacctctgt agctgtagca cggtatagta gccgccaagc
                                                                       720
tgtcggcggt aggatcgatg cggcgagcga atgtaggccc tatcccgggt atgcgagtaa
                                                                       780
gggtgccgaa tcggctgcat tcaggtcgat caccgtaccg cgaggaaatt tatggccgat
                                                                       840
cgggcatagg cttctctgac aggaggcccc acgtagtccg cacggtcacg atgctgtcgc
                                                                       900
ggcttttctt gcgcgattgt tccgaggatg ataaggcctg acgtaattct tctttcttc
                                                                       960
ttttctaccc ggttcatcag cgacgtttga acagcttcgg ccacaggtgc attgccactg
                                                                      1020
gccggccttc tttgaagatg aatagcccga cgatgaccat cagcaggagc aagatgctat
                                                                      1080
aatgctttcc cgatttgccg aagtggaagg agtctttcat ctgtgtacgg ggctgtttgg
                                                                      1140
cggttgggtt attccgagaa gagtagcccg tcgcgctgtg gaggatgcgg tcggtgccgg
                                                                      1200
ctgccaattt ctcatcgtgg gtgacatcag gaaggtctgt cccatctctc ggcacagacg
                                                                      1260
gaagaagaga gcgtcagctc ttctttgtgc gctgagtcca gactgccgct cggttcgtcg
                                                                      1320
gcaggatgat ggccggatgg ttcaccagag cacgtgccac ggctatccgc tgttctcacc
                                                                      1380
gccggagagt tccgatggct tatgcgaagc tctgtcgctg agttcagatc ggaaagcagc
                                                                      1440
cgttcagctt cgcaagaagc ctcttttcgg tctttccggc tatcagagcc ggtatcatca
                                                                      1500
cgttttccag agctgtaaat cgggtagcaa tcggtgaaat tggaagatga atcccagccg
                                                                      1560
tctattgcaa attcggcttg cttccgattg ttcatgccca ttatatcggt gccgtcgtac
                                                                      1620
gcaattctcc gctgtccgcc cgatcgagcg tacccagaat ttgcagagcg tggtctttcc
                                                                      1680
ggcaccgctt gtgccgacga tggagactat ctcccacggt cgatggcaat atctaccct
                                                                      1740
ttcagtactt ccagagagcc gaaatcttgc gaatgttgcg agcttctata atcatt
                                                                      1796
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 611 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...611
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227

		t-coastoot	cacctaccas	taacgactcg	ttggtgctac	60
gccgacggcc	ggaatgtact	tgccggtact	-tttessa	taacgactcg	aatcgatcac	120
gggtgatcaa	cggctatgcg	ccgcttcctg	Ctgattcgca	ctgatcgacg	accoparac	180
- + + +	+ cacaggaca	ofocttcggg	aagaccgaag	aggagaatug	CP 44 4 6 9 9 9 9	240
+ - a + a a + c a a	grafacttat	ggaggaagaa	cttcagtacc	ggalgactic	CBagacage	7 1 1
Legialices	Scatterat	gragaggaca.	tctcggacgg	cggactcgac	ccggggaaga	300
gagctttcga	Cgaagacgac	goagaggass	anatrroppa	cagcacttat	tcgtatcgac	360
ggacagatac	gaacatttee	gcaccacage	agacceggg.	tatccaacaa	goggotgaag	420
aaattccttg	tcgacaggat	gaacaacgcc	accgcagccg	tatccaacaa	8-86-68	480
t-ccost	attootcaat	gccgaccggt	aaagagcaac	Laceggacea	44666666	540
+ at agt caca	togaactnct	ccggccacga	cgggaarigg	agallatice	cguagatat	
cacacacac	agtatataaa	gacgatgtac	tgctcgtgat	caataagctg	ccggattagt	600
		880	0 0 0			611
ggtacacccc	g					

- (2) INFORMATION FOR SEQ ID NO:1228
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...5\overline{15}$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228

attctgcccg gccgtattct gatagaatac tggctaaagg ctataactgc ggatcgaaga catcagtagc	ttgtagaata tcgatgtgga gaggagtata aacaaggcca cccagagacc gaagtgcgaa atgataccca	cattatagcg gcaggacgca gaaatctatg ccagcaccag cgtgaaggct gtgaaaagat caaacggata	taccgaatac gctacgcatg aatgatgaag gccaaagccg tctgatgctc ctgagcacaa	ccagattaca tgaggaaggg	CC 666 m - 6	60 120 180 240 300 360 420 480 535
catcagtagc gacattaagc	atgataccca	caaacggata	ctgagcacaa	tacccacage	· ·	515

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1886 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1886
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229

```
tegegeatea ceageteace gtecacatee gatatggeag gettacgetg ggggattegg
                                                                        60
cageegeegg caeteceatt geattggtte geggtgtetg atcagagett ttgtcatgge
                                                                       120
attcaccgtt tcggcctctt ggtggataag gaggctccct gacgggcctc gaccagcttg
                                                                       180
gcacgtgcaa tggctctccg aagtatgcga gggcaaactg cttgttcagc tctacagcct
                                                                       240
gatcgaatcg acgatggcct gctccaaatt ctgtatcagc atatagtcca aagccgacgg
                                                                       300
aagcacagat ctgcattgcc ggcagtcctc tcggatattt ccgtatgtcc tgttcgtgat
                                                                       360
atgccacctg ctcttgactc agagctacct caggttgatc ggtttgagtc gcttgggcag
                                                                       420
aacctttttg tcgttgaagc ggcaatggct tccgagtagt agacgcgcgg cacctcttcg
                                                                       480
gaagaggact ctcgtagtag ctgaggacga atagcggcga gggctgtacc tctacatcgt
                                                                       540
gtcctgaatc cgcccacgta tccgactgga gtagcgtgtg cgcttctcga ggatttctcg
                                                                       600
gatacgacga gcaggttgaa cttctctatc gtttcgtgct atcctcacgt gtctctttgg
                                                                       660
tcgaagtcga agagctgctt tttttctttt ttttgtcttg ctctgtgccg ctttttctat
                                                                       720
gtcgaaagcg cgccatagtc ccgttcggct ccgcgagtgt cgcccaatgc ctttttggct
                                                                       780
tggggcgagc atagtagccg acgacaaagt caggatagtg tcccagcact ttgcgaagtc
                                                                       840
ggtaatggct tttcggttct cgttgatctg cgtgaggagg atgcacggtt gtagagtgca
                                                                       900
tgatagttct ccggctccag acggatgact aatcgaagtc ctcgatggca ttgttcacgt
                                                                       960
caccgaggta agagcggagc aggcacggtt gaaacgtgcc aacttgtcgt tcggcttttg
                                                                      1020
gcgaacgact ggctgtagtc gtccatggct ccacgcaagt cgttcgattg gtagcggaga
                                                                      1080
caccgcggtt gatatagttg gacagttcgc tcggctccaa ttctattctt tgtccagggc
                                                                      1140
tgccatagcc tctgcgttgc gcttgctctt gaggtgagca tggccatctg cgaataggca
                                                                      1200
ggagcaaaga gagagtccat ccgaatacct cgttcagttc gcgaatggct gcgacggtat
                                                                      1260
cctgctcgcc cagcctatcg cgctgagagc tatatgtgct tgcttgcttt tggggtagaa
                                                                      1320
tttagcagtt cggctacccc ttcccgtgct tcggcatagc gtttgctgtc gggagcactc
                                                                      1380
cggtcagatt caccagcatg ccctcatcgt tcggcatcag cccaatccgc gacggtagtc
                                                                      1440
ctgaatggct gaatcgattt tgcccagatt tgccgtgcca cgccccgaag aagatatgct
                                                                      1500
ttggggatga gcgcattgcc tgcaggcagg ccgaagcatc ggcttccgcc cctgtatagt
                                                                      1560
cttccagatg attttggcta ttccccgata gaaataaggt tccgccatcc acgggcgagg
                                                                      1620
cctaccactt ggttgaagta cccgatgctc accacgtagt cgttgagtag agagcattgc
                                                                      1680
gcccgatcgt gatcacccga tcgacgtcta tctgccccga gctgtggcca cggagagcag
                                                                      1740
gagcaggagg aagaataagg agcgttgaat gtcataatca gagccgggga gaaatggatt
                                                                      1800
tgactacggc ttacgttttt tgccggtcgg agctgtcact acgcggtacg aagtccgtac
                                                                      1860
ttgcctttga tgatatggnt accgag
                                                                      1886
```

(2) INFORMATION FOR SEQ ID NO:1230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1273
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230

```
ggcgaacgcc tcgatgcaag tgacaagaaa gtttacgaag aaaaggtagc gatgctcgcg
                                                                        60
aagtatcgat caaggatgcc aaaaagggac ggcgactcag aaagagaccc gctcgagtga
                                                                       120
ggatacetee agecetgtea cetettactg etgeetgeag gagtageeet tgtggtgata
                                                                       180
                                                                       240
atcctgatac tcttcccatt gccaagcgca gaaaagggaa agaatgagag aagtcctgct
gactaagcct tattggctac gctcaagtat ctgttcgagg agggagtaca taatccctcc
                                                                       300
tegteegttg ettgeatgeg geggtetaeg eggettteat egeetegtae aeggaetgae
                                                                       360
gcagcacgtc agccggatgg aagtcgagac cccctgtact cgcccgaagc cctgcgcaat
                                                                       420
gtctctctgg ccgtcatggt gatctgctgt acgtcgtata tatatgtacg caccggccct
                                                                       480
ceteetteeg tigtacegea cetgggtgeg ceatetgeee eegeteetgt tetteeceae
                                                                       540
ctcttctatc tgcgtctgag tctgttctac gtcctgccgg gttattcatc gttggagttt
                                                                       600
ccatcgtgat ggccctcata gtggcagccc tgagtatacg gctccctatc tgtggagagc
                                                                       660
acteggacte aagegagaag cettgeagaa ceaettgtte taettteget etgeaeettt
                                                                       720
gtottogtoa ttgoacogga gtattgoaco cogactoogo ggtgogaaca googgoatoa
                                                                       780
ctacgactgg tggcaggcgc tctatctctt cctgatcgtc ttggcaggtg cctgatcggc
                                                                       840
tattttgccc ctcgcttgtg ggctataatc agaagaaaaa acactgaaaa aaataatcat
                                                                       900
cgaatcggac cggatcctca tcccacgccg accactcact aacaatactt tcccaatgaa
                                                                       960
cttcttgtcc aacgtcatgt ttgggtctcc aacggcctgt tggtaccggt agtcgccgga
                                                                       1020
                                                                       1080
ctcatctatt cttcatcaaa tcccttctcc tcctcggcac cctcttcggc acgtggcaag
ctaccgccgc cggcaggaga ccttcgcctg catcatcgaa aacaaagcgg cctcgacacc
                                                                       1140
gaagccctca gagccgaagc ggccaaacgc ccccacctcc gttcgaaaat gtgctggccg
                                                                       1200
aagteetega tgeagattee geeegegeaa tetgeteate ggteggtaeg aacteteteg
                                                                       1260
                                                                       1273
tgaacagcgt ctg
```

- (2) INFORMATION FOR SEQ ID NO:1231
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...540
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231

ggctgccttg	tcgccattca	tatctccggc	aacaattacg	atatctgctt	tttcggtttg	60
		tgctcaggtc				120
agattgtttg	gtttatagga	aatgcccttt	gttgcttttc	acatggggca	ccatcgacac	180
ttatataccg	ctgcatgaaa	gataaaagag	tcctcgattc	cgcagtcgcg	tatcaaggtg	240
atgactataa	cgtcaaggga	ttcgattttc	gtgctcacaa	ttcagagaat	cccatcctat	300
tctcaaatat	atcaaaggaa	gtggagccga	tatcgtatgc	ttgaagaggc	agtactgagt	360
cggaaaagca	actctcgtta	tgtggggcta	cgactttcaa	gaaatatctt	cccgaatatc	420
gctacatgga	actggtcgca	tctcgagaag	atagaaaagg	cagcggcctt	atgctcctgt	480
ccaaatatnc	atctcggatg	tgcaccgcat	tccataccga	gtccgcattc	atggcttcaa	
540						

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 704 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...704
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232

atccccttac g	gtggaccata	cttgccacct	ttttggctgt	attgtcatac	tcttttataa	60
gagatacaag g	gagaaccaag	ctcgccgtcc	tgtggtgaac	ctgaggcccc	ggctattccg	120
gcttatgacc g	gagctattgc	agccttgaat	cattacgtgc	aaaaaaactg	gtggaagccg	180
gtttgtataa g	ggaatattta	cggaattgac	cgatttgctt	cggagctata	ttgccgaaac	240
tcgcgaatag a	atgccaggga	gatgaccagc	agcgagatat	tacaagctct	tcagggatcg	300
aacttcctga a	aaaaggaagt	cgcctgctgc	atggaatatt	gcaacggccg	acctggccaa	360
gtttgccaag 1	tataaaccga	tacatggaga	ggtgtggaag	ctattcgaga	tgctcgcgcc	420
tttctcgatg a	aggtgcataa	ttccgggagt	catgacattt	gcatatcctg	aattgctttg	480
gctgctgatc 1	tgctgccttt	gatagcgact	tggtatatcc	tgcaagcacg	taagacttcg	540
caacgatgac d	catatcttca	ttgaagccct	ttgaaggaag	tcgccgagtt	tgagggtcta	600
tctgcgccat 1	tcgttgccga	tattgagagc	tctttcgtcg	gttttctcat	tattgctttg	660
gctcgtccgc a	agaataccaa	tagctgcaga	aagattcgat	cgag		704

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1106 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1106
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233

attttggggc	tgaacgacat	gtcgctttca	ctcactttta	tagggcctgc	cactgaaatt	60
cgggatcatt	gtcgacaaag	ttcgacaaga	aaccgatacg	ctttttcccc	cttgtttatt	120
catttcgaat	accacaccca	ttagcggcag	gcattgtgac	ccatggattc	agaggtgcta	180
cccaatgaga	gatccacttg	tcaattttct	tctctccatc	ttgactgaag	agtaagtttt	240
tattgaattt	tgccctccat	tcagagagaa	cacatagtcc	acaaaactta	tttttgcgta	300
ttetteaagc	cggtgtaagc	gaaagccaaa	gcaaaagggt	tgcaccattg	ttaagagaag	360
aaggcgaacg	atagttggag	gctatatcca	cacgtacaac	tgcacattgg	agaagtcttc	420
cttatacacg	agtttcgcat	ttgcgcgttg	gcatcgcgac	tgaagaccgc	aactctactc	480
ttatateete	gggcttattc	atgageteta	ccgaccaaat	cttgatgtcg	gattcattct	540
accogttacc	acgatatcga	agtcttgaaa	ctgataatca	tccgatggtc	ccaatccctc	600
aacttttggt	atgtggcacc	ttggtctttg	gagcggagat	cttcacattg	ctattgccgg	660
totcotatcc	actgtgggtc	attacaagat	ccatccgttg	tccgccacac	tcatcctcgt	720
ttgtaccagt	ttttctgatt	gtactggacc	accttgacat	catctcctcc	catcgtctgc	780
acttagcaga	aggacagagg	gttgcgacgg	cgaaagccgc	caccacgaat	ttggtaaaac	840
ttttgtcttc	atagtttttg	tcttttttt	gagactcaat	cgacaggagc	cctccagtct	900
cttgaattgt	tgattagcga	ttagtttgtt	acttgatttt	cacgagagca	cgatggctca	960
teattetete	ttcaccettt	cgttccttgt	ttttactttt	tactgattgt	attatcgttc	1020
acccatogca	agagtetcca	aaatcgaaat	cggcaattcg	cacaacgcgg	aatgcatgtc	1080
	tgccacaaag			0 00		1106

- (2) INFORMATION FOR SEQ ID NO:1234
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 989 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...989
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234

cetceccetc	atgctttgat	gggagagcgt	atcggtatgg	atgtactcat	accatatacg	60
acgtatgtaa	ggctctgatt	gacaattatg	cagaagccat	gatttcgaag	gcttcaagga	120
agatctgatg	cgtgcactcg	cgatagatct	cctatcacgc	aagaaatatt	cagaggtaag	180

aaagcagaag agct	gacgat atgcttttcg	atgaagctta	caagtctttc	caacgtaaga	240
tegattgatc gcag	aagtgg cccaccctgt	ggttcatcag	gtattcgaga	cccagccgcc	300
gtgtacgagc gcat	tctaat ccccattac	gatggtaaac	gtgctataac	ataggatgca	360
atttgcgtga agcg	gatgaa actcaaggga	aagcatcatc	aaagaatttg	agaaagctat	420
cgtactgcat acta	togatg atottggaaa	gaacatctgc	gtgagatgga	cgagcttcgt	480
aattccgttc gaat	gccagc tacgaaaaca	aagatccact	acttatctat	aaactcgaac	540
ttacgaactg ttcc	gcaaga tggtagaago	catgaaccgt	aagaccgtgc	gatcctaatg	600
cgtgctcgga tacc	ggtacc ggaggctcct	tcccaagaga	gctggaacac	aggcggcaaa	660
tagaaatccg acat	gcagcc gaacaagtad	ggacatgagt	aagtatcgga	cacaaaaaga	720
cgatatagaa gccc	acagaa agcacaaag	g gatgcggcaa	gcagacctca	gggtgcagct	780
gctcccagac accg	ataaga aacgagaata	agatcgggcg	aaacgatcct	tgtcttgcgg	840
tagtggcaaa aagt	tcaaac agtgccacg	g gcgtaacctg	taaaagattt	atgagagaat	900
caccgactat ggta	tagaat agtctgngat	ttcttttat	tttttctctc	tacccgcata	960
	atccta ctatgaccg				989

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 837 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...837
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235

gagatctttc gacggatcat ggcggtggcc caattattgc tgtcggtaag caaactctga agcccttcat	cgtcgaatcg tactttccat ggacagttct cggctacaag ggtaagcgaa tgctcgttct atatttccag	ggctatgtcc ctcgtctttt tggacaaata ggcgttgtcg acagggcgca cctgatcttc tctaaatatt	agtggcactg acggatatcc gggttggatc ttcaacgact tactgatggt atccatgctt atatcattca cttactgcgg	tttttggcgc ttcttccgat tccatcccga cataggttac gaggtgctcc ggtacgcagc tctcctttca	agatggctcg ccgattcgat agttttcttc ctgtgcattt gttcgtcttg tcggaaatac tctaagtgaa	60 120 180 240 300 360 420 480
atgggagttt aaacctccgg actcctttcc	gattgagctc tatatgggca tcgtcaaata	ttttgctgca ccgagcaaat ggcgagaata	gttcggcaat gagctgattc agaaattccc agaaacgatt tcttgctccc	ttagtgtctc caggtttcca gtcagccgtt	gggaaaggtc ttagagaagt tcttgctccc	540 600 660 720 780
			aggacgcgat			837

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2566 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2566
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236

```
60
ccaatagctg agcagcatca gctgaaagat gatgcgcagt gcccaagtga tcgagaagga
                                                                       120
gagcgataat agagcaatgc gaatatgcct gttcctacag tatttccacc cgattgagaa
gcagtgtgtc ggcgtcgggc atggtgggcg cataataagg aggatgatcc ccgtgatgat
                                                                       180
gacgtaaagc aaagccacac ctctgtgagg atcagtagcc gattggcata ggcttgccct
                                                                       240
acggtgcaga gatcgtcact gctttcctcc gctgtttctg ctgtcgtttc atgaggttga
                                                                       300
gactggtggc gtatatagag gtcttcgatg ataccatctg ccatcctacg ataggagcaa
                                                                       360
tgatggtttt ggctccggta atgtccgcca cccaaggaaa atctctgctg ccgggatgat
                                                                       420
                                                                       480
tacatccgcg cggtcgggtt taggtggaag cgtaccattc gttcttcggt tgaaatgggc
                                                                       540
ttgagcaggt gtatgtcttg tgcagtgctt ctaccggcat gatgctatag cgagaagacc
                                                                       600
cctgtccgat ccgctcagac ggacaaggcg attgatattg cctcccgtcc gataatcgtg
                                                                       660
atgtcggtat attctttgt aatggccatg agttccggcg gaatgcttct cgaacatagg
                                                                       720
ggcgaacctt ttcgctgagc agacgtccgt accgatgtcg aacgactgcg aatgcttgat
                                                                       780
atgggtatcg gagaaagtgt aagctcggta ctacctccac cgacgtccag atagatgtaa
                                                                       840
ttgctccgtc ggaaataatc tgttcgatat gattgtccga aacgaggcgt gcccctcatc
                                                                       900
tccatcaatg atgtctatat ggatacctgt tttctctcgg attgtgcgat cacggcttcg
                                                                       960
gcattcgatg catctctcat ggcggaggtg gacaggcgcg atagtccttt acccgatata
totgoatoat otoatagtat coogcatgag cogtacoatg ttgtotgtot tttcctotco
                                                                      1020
                                                                      1080
tatgtatcct tggtaaaaga gtcttcgccc agacgaatgg gaactcgcat gatcagcact
                                                                      1140
tgctgagagg ctcctccatt ccttcgctat tgacacattt gatcagtggc gcacagcatt
cgagccgacg tctatggcgg cataatgtac cttttcattc tttaacgctt agtcaggcaa
                                                                      1200
                                                                      1260
agatagtogt tagoattoat toccaatoca tocotoogca tggtataaag toaaacgaaa
agggctgcgc gaacggagtc tctcctcctc gcacagcccc gtttcatatt tcgctaaagg
                                                                      1320
ggtagcgacg cggtttgatg tcgagcttga ccggcttgat catattctcc gggagagtat
                                                                      1380
cgtatccaga tcctctttcg acaggatgtc gtgttccaaa agaggtcgta aacgccacgt
                                                                      1440
                                                                      1500
cccgtttcca tcgcttcctt ggcgatcttg tcgaattctt atagccgatg atcggattca
gagccgtaac gataccgatc tgttgcggat atacccacgg cattcgtcct cgttggccgt
                                                                      1560
gatgccatga tacagagtgt acgcagcgta tcgaatccgt tcatgagcag atccgaattt
                                                                      1620
cgaagcagca ttgtgccatc acaggctcca tagcgttcag ctccattggg ctgcatcgcc
                                                                      1680
tgccatcgtt acggtcaggt cgttgcccat cacctatagc agatctgatt cattacttcc
                                                                      1740
ggaatcacag gattcacctt accegcatga tggacgaace eggetgeatg geaggeagat
                                                                      1800
                                                                      1860
tgaattcgtg caaccgcaac gaggaccgct ggcaaggaga cgcaggtcgt tgcaaatctt
                                                                      1920
gtcaccttca cacagatacg gcgcaaggca gacgaatatc ctaccatcac gaagtgtcgc
togttgocco taccagatog goactgagao gaatgtocca coggtgactt cacgaagago
                                                                      1980
ctctatgcag tattcggcat agttcggctg gcgcagatac ccgtgccgat agccgtagca
                                                                       2040
cccatattca cggtcaggac tcttcggcgg caaagtccag atttttgatt tcatcctgca
                                                                       2100
                                                                       2160
agatggagca aatccgccga acgtctgtcc cagagacata ggcacagcat cttcgactga
gtacgtccca tcttgagtac atgggcaaat tcgcggctct tggcagcagc gactcgatga
                                                                       2220
                                                                       2280
gatccagaag atgggggggg aacttcagat atgtgcgtaa aggccgaggt ggatagctgt
                                                                       2340
cggataagca tcgttggtgc tctcgagcag ttcacgtgat cattggggga gaggtgggca
                                                                       2400
aattcgcctg cccgtgtccc atgatctgca aggcacggtt gcaaatcacc tcgttggcgt
                                                                       2460
tatattcgtg gtcgttcctg caccgccttg gatcatatcc acggggaaat ctcgtggtgc
                                                                       2520
ttgccttcga ggatttcctt gcaggctttc acgatgccgc tttctgggca tcggtcaaga
                                                                       2566
gaccgagccg atgattggcc actgcagcgc ccatttcgtc atggcc
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 903 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...903
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237

cttcgatgat gcttggagtc ctctcagatc actgcgtaga tggtagcgtc tctttgcatc 60 cctgctgcgg gctatcaata tcgaacctat cctcgttcga tgcccggcca tatgttcgtc 120 ggttattaca cggatatatc caaaaaaaaa aaacattcct ggagacaacg atgatcggtg 180 atgtcgattt ggacgatttt tccctgatga gcagttggat tcgacgatga taggcaaatc 240 ccaaatcaga tgtccaagct gactttcgag aagtcgaaag aatatgccaa caagaatatc 300 aggaaaacga agctgacatt cactccggca agtcgggcta tatttcttgg aaatatccaa 360 agacgtgcga aggcgaatcc aatccatcgg cagtagcatc gcttttgccg catcgtcctt 420 ttgaaataag aatacgccgg atgctatgtg gcttacggct atgcaggctc tcagtacacc 480 tttctgacat aaaaagtgtg ccgaaaacgc tgctgaagcg attttcgaca caccctcatc 540 cttatgctta tatgaaaagc cgcactgcgg atagcgtaaa ctccgaaaac aagatttgag 600 gattccacca cctttgtaat ccgctgtgca aagcaaccga aaggtgcggc ccgccatcag 660 cgatgaaatt gtcctcggaa tagttgtatg atgagtttcc ccgatctaac agtgcggctt 720 attcctcgtc ttctcgtatt gcaaagttag caacattgtt tagatttgca attctttgtt 780 tcatgatttt gggtatggtt acactttcgg atcctaatcg gcgttctcga cgttcaaacg 840 tattacgata gttcggttgc ttaggtaatc tgctttgacg atggggaagt tttctccggt 900 ttg 903

- (2) INFORMATION FOR SEQ ID NO:1238
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1107
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238

```
atgctatcat gaaagcattg tcgatacgca atttccaagt gcgcgactaa tgacagggct
                                                                        60
gaagatgtat tcgacgagga aggttttnga cattataccg agatccggat gacggatgcc
                                                                       120
cgcagtaagg gggtggatac gaccggccat ttgccggcag tgggggatttg cttcgggagc
                                                                       180
tactccattt tatattcatt gatccgtttc tcccgtagta atccaataac atcaacccaa
                                                                       240
taaaaaaggat agtttttctc gaactaaaag tcgcaaaaac aacgaatagc aattgctgta
                                                                       300
cgaatgtaaa ctttgactaa ctttgcaaaa gcattttttc aaacataatc aacaagaaaa
                                                                       360
ttagaaatga aaactcctgc agaactgaag tatctaagga tcatgagtgg gctcgccaag
                                                                       420
aaggcgacgt tgtcttcatc gtatcacgga ctatgctcaa ggcgaattgg gcgaaattgt
                                                                       480
ctatgtggac ttactaccga aggcgaaacg ctcgaggctg atgaggtttt cggatcgatg
                                                                       540
aagctgtgaa gactgtttcc gacctgatga tgcctatcgc cggcgaggat tggaagtgaa
                                                                       600
ccctgatctg gaagagcaac ccgaactcgt aaacagcatc cctacggtgc cggttggatt
                                                                       660
atcaaggtta aggctgcaaa tgctgcgact tcgacaacct cctgagtgct gccgaatacg
                                                                       720
aaaaactgat agctcataaa tgcagccttt ggtaagcatc atcatgggta gtacttccga
                                                                       780
tetgecatta tggagaaage egecaaaatg etegatgaaa tgeagattee attgagatgt
                                                                       840
tggcgctttc ggctcaatcg actccggctg aagtagagac tttgcacacg aggccagagc
                                                                       900
tegeggtate aaggtaatta tegetgetge egtatggeag etteatttgt gtggegtaat
                                                                       960
tgcttccatg acgtctattc ggtaataggt gtacccatca atgccactct tgacggaatg
                                                                       1020
gatgctctgt agccatcgtt caaatgcctt ccgggatccc cgttgctact gtggggataa
                                                                       1080
                                                                       1107
tgctgccaga atgcagcact tttggcc
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2740 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2740
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239

```
cgaaaaggta gagataaaga ggccgtgagc ttccttgggt aagacttatt ttcagcacac
                                                                        60
ccaaagcggt agtttctgag aaaagtaccg gagtatctaa gagggttttt tgtcgattgg
                                                                       120
ggggaggaga tgtttgcctg tttggcatct cttccccttc tccacaatgc acttatgccg
                                                                       180
gacagatact toggttatto aatttaggca tttcactacg accatocott aggaatgggc
                                                                       240
                                                                       300
gagcgctgaa gggtaagaaa tggtatgaga gatgctgcct actcgaagcg gcgcctatat
ctgcctcttc gatgatactg acgatgagct tgccgtccgg cgttaggtgg agtcgttcga
                                                                       360
agcaaaagct cggccaagag atcgctggcc tctctgctgt cggtgtcttg ccacaaggga
                                                                       420
tggcttgata ctcggctatt tggtggcaat cagttcgagc atttgttcat gcgatgatct
                                                                       480
gccatcttcg gtgtagtatg gatgacatcc cgcacgacat ctgccgcaca gtctatgatt
                                                                       540
                                                                       600
gtacaggtgc tgccagcagc gaataggaag agacaccgag gggcgacaat cgaacccgac
agattggagt tcgtccacag ctgccttcac ggcagaacat ccgacggatt gaattcgagg
                                                                       660
agttcgggga agagaagttg ttgctgtcga tatgacgtct tgattcgtcg gccatgaaac
                                                                       720
gatcgtaaag aatacettgt gtgcgcggtg gaaatcgace aaagccaaac cectactcag
                                                                       780
                                                                       840
agtatcacca gataacggcc gcgatggaca tagcagagca tatcggtgga ggggtcgcag
atacggcaga gggagtaaaa tcggtcgagg cgaacagctc ttcgagcgga tcggtggttc
                                                                       900
                                                                       960
tgccatcttc tcggcatctc gcttggcttc gactgcttga agagttcgtt ccagcccata
teeggegatt gaegeegga etgeggatag geteegteag teeggtttet ttgaagggat
                                                                      1020
```

```
tatacgatga tccagatcta cgggcggacg aactacgttt ttccccgggc cttgatagca
                                                                      1080
gggatgtcga tcagttcttt gcggtcgaag tcaatggccg gtactgcttg ctggagctga
                                                                     1140
gtgcttcacg aatgaccaca ccgatgagtt tgaaaaagcc tgttcgtcgg agaacttgat
                                                                      1200
ttcagttttg gtcgggtgga tattgcatcg atctgggagg gttcaagatc gaaatacagg
                                                                      1260
aagtaattgg gcatgttccc tgaggaatga tcgcctcata ggcagccatc acggctttgt
                                                                      1320
ggagtaagga tgacgcatga agcgtccgtt cacgaagaag tattgcaggg cactcgtttg
                                                                      1380
cgagcaccat cggggcgccc tacgaagccg gatatattgg tatggggctt ttcatcccga
                                                                      1440
tgggtatcag atctttctcc attctcttcc gaatacatcg aggattcttt tcttcagagg
                                                                      1500
agaaggagge agateetgee cageteacee gaatggtaga tagaaaaage gaettgegga
                                                                      1560
ttgaccaage caccegtteg tatteggtea ggatgtgeeg aaatteegtt teattegttt
                                                                      1620
gaggaatttt cgacgtgccg gtacattgta gaagaggttc ttcacaaaag aatacagccc
                                                                      1680
                                                                      1740
agtggagagg tgacagtagc cacttcgcct acttcgagcc attgatggta aggcgcgtac
ccaattcatc ttcagccctt cgggtaggag ttccacttgt gcaacggctg caatcgaagc
                                                                      1800
                                                                      1860
cagggettea cetgaaaace categteega aggetgaaca gateetgaaa agaagetate
                                                                      1920
ttgaagtggc atgtcgctcg aaagccattc gggcatcgct ttggctcatg ccttgccgtt
                                                                      1980
gtotgtgacg ogtatoaatt ogogacoggo otocotgaca coagootgat aatggaagog
                                                                      2040
coggoatoca atgogtttto caatagotot tgacgacoga ggooggacgt tggattactt
                                                                      2100
caccggcage aatttgatgg cgatactgtc cggcaggagg cgtatgacgt cgctcataag
                                                                      2160
atgacctaaa aaccaaccac gatagcaaac aaacggctat gagcaaagcc aacgtaggag
tgttcgtccc gagcgagtgg attgtgtctc gccttgcagc tgtcgtcctt cagatgctgg
                                                                      2220
gtaccttcca caaatgttcc gcgtatacga gggcatagcc ggagtagtcg tgtgatgaag
                                                                      2280
actgtccgtc cagctctgct tgccctcctg ttctacttcg cgtctaatgc gttcgatacg
                                                                      2340
tttctccaac tctcgcgtcg ctgatcgtaa tagataggtt tgtggtcaaa agaccggggc
                                                                      2400
tacgctgttt atagaatgat cctaatccca tagtttttct ctattaaaga gaatggagtg
                                                                      2460
                                                                      2520
aagaaaagat cgaagaagcc ttcctctttg gtgtccgtat aggtcgggca atataaggag
agagccggtc tgtaggatcg gtagcctctt gccggctgca ggtgtcggag gaatggagtc
                                                                      2580
ggtctgtagg gcagcgatgt caatgagtct tttctctcct cttcggccag agcccgtgta
                                                                      2640
                                                                      2700
tgcacgaggg ctgccaaagc accgctnaag cgtcgcaaat cggacagcga tccgagcacc
tgcaaagacg gaatcccggc tggcctgcgg aaaagatcct
                                                                      2740
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 881 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...881
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240

```
60
tccaggacgg atacgccgca tagctcccaa ccatgcctct gtgctgatcc ggccgaagag
                                                                       120
cggtacgggc aaagagttga tagccgaagc tctgcacctg ggagcaaacg agcctcagcc
ccattcgtca aggtcaattt gggtgggttc ccgaaagttt gttcgaaagt gagctgttcg
                                                                       180
gacataagaa aggagettta ccaatgettt tteegacagg aaaggaeggt tegagetgge
                                                                       240
                                                                       300
tgatgcggca cgatctttct ggacgaaata ggcgaactac cggtcggcaa ccaataaaac
tgctgcgagt gctacaggaa cagacattcg agccgttggg cgaagcgtct cccaccgagt
                                                                       360
ggacatccgt gtggtatcgg ctacgaatgc ttcttggagc gaatggtagc cgaaggacgt
                                                                       420
ttcagagagg acctctacta tgaatcaacc tgatacatct gcatctgcct ccgctgcgtg
                                                                       480
```

		++	ageetteagt	gaagcctttg	cccaatcgac	540
agcgtcagga	gatatacagc	tgctggtgga	agccccago	statetetee	cccaatcgac	600
++	ataccattta	agataraagaa	PCTATECKAL	gtattegtte	aceccca	660
accentat.	acacaaacta	aaaaacgtag	regarchack	Clatte	~666~~~6~6	
CEEECAACE	acceptants.	taactacttc	ggttcgcagg	tgacggcagc	agaccactcc	720
agaaatcagt	gcccgggacg	LEGULECULU	epece et at CCC	agagacocto	actaaataca	780
gacgaacggg	ctttgccgac	atggaggaag	CERCLACCE	agagacgotg	actaaataca	840
acogaacett	agtcgtgctg	cacgagcctt	gggattgagc	cggcaagctc	tttccggcga	
-+-cccca33+	acggactgtg	atagteteta	aaacagaatc	g		881
atggagaaat	acegucees		Ü	_		

- (2) INFORMATION FOR SEQ ID NO:1241
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...447
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241

	cctactatcc	gtgctcggta	atetctetea	taaactcacc	gtatcggcat	60
agcagcacca	CCCgccgccc	5 c S c c c c c c c c c c c c c c c c c	tastacaacc	totocettce	ctccggtact	120
cgtaaacagc	cgtcccgcag	gggacticta	Lgalacgace		ctccggtact	180
tracttaart	cogcogotot	gtccgttgta	gccatgatat	gacggicala	gcgcagacgc	
ancantator	aataatccga	ttgccacgga	gaaagacatg	tccgccacgg	cctccgtcgc	240
agcagegee	acceptted	ggatatactt	ctccctgcgg	aagtgcgtag	agccctccct	300
ctccgccggg	CCaccicigg	ggacacaccc	++	aatagactct	getgecatae	360
cccttgcccg	aacggcagta	tatettgacg	Laattgatga	aacggaccoc	gctgccatac	420
gatggattta	gttagagact	ttgcggaact	tgccacaatg	ggagcgatac	gcaaagcgat	
otottotato	gtccccgtac	caccacg				447
	5000000000					

- (2) INFORMATION FOR SEQ ID NO:1242
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 596 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242

aggatcccca	gcctcaagcc	caagaaagga	cgcttcctga	gcaaagaaag	cgagccgaag	60
agtgggagag	cggtaaggag	cggttccgag	accttgagct	tggtcgcaca	gtgctgctcg	120
tcggatagag	gatgcttttg	tcggaatgag	tatgcaagtt	gggaaaataa	gaagaaaatc	180
gagcagctgt	tgcaggtctc	tccctttggg	aaacctttga	gagcaagctg	aaagtcaagg	240
cagacagata	aatattgcca	aactgaaaaa	ggaaatnctc	gaagccaaag	aacaccctat	300
cacgacttca	agtcgtggca	gaagttcgag	cgcgaactgc	gcctgtcaag	aatcaggata	360
ttatcacttg	gatgatgtgc	agggatctca	tgaagagaac	aaggtggagg	gattggatac	420
cggtactctc	tacctgaaag	aattcggacc	gacgtccaag	agcaggggag	cctcaatgtg	480
ctgaaccacg	gaaagccgat	gcgctttgcc	cgtggtcgtg	tacagaagcc	gacaggccga	540
ggccatgtac	acaaggagga	ggcttcctct	ggcgacggtc	tatatcgaga	aaggga	596

(2) INFORMATION FOR SEQ ID NO:1243

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 710 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...710
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243

tgatcctcag	atgatcagag	tttgtttccg	tatggcttga	aaatgaaaac	aaaaccaggg	60
aaaattattt	tattccatca	gcgaagtggc	gcggatgtcg	atctgccgga	ttccactctg	120
cgtttttggg	agaaggagtt	tccggcataa	agccacgtac	ttccgaaggc	ggcacacgtc	180
gctatacagc	caaggaatcg	aaatggtgcg	gctcatccac	caccttacca	aggaaaaagg	240
actcaacttg	caggcacgaa	gcaagctctc	aagaacgact	atgatggtac	tacggcaggg	300
aagaagtcat	cagtcgtctg	aaagaaatcc	gtcaggaact	atggatatcc	gtgatgccat	360
cgaccaatgg	gagcggaaaa	atatgtactg	aagaaaaacg	atgctgcgat	ggatcccgaa	420
ttcgatcttc	ttctgaaagc	cggaaaagca	gcggactctc	tgtcggtatg	aaagacgatg	480
agctcttagc	ctgcttgaga	gttgttcata	cagagtggaa	cggctgaaag	ccgaagagca	540
tatgctatcg	gtggagacaa	gctccaagac	ctgcgaatcg	tgggtgtagt	gagattcgtg	600
ctgagatggt	ggggccttcc	ggcaagcaga	ttctgatgat	actttggcgg	tcggacgcat	660
cttggctccg	gcccttcttt	tgcttcgaga	atattttacc	cgttaccctg		710

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 712 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...712
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244

accattctac	оосаарраар	cgtaagtatg	tcaccagccg	gcatattcag	accgtctgat	60
gccgcccac	gacaagaatc	tggctctttc	gtgtggagcc	accgataacg	ccgacagctg	120
gcgagaaccg	gacaagaaca	tactgcactt	tccgttctta	tcgagaccat	gcgccgcgag	180
getegratee	4+caanggg	cagccccaag	teatcatcaa	agagatagac	ggcgagcggt	240
gggtacgaac	anacttettt	cgatcaatct	gccggaagag	tcctccagtc	gtatatagac	300
gcgaacgata	gagettettt	agagatogto	atgatggaaa	acagaacgac	cgggtgttta	360
atagtgaccc	tatecettes	caagacaatca	togactcaac	aatgccgtac	tgacagcatc	420
tggagttcca	sacataatea	ccaccacttc	ttggaattcc	aaccetegaa	agggagata	480
ggcaggagag	geegeaateg	atcattacac	toggaaacoo	aacggcctat	gcctatgcct	540
gagcggcgca	caacgggccg	accattgege	tcatctctta	cecageagag	gtctatgccg	600
gaataatctc	caaaagccgc	ggacgccccc	aggggactt	ctgcgttcaa	cgtctgcaag	660
gtcaggtcgt	aaggcgagca	cacgaaagga	atancogato	ataagtgtca	cgtctgcaag ct	712
agcaaaaagc	ttaccaatat	gcgtgcttcg	grageegacg			

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 595 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...595
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245

cotatogago	atttoragaa	teccattgae	aagtatgcat	cgcagcttaa	tctgccgatg	60
CCLattgage	accegcagaa	200020200	atgacaatga	atatatacca	gatacaacga	120
ggaaggtgtt	eggetettat	gcccacagcg	gcgacaac66	atatecactt	ccotaaocat	180
gatttcaccc	gatctgatca	aggetetate	gctacggagg	atgtccgctt	ctcaatcaaa	240
tcgggaatag	acagcaaggt	ctgttccgag	ccgtggtcaa	acgcggtatc	- tteesesses	300
aaagcgtgga	gggggtagta	ccattaccca	gcaactggcc	aaactccttt	attecegege	
acggagacca	aactcggacg	cctcttccaa	aaaccgatcg	agtggttatc	gccgtgaagc	360
togagogitt	ttatacgaag	gaagagatca	tcccatgtat	ctcaactact	tegaetteet	420
ctacaatocc	ottoppatca	atctgcggct	ttatacctac	ttcggtaaag	cagccggctg	480
gtataatget	Per999222	crattctaat	cegtatetec	aagaatccgg	cctattatat	540
accigaagac	gaggagge ag	cogracatta	-00	cgcaatatgt	tctgg	595
cccggtttgc	atgggggaga	Lagaalgilg	CCEREERCEC	292222292	00	

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- (2) INFORMATION FOR SEQ ID NO:1246
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 622 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...622
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246

cggagcatcg	tggttagtcg	tgttgttggc	gtatgccagg	gcaggtgggc	tgtagtactt	60
			ttgatcttta			120
cgatgataag	gagaggcagg	agggtgatat	aaaaccgtat	ccgatccatg	taaaaccacc	180
			ccggccccca			240
atggtatgcc	gatttctctc	aacatcaaat	tggcactggg	agtcgtataa	gtcacagctt	300
ataccgataa	ccgaaccgac	tcaatagaat	agccaccacc	aatggccacc	agcaagtccc	360
agcttgacgg	gctgaggaat	accgggcaaa	acatcggaag	cgaacccaaa	aggataccga	420
gaccgatgcc	gatgaatatg	gcattaggtt	cggttcgttc	agtcgtttga	caagaattac	480
cgatcagttc	tccactttgg	gcattactaa	ctcactgccc	actacagtca	gacgatcgcc	540
acctgtagcg	gaaggaagcc	aatgctacca	tctcaacttc	ggcacggtca	cacgtgtcac	600
attcatgcca	tgcattttgc	gt				622

- (2) INFORMATION FOR SEQ ID NO:1247
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 542 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...542
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247

ggaaaattct tccgattctc	gaccctgaaa	atagatttt	tggaaagctt	tgaataatat	60
gtctcaacct atcaatgact	tataaagggt	cggttgggat	acccttagtt	agaagggtgg	120
agacaactcc catttttgag					180
-6	_	0 0	00		

		+++20+22+	totttagtaa	tetteegaat	accettagtt	240
ggtggagaca	actacacacc	LLagiaace		attataatta	ggaaaccctt	300
agaaggtgga	gacaacgttg	tcccaagcct	gaacggtage	griginging	ggaaaccctt	360
anttanaann	otogagacaa	caaacgcatc	gttataagtt	ttttgattgc	gttgggaata	
	6-86-6-t-G	gacaacotto	tocaagootg	aacggtagcg	ttgtcgttgg	420
cccttagtta	gaagggugga	gacaacgeeg	annogentes	+++++	ctgtgattgc	480
gaataccctt	agttagaagg	gggagacaac	aaacgcaccg	ctataagttg	ctgtgattgc	540
ottoogaata	ccttagttag	aagggtggag	acaacacctt	tgcttgcaca	tcctcaggac	
						542
ag						

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 565 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...565
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248

cactetteta	taaaatorot	gatgtccatt	cctttcagat	tctgttcttc	ccgatacgga	60
CgCtCttcta	caaaacgege	techancast	gaccoatcoc	tecageagga	tatecetate	120
acaaacgctc	cacctegega	CCCagacgac	gaccgaccgc	tccagcagga	atccacatta	180
ggacatattg	cgcggatgct	gtccgacgag	gtaatttcgt	cgaagatgcc	accuacacing	
otcagattga	aattgcgcaa	atggacaagc	acttggcacg	ccagttgctg	eggegtatea	240
Pocabacoca	asantragar	rectetttee	ggtagtgctg	tagcgcaagt	gtccatgtag	300
LCggaggacg	aaagccagac	checocococo	TC222ttCGG	catocccaoc	tettetegag	360
cactctccgg	catacggtat	Cigagaggca	gcaaacccgg	catgcccagc	++00000330	420
aataagcctg	aaaatccttg	tgtaccgagt	cgatatctcc	gagatggcat	ttgccccaag	,
tectettet	ctgaagaggt	atcttctccg	ggacggctgt	tgagcttcac	cacagcgagc	480
coccocctt	ctgacctcga	ttatactact	totocatoag	gaggtatagc	ttgntcangc	540
				0 00 0		565
atacatccat	gtgccatact	tatcg				- '

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 872 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249

					*******	60
ggatctttca	accccatctg	tatagtcgta	cggcagactt	ttatcaggat	ttgccagaag	60
cctttccatg	ttggatgagg	tggttttatt	ggacattttc	cggcacgaga	actccctttg	120
ccapatataa	ccagtcgtct	gatattgatt	tgatcgagaa	tcccaataaa	acgctggtga	180
000000000	tetactaatt	atttacacoo	caacgagata	ccceatetce	tattgatact	240
gcaaaaacga	CCCgCCgucc		cotonono	natatotoca	aacttatect	300
cggagcggcg	atatcgatcg	gttagtgatt	cctgncaaac	aatattttta	aacctatget	
aaagaaggtt	ctttatatac	tggggttctt	tcttgtactg	gccatcttgt	tgcagccata	360
gttttctttt	cggactattc	cgatagcact	cgtgctcagg	tttggaagtt	cgagtcgagg	420
ot and access	acatocatto	адсалаладас	cgatgtggag	cgagacttga	agcgtctggg	480
graagargaa	acacgcaccc	ugcuuuugus				540
tttcaccccc	atggcaagct	gctcgactct	atcgatcttc	acagaacgga	aagaaacccc	
gtgctaattc	ccttttccgc	ggagcggaat	tgtatgcctc	tccatccgcc	aactgtatct	600
garagtogaa	caaaaagatc	cectctttat	ggtagtagat	ccgatacctc	tttctatgtt	660
Buca6c66aa		aattaaaaat	tacaatatac	tacccccata	ctastaacct	720
tctaccgaca	ggagcgtgat	Cgitteaact	tgcagtatgc	tgccccgta	CEGAEGGEE	
caggggatat	atctcgtcct	tagctaccgg	ccctctcttc	gacctcattg	catttatcaa	780
gcgagatcca	ttctggncaa	actttttcgc	tcaaggttat	gtgcccggat	aatgncagaa	840
					_	872
catattaagt	tccccgtctg	Recitadacie	5 ^u			

(2) INFORMATION FOR SEQ ID NO:1250

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...544
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250

agatcatacc	ggatataaat	gccgttggat	gtggcctaaa	gttcgctatg	cttcggttta	60
			actaaagggg			120
			gctcaatgac			180
			gagggtatga			240
			ggtttaaaaa			300
			aagaaaatga			360
			ccttgctcag			420
			tgccgtcaaa			480
			atgatttttg			540
cccc						544

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1553 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1553
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251

				agaagetta	cacaccatca	60
ggtgccaacc	tcccacagag	attgaagacg	gcactatcat	aggaggeeeg	ccacaaattt	120
actattoacc	atopoogaca	aagtagtgga	ggctgtcaca	g c g g a g c g a c	ccecaae	180
ataataataa	ocoottotea	Cggccggaga	gtgggcgcaa	LLALLACACE	gageeege	240
aggetettee	cttccgtacg	gttatcctta	catcgggatg	cgccaagicc	Cgatacaaca	
aattgagett	pocpacatte	ggggcatccc	tcgcgttctc	gatgeeggae	agigaatgat	300
agttattcgc	teeceetaat	tgccctgaag	ctgaaagaag	taagggattg	gatgatatta	360
agecactage	gategtetae	aacattgcat	ggacgaacag	aaagctgtca	tcgtcctgct	420
acadactact	agecteggtg	taagaacatc	catgtaggcc	ctaccctacc	tgcattccta	480
tananganta	agcccaggeg	ctgatcgaaa	acttcggtat	agcaggtatc	ggtacggtca	540
Caccgaacg	agegaaageg	togcataaga	ataagaagtg	gtgtgcaatg	aataccttaa	600
agaagatatt	cggacgccga	actocattoo	tttattctcc	atcttcttga	ggtatagaca	660
gctttctcgg	aaaagccgga	tannacttt	gtaagctttt	cacagagtac	ttagaaccat	720
caaaagtatt	aaatactctg	theasass	Scandececc	cttttgccag	aatagatcct	780
ttcgatgaat	agttaaacta	ttttgtggaa	agcttaagag	ataaccata	topoccoact	840
aatcttcttc	gaaaagtggc	taatcaaacg	tgagttcgat	gcaagcgaca	agtttgacgt	900
ctctcttgtt	gggatattga	ctataatcga	atcagaaaat	gaagggaaaa	agetegacge	960
ctcatcggat	gtcgaagcct	ctcgaagctg	aatttctcaa	ccgagaaatg	aaatacgctg	1020
202220200	tattgcatat	ttcttcagat	cgaatccgca	ttgttttata	gccaccega	1080
acatacocca	aagggggtcg	agctacgccc	tacagcgact	cgggctacgc	Cglagagela	
ccgagetgeg	ctctacggct	cttcaagcta	cgctgtaggg	ctcaccggcc	gggccccacg	1140
gctcagctcg	gccacatcta	cggctcacgg	agcggactct	acggctcggc	Legelacgel	1200
atagagrata	cctcgccgag	ctctaagcgt	agctcgaaga	gccgtatggg	atageceget	1260
atoctotaca	gaatccgcca	tctgccttgt	ggtatagccc	atcttccggt	gcggactgca	1320
acceceace	asaccastcc	gaatttcaat	gttggtccga	tccgggcaga	agaggattgc	1380
acatoggica	attectes	Pagescasco	tataactccc	agatettagt	gtgtaacccg	1440
cccctataca	allgoolgaa	ttaacattto	tacgccgaac	teacettaat	caatgncgca	1500
ctaatcgggg	aacgaataca	LIEBURIT	. tatecteaa	ctttcgggat	ctc	1553
agggacatca	. gcaaaaaata	accccgaagg	ttttgctgaa		-	

- (2) INFORMATION FOR SEQ ID NO:1252
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1618 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1618
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252

```
gccgtcagtg atattgattt ttccatccct tcagggcaaa cctatgcgcg gtcggaactt
                                                                        60
ccggaggggg taagaccact atagcccgac tcatacctgc ttttgggacg ctacccaagg
                                                                        120
ccatatacgt atcggtggag tggatgtagg gatatggcaa aagaagagct gatggacagg
                                                                       180
atctctttcg tctttcgaat accaaacttt tcagaaccac cattcgtgag aatattacct
                                                                       240
atggcgtccg gatgcatccg aggatgcttt ggctcgtgcc atcgaccttt ctcaagccgt
                                                                       300
gaaattatag agcgtttgcc cgatggactg caaacgaaga tagagccgat ggcacgtatc
                                                                       360
tctccggagg ggagcagcag cgcatagctt tgctcgtgcc atactcaagg atgctcctat
                                                                       420
tgtggtgctc gatgaagcca cgcctttgct gatcccgaaa acgagaaatt gatacagcag
                                                                       480
gctttgcacg actgacgaaa ggaaagacgg tgctgatgat tgctcatcga ctgacgagct
                                                                       540
acagcatgtg gatcgtatcc ttgtgataga gaagggacga atcgcagaca gggtacccac
                                                                       600
gaagaactcc tgacacaagg tggtctttac aaatccagtg ggaggaatac cagcgatccg
                                                                       660
tttcttggac attatgaaag aagaaaacac acaattacct ctaatcgaaa cgaaacaaac
                                                                       720
ctatgatacg atattccaac accgattcgc tctctctcgt aagggtgcgc aggatcttgc
                                                                       780
caaagcattg catggactac ggttttgaat gtcggattta tgttgcctgc catttcactt
                                                                       840
ttcttttcct cgaagactat ctgcaaggat ccgccacaca tgtatttggt attatatagc
                                                                       900
catgggagcg gcttttatgg cggtgctctt cttatagctc tcttccaata cacaagcctg
                                                                       960
tacaccaaga tatatacaga agtgccaacc gncgcatcgc cttggctgaa aaactacgca
                                                                      1020
aactcccatg gctttcttcg gagagaagaa tctgtccgat ctgacttcca cgatgatgag
                                                                      1080
gatagtacgg tgatggagac tgtcttctct cacagtatac cccagctttt gcatcgttgg
                                                                      1140
tcagtctctt tttgatcggt atagggctct tctgcttaat tggcagcttt cgttggcact
                                                                      1200
cttttgggtt gtgcctgtag cagcctagca attgtctttt ccaaaaagat gttgaacaaa
                                                                      1260
tcattccact cgaataccat gtcaaacgag aggtcaccga gcatatacag gaaggaatcg
                                                                      1320
aaggatacag gagataaaat catataatgg cgaagaagaa tttgccgagc gctcgatgcc
                                                                      1380
aaactccatg cctatgagaa gagccttatt cgatgtgaac tgttgtcggt gccgtcctta
                                                                      1440
atgcttcaca tataatcctc aaactgggac tgcctctgta atcataatgg gagcttatct
                                                                      1500
cttgtcagaa ggaacaatta tctattcact tatttagtct ttctgcttat tcggatcgac
                                                                      1560
atatataacc catagtgaag tattcagcaa ttgctactct gcagtacctc gatgtacg
                                                                      1618
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION $1...5\overline{12}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253

atctcatcaa	tcaaaacata	gtatttcctg	cccatatctt	ttgtttgctc	atgatatagt	60
cgtataggag	attgggatta	cgatacttga	tatccgattt	ctatcaagag	ctacctccac	120
gaaatcttct	ttttgagctc	cttcctcatc	aatcgattct	taaagagagt	gaagagtagg	180

						240
+cactttc	ctgaactctt	aatcccgtaa	caatcttcac	cttaccattc	catcgctttg	
aatgatttt	Cigaucicic		+-++n+cn+a	astaggetet	cttotoattt	300
cgaatactgt	gcaatgtatt	catttctgtc	tattattata	aacaaggeee	cttgtgattt	360
	ttaatcatat	attacaacto	ttttgtcagt	gcaagatatt	tttttgcttc	300
ctctgaaatt	LLAGICELEL	accacaacca		++++cn+a+3	accasaastt	420
gaactaacaa	aaaaaataga	ggaacaaatc	tatacgatge	LLLLgalgia	gccgaggatt	. – -
Baaccaac		setttaagat	ggggaagaaa	cegaaaatta	ccgtctttca	480
ttgcgaatac	atttcaaaac	actingage	888844844	- 66	J	512
acategggaa	cggcgttatt	ttccggtaga	ag			712
aaaccgggaa	666665		~			

- (2) INFORMATION FOR SEQ ID NO:1254
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...478
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254

	ccattoccaa	ggtgaaaccg	atagccgtgg	atattgcatg	acgaagctct	60
gcgaaagcaa	atanteette	togataacca	aaatagccca	ccgagcacac	agcagttcgt	120
ggagcagggt	ataatte	cegacaacca	toatagaggg	gaggagatac	tttcttgagt	180
cgtaatcaag	ggcaagaata	cacccaggee	teaccasast	aaatecaate	gtctgcataa	240
atgatctcca	ccatctcacc	aaggcggcaa	ctaccaaaac	aaddaacca	apotoccagt	300
agcccatccg	aaacgatcca	aaacgaactt	Cigaatcagg	tattacette	aggtgccagt	360
gccaatacga	atgtcacggc	tgcacccata	ccgattgagg	Lectaccec	ttcgatacgc	420
ctaagaatgg	gcatataccg	aggaactgcg	acgcacgacg	ttattaacga	aaaccggcgc	478
tatgaataac	atgaaaaatt	cataatgatg	ccaattactt	aaagtgagtt	atgetett	470

- (2) INFORMATION FOR SEQ ID NO:1255
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255

ctgaagaatt	gtaccatgtc	tgccacnttt	ccgttggatg	ttcgctcgga	acaaaagcca	60
gattcacttt	cttcttcggc	ccgctcaaat	acaatatgta	cgcgcttacg	acaaagggat	120
gaaagccgag	gacaacctcg	atctcgacac	ttggtctact	tgggtgccag	tatcttccga	180
tggatcaatc	gttatagatc	attccggcct	ccacattcct	gcagcagtat	tttagcaact	240
gggggtgatc	attcttttgc	tcacgctggg	gatcaaactc	ctcatctctc	ctctgcttac	300
			ttgctacggc			360
ccaagtaccc	gggcanggat	caggaatcca	tgtgaagcgg	cagtctgcta	ccatgaatct	420
ctatcgtgcg	gccggtgcag	gccgatgagt	gggtgcttgc	ctatgctctt	ngcagttccc	480
tttcctcata	ccatgtacat	gtatttccct	acgactatcg	acattcgtag	cagagtttct	540
ctgggcggaa	gacctctcct	ctatgatgct	ggtttcagct	ggacg		585

(2) INFORMATION FOR SEQ ID NO:1256

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1050 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1050
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256

```
cctatataga gatagagacc ttctctttt tcaaaggtct ccttaaagtt aatgatccgc
                                                                        60
cgagcaattg cacttggaac cggaatgtgc aagtatcttc attcatttgt attgcggtac
                                                                       120
gaatacatta cctttgcgcg caaaaataaa cccccatcaa ccagaaggat gaaaaactta
                                                                       180
gtcatcgtag agtctcggca aaagccaaaa cgataggacg tttcctcggt tcggattata
                                                                       240
cagtateteg agttacggae acateegega ceteaageee aataaattea gtgtgatata
                                                                       300
caaaacaact acgagccgga atacgagatc cctgccgata aactccggta gtcaaggaac
                                                                       360
tgaaatccca agccgaccga tcggatttca tcggctggct tccgatgagg atcgcgaagg
                                                                       420
agaggccatc gcatggcatt ttacgaagca ttagggctga aaaacaaaca gaccaagcga
                                                                       480
attgtatttc cgaaatcacc gagacagcca tcagagctgc tatcgaaaat ccacgagatt
                                                                       540
agacatcaat ctggtcgatg cccaacaggc gaggcgcgtc ctcgaccgat cgtcggcttc
                                                                       600
gaactttctc ccgttttatg gagacgtatt cgtcctttct ttcggcaggg cgtgtacagt
                                                                       660
ccgttgcact gcgtcttatc gttgaggaga gcgtgagata aatgctttcg tgccggaagc
                                                                       720
atccttccgc tgtacataga gttcgtcctt cccgacggta gaatgctgac ggcggaattg
                                                                       780
cagaacgatt caagacgaag gaggaagccc gatatttctt ggagcaatgt atgatgccca
                                                                       840
ctttcatata acagacgtta cgaagcgtcc gggcaaacgt tcccggccac tcctttact
                                                                       900
acctcgacgc tccagcagga agcagcccga aactcggcta cggtgtggca cagaccatgc
                                                                       960
gtatcgctca gaagttgtac aagaaggctt atcacctatt gcgtacagac tctgtgaatc
                                                                      1020
tgtcggatag gcnctcgtgc actcaaaaga
                                                                      1050
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1167 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1167
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257

-+	++a+acataa	togggtogat	gcgcgtcata	ccgatattcg	catcacgcga	60
ctccacgccg	catatteeta	tccgaacgtc	atccaaaacg	agcgcgcttg	atcgtcggga	120
agatgagtca	gatattette	anttoctato	atagaggaga	taggactcgc	gctcaccgat	180
aattcttcac	gagigatice	agetectacg	tacaattcaa	tetetateca	aceeccetto	240
actcggatag	gtcagctctt	gigiacticc	agatattaat	tctctatcca	aagtcgtggc	300
tcccatactt	accettetga	gtgateteae	ggatgttgat	ttcgggattg	aatctcatco	360
aaacgccttg	tggtggtcgc	caccattgca	gtccacaata	tcggataatg	aaccccacca	420
aaatgatgct	tggccgcata	agccgtatat	acctcgtcac	acceggateg	aagcegeaac	480
ccappatage	agtcaggccg	gcttgcgaaa	acgatcctga	taagcccact	gecaacigia	540
ttcatacttg	cttcgtcgag	aggctcgtag	ttggccgtat	cgagatagtt	Caccecacac	•
gcagacaggc	atccatgatc	gtcagatcct	gatagggaag	tgctacgtga	tcaccaattc	600
cootttgaaa	ctctcgaaca	gagccaccag	ttcttcccat	tgtcggcatc	gacctgagcg	660
otttogatcc	ppacettttt	gatttcgacg	caatcttgtc	gcacttgctt	ctcgtgcggc	720
taactaacat	gatetegtga	atacatcegt	gttcatagcc	accttcttgg	ccacaacggt	780
tggctaacac	caaccccaat	aatoaooact	ttacccattt	ttatatgatt	cttgtatgat	840
accidactge	cggccccgac	22024222	даасаддсса	acaatcggca	aaaagattcc	900
tattactcgc	Ciglagegea	aagacaaaga	aggatgeate	tratoragga	toggootacg	960
gcccccactc	acceggeeee	cctaaagcgt	aagatgcatc	ctangongg-	toggootacg	1020
caccaaaatc	ttcttacatg	cacgccataa	aacgiggige	gcaaaccccc	ttgttttggt	1080
tcgggaagta	aaaattctcg	cgccacaacg	aaaaagtttt	cgcaccactt	cgttcagaaa	1140
cacgcgccac	aatcagatca	tttgcggttc	gtatttccga	caaaactatc	cggactaaaa	1167
ggaagttaag	tagtcatgtt	acacggc				1107

- (2) INFORMATION FOR SEQ ID NO:1258
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...453
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258

gtgaagagcc	gagcgaagaa	gatgaagcag	ttcagactga	agaaaatctt	tatgccaaag	60
tgctaaaatg	attttataag	agagagagga	tattcatctg	gcagtacttt	tgcactaatg	120
gggaattacc						180
agttatttt	aatagctgct	tagaaatgtt	tatgttcggc	tgtctcctat	tctcaaaagt	240
aactcaacga						300
gcaaattcca	aaggatttgc	tggaaaatat	ggataaaatg	ggctggacaa	ttcgtcaata	360
ctcaatgaat	atgagggag	atattttaat	ttattttcaa	tatagaccct	caggttttta	420
atcttgtcgg	gaaaaaagtc	gcttttgggg	aag		· -	453

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1008 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1008
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259

```
ctacgatgct cggcgccacc ctgctaaagg cctataaact ctacaaggag gcggaataga
                                                                        60
aattttcaga gaacacatga ccgtgctcct cgtgggcata ttgtggcctt catcgtagca
                                                                       120
ctggccgcga tcaagttctt tatcggatcc tcacccgata tggcttcaag gcattcggct
                                                                       180
attatogtat cttggtggog gtotgottat ogtattgatg ototoagggg tatoottago
                                                                       240
tgtctaatcg gaaaaatgaa acaaataaat cgtccgctcc acctgcgcga gggaaagtac
                                                                       300
tatacttcga caaacctctc acatggactt cgttcgactt ggtaataaat tccgctatcg
                                                                       360
ggcttgtcgt cggatgggta tcaagaagtt gccgtagggc atgccggcac attggatcca
                                                                       420
ttggcatcgg gcgtgatgat ctgtgcacgg gacgtgccac gaagcaaatc gatgtgctgc
                                                                       480
aggccggcac aaagagtaca ttgccgccat cagactgggt gctacgacac cgagtttcgc
                                                                       540
aaggaaacgg aaccggatgc tttcttcccg tacgaacata tcacgcgcaa tcgatcctgg
                                                                       600
acatactacc togattcacg ggaacgatag aacaggtccg cccatattct ctgctgttcg
                                                                       660
cgtgaacggg aaacgcgcat acgattggct cgaaagggga aagaggtgga gatgaaaacc
                                                                       720
cgtacgttgc agatcacgag atcgaactac tggagtatgc cctacccctc atcacgctac
                                                                       780
ggatgtatgc agcaaaggca cttatatacg tgctctggct cgtgacattg ccaagccctc
                                                                       840
gaatcgggag gacatttgga ggcattgcgc aggacaagag tagcaatgcg cgtatcgaag
                                                                       900
actgcctttc gatggatgag ttggaacaat gttcgaccgt cttggttttg cttatgaacc
                                                                       960
ggagttcgaa caaaaagagg caatccgtct tccacaccta caaataaa
                                                                      1008
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 699 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...699
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260

```
taaaatgatg atgacagact gtttttcgcc ggctgcagtg gctccaaagc ttaccgtcac
                                                                       60
tcactttctg tggaatgatg acttctcaat cggtttcaat tcgatggggg taggttggat
                                                                      120
ctacceteta ttegaagggt acacacatt ettgtegaag taaaacatet tgeeteeagt
                                                                       180
tggatctacc ctctatcgaa gggtacacac aaccatagac gtaaggcata cccgtttcga
                                                                       240
tetgtggate taccetetat tegaagggta cacacaacat aagactatat ettaataace
                                                                       300
aaattotgtt ggatotacco totattogaa gggtacacac aaccaagggt ogggttottg
                                                                       360
accttacctc cagttggatc taccctctat tcaagggtac acacaactat aaaggtttgt
                                                                       420
tcaaggaatg tgctaccgtt gatctaccct ctattcgaag ggtacacaca acgatgcgga
                                                                       480
caacgteet tacteegtet tgttggatet accetetatt egaagggtae acacaacage
                                                                       540
gattageteg teegeegaca egtettgttg gatetaceet etattegagg gtacacacaa
                                                                       600
catgattett gattggtgge ttgggegttg gaaatgteag tagtgtgggg attetteete
                                                                       660
                                                                       699
gttggggctt tttcgctaaa tttgcagcgg acgaggtgc
```

- (2) INFORMATION FOR SEQ ID NO:1261
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 964 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...964
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261

cotcoappet	gtttcggtgt	agtatcggac	atgtcaagag	acgtatttga	ggttaggagt	60
statacttas	CCCCCCCAAQ	gagcagtagc	ggcagcaagc	gaagacgacg	aaabcbabba	120
tottagtaga	agratatttc	agggaaatcc	atcaagggca	cttgtcacat	aagagagata	180
tattggttta	agcacacted	cacactaaca	gactgcatga	cagtcggcat	accgagagcg	240
gtagtgcctc	tooggatata	CPCPCCPCC	taateccca	tagggaagca	aagcaagtcc	300
ggaaagaggc	ticgcatacg	tancanacat	cagtacgcca	aaacctgaca	agcgaggatg	360
caatctcatc	gtcgggaggg	Lgacgaacac	aaccaccatt	gatroogtag	gagaggaagC	420
aagagataca	tgactatcag	Catteggtaag	aaccgccact	gatcgggtag	oppgtagcag	480
catacagata	tacgtctata	aggtgccgat	gagcacgaac	gccacggttt	tragartata	540
cttgcccaaa	gggcgatgga	catactgccg	ccggccgtct	ccacctacce	tcgagctgtg	600
atctcttgat	ctccatggct	atgctacaca	ctgtgaccat	gaagatgaca	gacccagtac	660
gccgggtatc	atgatattgc	tcaggtagat	ggagtagtga	gccacggatt	gcctatgggg	000

			ccatggcctg			720
			taccagttcg			780
			tagttggtat			840
			tcgggtatat			900
ctcgctgact	gccagccgag	ccttacgcac	gtttcgaact	gttgaccatt	tgggttgctt	960
ccat						964

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1173
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262

```
ggggtattcg tcaatccggt ggtctctccg gcggtagctc cgtcgacact tattcgcttt
                                                                        60
tcactcatgg ctacgcatac gaaggagcaa ctcgacttgc catcgaaaag ctgcataagg
                                                                       120
tattcaagca gaacggtgtc ctgtaaggta attaatgata acagcgtgtt gcggacacgc
                                                                       180
tcctttggag gaggatgtaa tgaatacaac gataatagga gtagcaggcg gaagtgcttc
                                                                       240
cggcagagta cattggtgaa aaagctctgt gaggctttcg tcgaagaaga tgtgttgtac
                                                                       300
tctgtcacga ttactattac aaggccaatg accacctctc cctgaggaaa gaaagaagct
                                                                       360
gaactacgac catcccaatg ctttcgacac ggtatgttcg tcagggatat tctctctctg
                                                                       420
aaggcaggca aaacgataga ggtccggtct attctttcgt agagcacaat cgtttgcaag
                                                                       480
aaaaagtaac gttcgtcctg ccaaagtgat cgtactggat ggaatcctga tattcgagac
                                                                       540
aaagagctgc gggatctgat gaatgtgaaa gtattcgtcg ataccgatcg gatattcgat
                                                                       600
tggcgcgccg ccttgtgcgc gatgtccagg aacggggcgc aatatggatt cggtattggc
                                                                       660
acaatacttc agtacggttc ggcctagcac gaggattttg tggaaccatc caagcggtac
                                                                       720
gccgatctga tcattcggaa ggtggattca attcggtggc gctctcactc cttgtcgaaa
                                                                       780
aaatcgatcg gtgattcgta aggaagaata acagccggat actccgatct ttcctcaaaa
                                                                       840
ccaaaacctt aatgcgatta aaaccaaggc tttctttcca aacagcattc ctgtattgtg
                                                                       900
gtggatagct gccatcgtat ctgccattac gaagctgctc cgcacaggca caataactat
                                                                       960
accatattcc gctcctcttt tatcatttct cccgacatca gtcgctctat tcggcctatc
                                                                      1020
cggcagagct cacgatgttt ttctctacgg ccctgtcttc tctatccttt tcgccccttt
                                                                      1080
gcccttttgc cttcttcat agggatgctg ctgtggctgt gcttttcgtt gccggatgcc
                                                                      1140
tttgggctgt cagccaatta cccacgagcg aaa
                                                                      1173
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1426
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263

	acgcatcgtg	atatagcooc	cataggggtt	ttgcagaccc	gaaaatgttt	60
cccgtagcgt	tcctgtccca	cacttotaao	gcaaaggccg	tettacetce	ccatacttct	120
tcttcgagcg	ctctaccctt	ntacnataat	ottataggca	gcataaaggg	gatagagacc	180
ctcgagcttc	ttgatcccaa	antantactt	ttagggtgga	atacctcatt	cgttataccc	240
gctcttggag	ttgatcccaa	aatgatgett	ce6566-66-	etcttcectc	ataagcagta	300
tgatgtcgat	gtagcgaggc	aatgcaatgg	gagcagagaa	Caagagtcag	tactetttct	360
gccacctatg	ctgtccccga	gatgcatgtt	caccacacge	ccctatacac	tectegateg	420
ttgtcggggt	tgcggaaagt	agagaagata	gagcaacacg	cccactcac	gaaatatgtc	480
tgaacttatc	cgccatacga	gcatctcacg	gatgegette	tancaccaca	aggrataaat	540
ggggtcgtag	aacgcttgaa	gcgacgaaag	accgccttgg	Laacgeegeg	aggeatatate	600
cctaccaaga	ctoctcatco	acgagattgg	caaaattgtc	aatggttatt	CCCCacccc	660
atccttcatt	tcagccccat	agagcatcag	aggcatggga	tggatatgcc	tcggaggata	720
gaaatageet	ctoggogttg	gtcgccttgg	ctttcagttc	giccagicgi		780
caaatattaa	geettettt	tcctcttctc	cagtcgctct	ttotototoge	acigocoacg	840
aataaacctt	potpattgat	atctatgtca	ccggactttg	ccatcgcctt	ggtttgctaa	
tantaccttt	ragttrotro	aagtogtgoa	gctctacctc	ggaagiiiga	grageregee	900
attatagagt	geceeattet	caaagccatc	cgcaccactt	tttctattig	LECECECTE	960
anctatecas	gratogtatt	acatcgtaag	gcttcatccg	gergeeree	acagagacga	1020
+ aaaacaaaa	ttgagaaaat	cccccaacag	cttgcgatca	CLCLCBCLCL	gittgettet	1080
ttotatoata	ccttggcagc	ctcggcaagg	acacggaggg	rgcggrcgga	gcaaagccga	1140
aggrataara	ctctgtcttc	atgtacccat	tgtgggataa	ggcgtttgta	CgCggaagac	1200
agtttgcata	tagccggatg	cggagtacta	tatgaaccgg	ccatcatgaa	gacgccggcc	1260
caaggettaa	toctacaccg	gtagtcagtc	gtccgcatga	gagggtgatt	glalaagici	1320
catcoootct	ttgccgatgg	cttgattgac	taactcaagg	gcatctctgc	ttcctcctcc	1380
tcatcatctc	cgtcccccgg	ccacattggc	caccttaaag	aaccga		1426
2000000000		50	-			

- (2) INFORMATION FOR SEQ ID NO:1264
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2670 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2670
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264

	+ a + + a + a + + + a	+a+annaan+	atcagctatc	CGSSCSGCSS	ocoasocato	60
gtggaggatt	agacacacata	ctttactcta	attttggaga	ataataccaa	acqaqqtqtc	120
eggicgggat	agegeagacg	acatagacat	aagacagcca	acotoataoc	ctccgtcgtc	180
ggaactaacc	caaccaaacc	otagatacoc	acgtattcag	agtatcagaa	aggataggcc	240
tacggcaaac	tragagtete	Cottagagac	ggagcgagag	ctesttcect	atatccggat	300
ctactastac	coassactcs	tractogrto	atcctgcatg	gacgtacgtt	tetcteectc	360
grgcrgarac	atatacagac	totoocatao	cacattctgc	cectactact	cgaaagtttt	420
tongongan	acgegeagae	tccgaaaaaa	ggggaatgat	aaggeetgtt	etecaaataa	480
tatagaagaac	atactccata	ccttaattcc	ggaggcaata	tgaatcgaga	aagctttttc	540
tactogcaca	tetettatt	acteteceae	tccatctgca	asocatcoct	ccatecaaca	600
coctgoings	tagaacttat	atatocaatt	cggccaaatg	tttcctcctg	ccatcostot	660
acacggcaga	nancogates	acaccegate	cggcattccc	tacctcttat	agctgcttct	720
ctaccatgia	tanactagat	gacastatco	gagagetteg	ctttaccaat	accagaaact	780
tteeseesees	stages	tonatonact	cgttcctctt	atagcacagc	tttgatgagg	840
costtogget	atagacaacg	cagccagcc	tggggaaaaa	tattatatca	gatgeettgg	900
ggattegget	tataaggacg	atgataatta	cagagaatat	trattragar	aattacatcc	960
granggract	actaccaatt	atacccatca	cggaaaatat ggacatacgg	caacagcttt	Perceases	1020
ggatggaact	totogenate	acacccacca	gcccttggta	tagrarage	agetatacat	1080
acactteett	acagggatca	accatatoat	gaacaatcgg	cattoggcag	coatotoctt	1140
tacacacacta	acggggacca	attaatcaa	gaattagcta	ttagatcagc	gatctgatct	1200
tecagagete	tacaaaggac	accegecege	gaccaagaaa	Caddaaadaaa	ctctooaoao	1260
cotgegatee	totottotac	coccaaagec	tacatcaacc	aacaaataaa	ctttgaaggc	1320
catggitati	acataccasc	cgggaacaga	tgaacctgaa	gacgaccttc	aaccgaactt	1380
tacteactag	atacasatca	gatcacaatt	cagcgtttcg	васвассесс	gaaagtcctt	1440
rgeregergg	gracgaareg	anttttonta	ctccggcgat	ctcactcooa	ctttctgccg	1500
atgtgagaaa	ggccggcaaa	agetteegta	cgtctgggca	gagatectoe	cctcaatact	1560
gigiagaacg	actttaccaa	tacccaage	gagccggacg	aaatototto	gaaattaacc	1620
gricigraag	tttccaacca	cgcccaagac	tagaataac	atacacetec	ccatcacat	1680
gacgetegag	actestacea	gcgcccaag	tgggagtagc	tataccatct	tatogaggaa	1740
gggtatagaa	geteatgeag	ggcaccagcc	tggcgggcag	ttaccaaca	tttgagtttg	1800
acatecact	ggicgaccac	ctttccctc	ctaccgtacc	agaataact	ntacagantt	1860
cagicggact	acattectate	citicogcig	acgatcgagt	atcotottt	cccanactas	1920
caaagcggcg	agcacaccgg	gtacctgcg	caagcgaacg	caacatacca	agracttor	1980
totastasta	accgacgcgc	tteettaeea	atatattcca	actcatctee	trerearge	2040
atagatat	agggetgeet	acasscacca	ccagatggaa	acccacccgg	cccatatcaa	2100
atacgatett	cccacacaa	tttaccasas	gaggcgtcgc	tacaacacca	gaatoctcga	2160
gatastagta	catagagaga	ttatccaact	cgatcctgca	aagaagcatt	ccaatccaa	2220
geteetegte	tetteggaga	angaaantto	cccgataaag caaacgctct	caaccattat	ctccactaca	2280
cggcacacac	ctgaaggaat	aggaaagete	tctctgcata	agatragra	aactcatcca	2340
aaccgggaag	ccgaaggaat	cattagage	cttactatac	atctcatatc	ccasatcoc	2400
atgastcogo	tetacteane	acconstaca	ttgccggcac	cacotatate	aaatcctgaa	2460
acgaattege	aataccacta	ccaagtaca	tgaagttctt	atogettoes	accascaca	2520
castcatca	ctcaccaccac	tasacaacas	ctcaaaacat	accasasocc	tttcctatta	2580
ctccatccc	cacattoos	anctantana	ctcaaaagat	accotatoon	tooocattco	2640
			actnactcag	Leckratege	LEBECALLUE	2670
ccaacgcaac	ggtattggca	LUERECACAL				2070

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 792 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...792
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265

tggcgagccg	atcncggnag	agaatatcgg	taagcgagtt	gctgccgatt	cgataccggc	60
cttcaccgca	ggaatgcttc	tgtactgaac	acgctgggtg	tgtactcaaa	ggactgttcg	120
tcctcgtagg	aataggtctt	atccttgtgt	cgttttcggt	cttttcggcc	ttatattaga	180
gctgtttgca	gacggtacgt	ggcacatgct	cctttgactt	cggactggat	ttctattcct	240
tcttgatgat	actctgtgcc	acgatctccg	tatttattat	agtagccgtc	ccggtatggc	300
catcgttttc	agacatcaag	ggcaggggag	aaacgggatt	attctgcagg	tctcaaatgg	360
ctgggcttga	ccatttggct	tgctgccgct	gtctattggc	cgtagtcttc	atattgataa	420
cccgtgaact	gggtttgaat	tcttcctcca	tcgccattca	gtatgatgtc	agaaatgcct	480
aaaaaacatt	aggttccttt	taggacaatc	catagtaaag	gtttttgcgt	ttttgttcaa	540
tcttcgtttt	agaatcttgc	cttttgaaaa	agaataacat	cagctattat	agtatgagcg	600
ataattgtca	tttgactgag	aaatcatttc	gaagtgtgtc	ctcccgaagg	attccgtcct	660
gactttattt	ttccgaattt	gtctccaaac	tggtattgga	tactcctttc	tattgtcctt	720
ttcgccggat	ggggttggtg	aagtataaga	gggccggcat	ggctcccagc	acctattta	780
cgacgtaatg	gc					792

- (2) INFORMATION FOR SEQ ID NO:1266
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{30}$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266

ttattcaaaa	agttcctcat	tttcggacag	atgctgttct	tgacttgcta	atagtgttct	60
tctcactccc	ttattgacag	atcattcgcg	tgatctccct	cgaataggga	ggtaaccaag	120
cagtactacg	taccggagga	aagacttggg	gcgatgaact	gaccgatctg	ctttttagcc	180
ggccggatag	tgggcacagc	tactcgaccg	gttgttccta	ctccttgaaa	aaattgccga	240
aagcagctct	ttcagccagc	cgattcggag	tatgaccaat	cggaggagac	caatatatgg	300
agttggagca	gatctatcac	tatcgcaata	tgctgaacag	gctagaggac	tggtcgaatc	360
ctatgccatg	gatatgtcag	ttcgttctgc	agtcttctgt	tgcaaggatt	ggtatccgga	420
gtgagcatcc	cattcgaggg	aaacctctgg	tcggcctgca	aatcatggga	atagatcaaa	480
cgcgatcttt	gatttcaaac	atctgatcat	tctctctgtc	aacgagggta	aactcccatg	540
cgtgtctatg	aaacgacaat	gataccctac	acattgcgca	gagggtatga	cttcggtcaa	600
tgaggtaaac	gaagccactc	aatctatgat				630

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 891 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...891
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267

```
aatgaaaact gcagaagttc atcaggatca gacgatattt caattgctta tcatgagtgt
                                                                        60
gtgattgtag ttattacgga agactgaaaa gaaaaagcct tcgacggcac cgaatcccga
                                                                       120
atcgaaaggc ttatccccaa ttattgtgca tgtatcagtt gtcggtataa gtcatactgt
                                                                       180
aaacgccgat acgcgcgtct tatttttttt tccgagctgt agtttgacgc cggacgggaa
                                                                       240
catgaattat tcagctggga ggtgtacagc gaattggaag ctcccgcaac ctgagcttca
                                                                       300
caggcagcag tacgagaaca aggtccttgg tgatataagg cttccctcgg gagtcttctc
                                                                       360
cgtattgttc ttgatatgct ccatcagcag gcactgatat tgctaaaccg atactcccgt
                                                                       420
ttcttaatgt tgtatatggt cataggaatg ccgtgcgagg ctgcatcagc tcggtctgtt
                                                                       480
cttgctcgaa aagtttctca ccgaatcctg cggcaagagc aacaagtagg agggcggacc
                                                                       540
agcatcaagc cctcagatgg cttcgaagca ctgatattga actgtgctca ccgatttgcc
                                                                       600
aagccaaaga ggaagacaga ttgctcgtga aagcatcgta aactgctctt tactgattgt
                                                                       660
cagttgcgtc atcacccctg ccggaccttc acacaagtga gagaatcatt ctcctgcaac
                                                                       720
aggtgggata tttggagttc ttgatatgat tgacctgata ggattcgctc gtgtttacga
                                                                       780
atgttctgta gctgttgtgg tggaatcggc cgtaaccttg tagctatnga agaggccatc
                                                                       840
tgcgtattgt cacgctgagc acaactcccg tacccgtcgt cgagtcacat a
                                                                       891
```

- (2) INFORMATION FOR SEQ ID NO:1268
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...353
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268

tgcgatgtga	aattcgattc	cccatggttg	atggttttta aaaagtgcta	ctatatttgc taggattgat	ggccaagaat atagaacgat	60 120
attgacaaac	agtttacgac	caaataaaat	gaatatgcca	catatactcc	caaagcaaga	180 240
	2022212220	aagaataacg	cttccatagc	ctcctcaaag atccctcccg	agteaggeae	300 353

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 968 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...968
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269

	accanateaa	tartaarcat	agccgaagct	ctgaccaatt	cgtctttgct	60
cgatccggca	gccggaccgg	agatataaac	ctotcoocaa	ctggatgtgg	ccctgccgta	120
ccgcttcgta	atggtatega	gggtgcgagc	catagaagcc	tgttcggact	ttgccgtcga	180
acgaaggcga	agatgcccgt	cigiaccigo	tototatoca	toacacagaa	atatgaggac	240
tctgggcatc	aacatcctac	cggcaaggac	tenetecca	tgacacagaa	acagcattcg	300
aaaaagtgct	gagtcccggt	acggtgatta	tcagtgccgc	agccgaagtg	tatcoatttc	360
tcgcatcgtc	agccccgtcc	tcagccatat	agccgctacc	gcttctacta	catchagata	420
agcttctgcc	cgttctcatt	gggaggatcg	gctttgccca	gagcttgggt	actateggeg	480
atgaagtccc	cactgtacgt	gtccggaata	cttccgcgat	gcgttcaata	CCgLaCagga	
actcattgac	agggtctggt	tctggccgga	cacgacatat	ccgcaggcgg	tetgattacg	540
ctcttctgga	aatgtgcttt	gccaatgtag	taggcggtct	ggaggtggat	tggataacct	600
cotogaagac	gacctgatca	aagtcctctt	tgccgaaacc	cgggtatcct	cattcaggta	660
280888	aagccgttga	taagatctga	ccgatgccgg	catcggtttc	ctcccgatag	720
anghacehen	CCAAGGCGAC	acctcttgat	acataaagac	ggagccgaat	acctgttcgg	780
totopocaca	tacacascat	ttootatgag	tcgtcctacc	tgctggactg	cttcagagtg	840
tattattata	rgcgcgacgc	cocttcoaga	actataagga	acaccggtcg	tatatcactt	900
gcaatacctt	ggccggcaac	totanagean	togattogat	cccgatcgaa	agacggcatt	960
	ttacgggtga	ccigaagcga	CEECCEECC	2228228	- 8 06	968
cggcattc						

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 725 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...725
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270

ccattgtgta	atctccccct	tccatcacat	gcttttgccc	atccacgatc	gcatcttgtg	60
atcgagattg	cagtcaaggg	tgtccctcat	actaaagagg	catcgaagaa	aggtgctgtt	120
ctgaaaagca	aacgagatct	gaatccttat	cctgtttttc	aaacgatagt	gaagcatcgc	180
cggcacgtgg	catcaggccc	cccacttata	gtagattgta	tagctgaggc	attctccggt	240
cctgcgaaat	cgttggagat	gggttgctga	gcttgcaatg	atatagaggt	gatgttatga	300
tgtatagagt	cgtgaggatg	atgactatgc	agttgaatgg	attcgtttct	tgcttatatt	360
ntgttttgct	ttcatttctc	cttttcttt	ctccaatgat	tcaaatatag	gcaataagcg	420
gttagtagaa	ataaaaggag	gagcctgtgc	cagacctcct	cctcaaaaac	gaatagactc	480
tttagtagtt	ttgggtgtaa	atactcccaa	agttatttt	tattcgaatt	atagatttcc	540
tgagttttc	gattagcttt	tcaccacgaa	gatctcgctc	tataataggc	cgtcaggacc	600
caacagtatg	acttgcggaa	taccttgnat	gccatactat	ccgtagccac	attcttagca	660
tcgatatctg	aggccatacc	acgttggact	tctttgcttc	agtgatcttc	atttatccaa	720
actac						725

- (2) INFORMATION FOR SEQ ID NO:1271
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...648
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271

gcgcaatg	ta tcgttcacgg	ccaaacaagg	agaagtcaca	gccctcgtcg	tccgtcgggt	60
ggaggaaa	ga gcacatcggc	caagttggct	gcacgctttg	ggatatagat	ggaggaaaga	120
tctttttg	gg aggggaagac	atttcgcaat	cgaacccgaa	accctgctac	gtcattatgc	180
catcgtct	tc caagattact	gctcttcaat	gcatcggtgg	ccgataatat	ccgcataggt	240
aaaccgat	gc tacagatgaa	gagctcaaac	gtgtagctng	gttggcaaga	tgcgcgaatt	300
tgtagatc	gt ctgccgaatg	gatatgacac	tttgatcggt	gaaatggtga	gaacctttca	360
ggaggtga	ac gtcagcgcat	ttctatagcc	aggctttact	caaggatgct	ccgattgtgc	420
tgctggat	ga agctacggca	atctcgatgt	tgagaatgag	acactgatac	aggccggtat	480
atccgaac	tg tcaaaaacaa	gacagtcctc	attatcgctc	atcgtatgcg	cactgtagca	540
	aa gattgttgta					600
	ca tgaacggtgt					648

- (2) INFORMATION FOR SEQ ID NO:1272
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 821 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...821
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272

```
60
cacgctatgg ccatagactc gcgagaagac tttggtctga cggntccgca atgcaacgat
                                                                       120
ccgtatgatc agcgtggcat agccgatcag cagcagcagg agcttaagaa accctgctct
                                                                       180
togocoacgg tacagaagat aaagtootat cotgotoggg cacatattto agtttggtot
                                                                       240
gtgtcccttt caggaaccct tgcccataaa tccgcccgag ccgatagcta tcttggactg
                                                                       300
gtctaattgt atcctcctcc ccgcaaatcg tcctctattc ccaaggcaac cctgtacgca
                                                                       360
totgotggtg gggotgcato actitgttga atacatagto cacgaataga agtagoccac
cgaacacaag gcgaaaacgg ctatcagcgc atcgacagta cataccgctt gatggccatt
                                                                       420
gacaaagccc atacgatcaa tctgccaaga gaccgtatgc cacgaggaca aaatccaccg
                                                                       480
acacgaagta gacagcacta tggctacggc ataggtgaca gcagtaagcc ctgccgccag
                                                                       540
                                                                       600
acatagaagc gtcctcgctc cttggtatag atccgcacga ggaagaatct atcacaaaag
                                                                       660
ccatcgagac cacagaccat tcggcggcat ccgtatgccc caccacacat cgccctgcaa
                                                                       720
cttcagagcc gtgacgaaaa agaggaggca cagaaggcaa tgccgatgaa tacgccggac
                                                                       780
attccctcac gataggggca aggaaaaaag ctatatagac gagggcagac cccgtttcgt
                                                                       821
ctgacaggat aagcagtacg ggatgaggat aatggcaaaa g
```

- (2) INFORMATION FOR SEQ ID NO:1273
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...472
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273

ttgaaagaaa	cggaaggaaa	aatctcgcag	acttctttat	ttgagcgatc	ggctccgggt	60
ttgcctgctt	tgatgtaggc	gttcatggat	ttaatgtctt	cgggttgcag	cggctacggt	120
cgcagcggta	cagctccgtg	aagggattgc	atcgacgatc	ctctgcaaaa	ggtcgctttg	180
ggagggaatg	cctttgtggc	gaagtactgc	tcataggtgt	attcgacgaa	agctgtggta	240
ggcccatgcc	acggcggtcg	aggagatagc	cgtcggccag	ctccaccgga	gtgcgaaacc	300
atcgccacga	cgaagatcgg	aaggggcagg	acgtgccacc	acaactttt	gtcagccgag	360
agggtgatag	gcacgagatt	gcgatagtcg	cccgcgtctt	gtaaatgatg	atcggagcca	420
atgccatagc	cggcgtcatg	gtgctactcc	atcggggcca	ttgccctcct	nt	472

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1342
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274

```
agttcagcac cgatttcgtc cagccggaca ccgcttttga aagcgtacgt gctggagtat
                                                                        60
ctcacgacgc aacttcaaat ccggacgttc tatcttgaac aggtagcacc ggccatacga
                                                                       120
gtgaccaacc ggtcctccat cccgttaggt ctacaggagg tttgtccgac gtcaagacta
                                                                       180
tctgtttgcc aagcattaga ggtgattgaa cacttggaag aaagctaatt gcgttttctt
                                                                       240
cttgcgatca accattggat gtcatcgatg atcagtacat ccacttgctg gtagatgcga
                                                                      300
tgaagtcatt gatcgtcccc atacgggctg ccgtagtgaa ctgatctcga acaaatgact
                                                                       360
cgatacgtat agtactttca accgggggtg cactctctga cacgaaggcc caaggcatgg
                                                                       420
cacaagtgcg tcttgcccac acggaagctc catatataaa gaatggattc atcggcgtat
                                                                       480
tgcccgggct gcggcgatgg cttcagccac tgagcgagct acatagttgc attcgctctg
                                                                       540
tagaagttgc ggaaattgag cctgctattg agctgcgtgt cgaaatccgt gcttcgctat
                                                                       600
gggtggctgc attgggcatg tgcctgtgta gcaaattaca tcgaactgtt cggctgcctg
                                                                       660
tccaccgtcg gcacaaccgg ccaatgcacc gtgccgggat atttgggcga actgttgtct
                                                                       720
acaagggcat tatacgtaat gatgcgttgg gacctataac acgccccaac accgtacgca
                                                                       780
gctgtctacg aaattgccct ccaaaaactc acagaagaac tgactcggca ctttaaggta
                                                                       840
agcgtatcgc cctcgataga taccggtatg ataggcaaga acatgtacgg tatgctcgct
                                                                       900
catccacaat atcctgaagg atgcgaagac agcgtcccat atttcattta cattggtcga
                                                                       960
gtggtagttc atctaaaaaa tatcgttttg agagcagtcg ttcattgctc ttttggggat
                                                                      1020
agcaaaggtc aaacaaaaga gtaaaaaaac aatcgacaaa aagtgtagta taattcagtg
                                                                      1080
aatcgtatct atattgtttt cagatggtta taaccttgag atataaaagc gaaggaaaca
                                                                      1140
acgctattcc actgcattcc agacacttat acgaaaccga ccaaggcgcg accgagttat
                                                                      1200
caacacccaa gacagagcct cgattagttg tgtacaaaga ggttgcgagg aaggagaa
                                                                      1260
aaatttttca acagatcttt atttacaatg aatcgaaata aggaaaatct ncggtgctcc
                                                                      1320
ctaaatcagg atgtatccaa tc
                                                                      1342
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 852 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...852
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275

	cgagaaaagt	agactcagtc	aatootoaao	caatcttcag	ccatcacgat	60
atcttcaatc	Cgagaaaagt	gggcccagcc	aatcccgaag	ctcctcagta	acaactatet	120
agaccgtgta	ggtataagaa	cgaacagcct	gereeggear	Ciccicagea	gegaecatet	180
cctgcagagc	ttctacctct	gcctctatgc	gtctgtctcc	tcaaaccggt	gcaacgaaag	
tcaatgatto	caacactctt	cgttcggaat	aatctcttga	gctgctactt	ccaatggcat	240
aataacatgg	gtaaaaccag	ccaaagcagt	gagcagactc	ttttgaagta	gttcgtttca	300
tagttatctc	cttttttaat	tagtatctca	tcttgttgct	tctttcgcct	cttaaataag	360
gtgatacaca	aagataaaaa	tatatttcgc	cgcaagctat	tcttcaacct	aaaaagtttg	420
totacacaa	gaatcggaat	ctttttcttc	gacaaaattg	aagtcaatca	ggagcaagga	480
Latgatgtag	gaaceggaac	actactacta	cttactttta	taatotttca	ttecttccec	540
ggttctcttt	aggtcaaaag	actgatgtta	CCLECCICA		aganactota	600
atatattggc	gaatggcagc	tatccgattg	gcatcgctcg	gatgegtate	agaaactcta	
cccgcccgtt	accttgggca	gccatctttt	gccaaaagta	attgccgnat	tcgggttata	660
accoorcate	occatgaaga	caagtctatt	ttgtcggctt	catactcctg	tttccgattg	720
teesteese	Staatageac	ttataataa	atoccatago	cctecceat	gaccgtttgc	780
tagggtagec	graarageae	Cigigatica		acceptant	tacatacata	840
agtgtgctga	cttggtggag	actgctgcgc	ccagtatatt	accacccacc	tgggtagata	852
ttcctgactg	at					632

- (2) INFORMATION FOR SEQ ID NO:1276
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 854 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...854
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276

cggcaagttc aaaagcgata	atcgcattgg	ttaatcaggc	ttcctcaaaa	aaagggaagt	60
ctgattttta catccatgca	aggagcaata	tgatataaat	gtctattgcc	gatgttgcca	120
tttctcttga aatttacgag	tgagttgacg	atttcccctc	caataatagc	caattcgagt	180

```
gtcagtttct ccaactagtg agcatcgcaa aggctttctt ctccgtaaaa ttgcttttca
                                                                       240
aagcgctaca gtttggttat aattcacccc gacactgcga aattgtccgt acaagttgtc
                                                                       300
agtttttggt agtaatcgag caacgaacga tccactttta tcatcgaaag gtctcattaa
                                                                       360
agaccettge ettgatgaaa geggetetat ttgaageece gattgetega atagegttag
                                                                       420
gaaacgagca aattotgtgt cgtaaatcga accatacaac aatggtcggc tcgttcattc
                                                                       480
ttgggaggtc ccccacattt ctctttgtca ttactttgga ttttaatggt ttgtaattcc
                                                                       540
                                                                       600
tcttctggaa atagaacgtg ctaaacataa ttgaaatcca ttagagaggt tcacgataaa
                                                                       660
atagccaatc aagacaacga aaacttctat ccaagaaacc gacttcggag gtgttctgcc
                                                                       720
ctctgcaaga gcaagggttt tgagttccga aataatttcg ggtaacgcaa gacatacctt
gctatttgca ctgaccaaat aaattcgttc cgaagaacga tatgttattc tctcgaaatg
                                                                       780
                                                                       840
tatgtttcaa agccttgaaa taccgactta tcgtttactg caaagttact aaggttgggc
                                                                       854
ctaaatccct tacc
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1178
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277

```
atgaaagttt ccgcccacgt gtttactacg acttttgccc ataagtatga ttcctgccca
                                                                     60
acctaagtat ggtcgatctc atttttcatg aaggaccacc gcaatacaga ccttgaagga
                                                                    120
gtgtattcgc tgacaaaaaa taggtgaaaa aatctctatc tttgttcgaa ttgataatag
                                                                    180
                                                                   240
tatctgatta tgacaatctc gaagccatac aggcaccgat aaacggattc gtcaaagatt
                                                                    300
ttcatattcg tttgagcatg cactcgattc ccaatcggag tggatgacga aagcataaag
atcttgaacg gttccaccgg taaacacgtc cgtccgctcc tgacggattg gtcgcagccg
                                                                    360
tctgtgccgg caaaacgaat tcgacgactc ttaggcggct gtcctgctgg aaatgatcca
                                                                    420
tacggcaacg ctgatccacg agacgtcatc gatatggctt ctacgcgtcg gggagtaccg
                                                                    480
                                                                    540
acceteaatg ttttttegac aategtgtgg eegttttgat gggggaette gtgetetete
                                                                    600
cgccttgatg cgtgccatcg ctctgaatga tattcgcatc atcacgatat atcccggctg
ggacgtgagc tgtcggaggg tgagatcagg cagttcggac agccgacaaa gtgataatag
                                                                    660
acgaagacat ttatatgggg gtgatcgaca gaaaacagcc atgctcttta gtgcttgtgc
                                                                    720
agaggtcggt gctataccgt tcaggctcca gtagagattg tggaaagggt gaagagggta
                                                                    780
gggggttgct cggctatgct ttccagatca gagacgacat attcgattac tatggaatga
                                                                    840
                                                                    900
gctctcaaga acgagcagtc tgcgctgcga gtcattgtct caccattctg gaccaaaaag
                                                                   960
ctttctcgga agaagattta agcttcttac ctcctttgcc atagagcatg ggggtatagt
                                                                   1020
ttatgccgaa gaaaaatggc tgaatttata gacaaagcaa aggctgagtt ggctgtttcc
                                                                   1080
ctgactcaga tgctctgcag tcgttgcttg ctttggctga ttttatctac aaagagcgaa
                                                                   1140
ataataagtc ttgtactcat tctttcttaa aagccggc
                                                                   1178
```

(2) INFORMATION FOR SEQ ID NO:1278

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{78}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278

cgtttgaccg cgggcaagcc ttccgattca gcactagaaa tacatccgtc cctattttca acatacgttt	gacatccgaa tctaccatcg tctatgccat ttcggaataa acatcctcca tgctccttgg tcctctcca accggagagg	gttcagatcg aagccaaatc ttttcggaat accagatcgg tcggagcgag gctatggctt aagctctacg acgatgctga	atcaagatcg ccgtccgtat gtgccggcta caccgaactg tagcaaaggc gtcctgtcgc atgcctgcag cccttcttt	gccggcacct gaccggccga atctgtacag cttgacgaat cttgcacatg tctccccgag agagccgctt tggcaagttc ccggctcatt	ccatcgggcg cagggcatcg atccgaaggc gtctatggca gaatatcggc ttcgtggacg ttgatcaggt	60 120 180 240 300 360 420 480 540
acatacgttt tccttgcgca ttccagattg	tcctctcca accggagagg tgcatccctg ggtcgcccaa	aagctctacg acgatgctga tcgaatccat	atgcctgcag ccccttcttt aaacggcaca	tggcaagttc	ttcgtggacg ttgatcaggt gataatccga	

- (2) INFORMATION FOR SEQ ID NO:1279
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 709 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...709
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279

cagggatcag accg	aagatc ggaggggaa gaaaaa atgaagact tatacg acaaagccc	g cgatttcgcc a atggctacaa	aatccatgat cgactcccac	aggccaaagg gaccagcaac	60 120 180 240
caccagttgc taat	ggacaa agcagaaaa	c cgctaaagcc	gagcagaaaa	agaaatgaga	
aaagactgcg agaa	cctgtc gctccgaca	a ccaacctttg	gagatcccac	gttcaagcct	300

acacgctgat	cggtatccgc	acccttctta	tagtcgaacc	aatgttggct	atattgctga	360
ccgtttgggc	agacaccgct	acgatcaaag	ccaagcggcc	tgtggccagc	gaaaattgcc	420
gtcagctata	gcataagcaa	tgctacaacg	acaggactga	cagatgccgg	cagggtatga	480
			gcgggggtga			540
aaagacttcc	cggtagcgga	cgcatattat	aggaagaagc	catcacggtc	catatgctcc	600
ggccgaacga	atagccagat	aatcgccgcg	tttgagtcgg	gcatgagcaa	ttcacgctcg	660
aatacatcgc	tggatcgcag	attgggcgac	aacatcgatt	tctctgcag		709

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...627
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280

ggcagaggat	gatgtggaga	cgatgacgac	taccgacctg	catacctatt	atcgcatcag	60
aagcaaaggg	gcgtgggcaa	cgtcaagctc	tttgagatga	actgcacaaa	cgctatgcag	120
ccatcttctc	tgcctttatc	ctcaccatat	cggtgcttcg	ctctcttcac	gcaaagtaaa	180
aggagggatg	gggatcatat	cgctatcggt	ctggggctta	gctttgccta	tatcctgttt	240
atgacgttgc	cggtacattt	gccatcagcg	gatctttgcc	tccgtttatg	gcagttggtt	300
gcctaacttc	gtgtttacgg	tcattgccgt	ttccctttat	aaaaagctcc	gcgataggca	360
gacttccgga	tgtaacgata	tccacaacta	tgaagagaaa	atacagaaga	atatcctcat	420
aaagaacaaa	cgtgccactt	tgattacgag	attttggacg	tttacacggc	gggcattgta	480
ttggtcggta	cgagatcaaa	tcgctccgac	tgggcaaagg	cggtttggtt	gatacctatg	540
ctacttccat	cggggagagc	tgtgggtgaa	gaatatgtac	atagccgata	ctctatgcac	600
	atgtgctcgc					627

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5789 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...5789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281

		_		+	basananata	60
agatttttc	atccggccag	gtcagtcgat	agcaggccgc	tacaggcgtt	cgggagagta	120
gtgcatcatc	agttcgcgct	gtacatcgtc	cacgatgcgg	cattaaggaa	gatacacatg	180
atactttaga	actgtgccag	cagatgggct	tctctttctc	cggcatggga	gracaccer	240
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tacaatacaa	cttgaaacga	ggagataccc	ggcgtgatat	gatagegear	gccgagcggc	360
coasosotoc	catttgctct	tggatagcac	cgtagatgca	gggtcgcccg	Latguaggeg	
taccactaat	ttgcctcggc	ggtaaaagtc	cgcatgatct	cgaactgttc	Ligiagatic	420
atrorageco	aacttctgac	ctggcaccgg	ctttggcaca	agcggtcagt	CCgCgaggga	480
caaggetgee	gcatagagaa	tcagatcggc	cttttccaag	aactgtctgc	Cacgcaccgc	540
accapatopp	patcectee	acccgctccc	actatttcga	tatggccgta	CBBBCBBaBc	600
caactatcta	tgccacggca	aaggtaaaat	cgttacctcc	gatagetgee	Cillingui	660
ctctatcaca	agacttccca	tatccgtact	ttccgtgccg	aggettegge	tacteegtag	720
caacccotaa	cggcaatacc	ttttccgagg	ggttggctac	ttccaccggc	tgtaagtett	780
otcootatat	atatgtagcg	gtatccctcc	gagacgatgt	acgagatcgg	ccaaagcggc	840
tetteggett	teatetceat	cgtggctatc	cgaccgatgg	ctcgggggca	taaccigaci	900
proprattic	ggagaagatg	tgttccgcaa	tccttcgggg	gcacatagcc	Lgcgacaacc	960
tactccgatc	gtaagagcag	aggatagtag	cagatcatcg	gcaaccggct	Ciccaagige	1020
COOPCAPAAC	aaccaaaatg	aggtcgaact	ccgcctgatc	gacagcatcg	aatgagtaaa	1080
aaggcggaca	tgaggcggac	aagacctttc	caaaaaatct	tctcctccc	cgaagtette	1140
aataccaatg	ccgtacgtgc	tccccccacg	aagagcaaat	gggacgattc	atgicgccig	1200
tattggaaac	ggctttccat	ccatagtcga	agccagcgta	tccaatgccc	agagtcctgt	1260
traatractt	tgggggtaac	caccggttcg	ccaccgatgg	cagaggcgat	cagccgcgtc	1320
agacgttagc	tccacccata	tgaccgctca	gaacggaaac	cacgtacctg	ccgtactgtc	1380
tacottcact	acggccggat	catgatgttt	gtccgccaca	taggcgcgat	gctccttata	1440
cadattccca	toggacceat	gaaaacccaa	catcgtatcg	ggcaaaagat	tcggccatca	1500
actocacaat	ggaagagacc	aggaaacatc	ctccgtgcag	tcggtaaaat	tcgcgccgac	1560
gcccgcaat	ctttctctcc	cgatagttcg	gatgcaatgg	tccgcgccaa	tgccagacgg	1620
ggcaaaaacc	acadattato	gcagtatgat	toggtttoga	catgatgggt	agtgtctatt	1680
caguggatau	tacttagagt	atotogatag	gattgtgccg	tcagccgtca	gtcggatgga	1740
+ = = = = = = = = = = = = = = = = = = =	tccatcccac	aggetetatt	ccegteagea	agaggtgccg	actctcttcc	1800
catacagaga	tgataccage	aggecocctt	ttgtcataac	actgtgcacc	ttagcgatca	1860
gacacggagc	cancetecat	gaccgccgat	aaaaacegca	tcgggcggag	cagggaagaa	1920
ttttataaga	ccataaaatc	tccatccaa	tacgctatgc	gggtgcaccg	aagcggcggc	1980
tattereas	catcagttco	gcaccttcgg	acggatetea	aacgcagtga	tatgcaaatg	2040
rgricacggg	, cattagette	gatogaaacg	gatecegtae	aaaaacctat	atccaaaag	2100
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gatgaggttg	caccatta	gegeeatega	agcactttcg	gacagccgag	cggagcacga	2220
catciticgit	. cgcccgccga	anccasasat	atcagcagtt	ggggcgttcg	aagtcgcgat	2280
ctgcaaacga	toggeegage	. agccgagaga	gcattgctct	teggeettt	ccatccgagt	2340
eggetgeete	. ccgcagggag	, dacegeeeds	taatcgaaca	ttcgcattgc	gatagcggag	2400
acctacggac	. algeatagee	. cccatageeg	tettetetae	ccgctcgato	gtgcacggtc	2460
gggtatgctc	gigginggin	. agaatgeege	tacoatcoa	tatogtggta	cggcatacga	2520
gaactcatgo	catggettge	. ccgcaagcga	. cacgaccego	. caccgtggg	acggcatcgg	2580
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aactattcct	catactcccg	a taacgggca	aalacatcat	. etageggeat	tgtaaatcta	2760
tccactcggc	atccgcaggg	agragicego	, gcacgaccc	acgageege,	tgcctccgct	2820
gaatatctt	g ccggaagcaa	tagetgteat	aguguaggas	2 Skaakaaak	g atgagggtca	2880
tegeteated	cgagtatgac	gategetge	guiguacus	aggagaage	t cctccgtaag	2940
tagcttcaca	a ctcgcgccc	ggtctgagti	_ guidgeat	toggoggta	g agtatggcat	3000
gaccagcgt	g gcagccagat	tgctgccgc	. cccacggcci	. cogacgata	t cttcggaatg	3060
gagcggaac	g gcttcacggo	atgtttggat	L teetgtaet	s sacgaatee	g accggtgccg	3120
caatgatcc	c ggccggagag	g getttgete	acggatcaga	t coggedage	t cctgtaaggc	3180
tgtgggtgca	ttgccgagg	gaaaagagca	a toggggtgo	cctccacgg	c caggogtatg	3240
cctgctgcg	t togggtgat	g ccgtgacga	g cggccagtto	t tgccacgcg	c ggatatgcag	3300
atagcattt	g gcctccacao	ccagacgct	cagtgcccc	ttggaatac	c ggaggtaacc	3360
atggtcaca	t ctgtgacaai	t cgtgcgcag	cgccggctt	gatcatttc	a tacagagaag	2300

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ccaccggacc ggcatccgtg tgaggatatt ctccatgtcg aagtccgctg tggtatgaat
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ggcatggagc aagcccactt gtggtctaaa ggccaatcct gacggtgcag ctctttctca
                                                                       3480
tegtgeggaa actettgate ataateteet geeegatace tittggettga tetettette
                                                                       3540
ggggtagtag ccgcgagggg tgataaagtg cccttcgagc agtacgactg ggaattgcct
                                                                       3600
acgagtacca cagtgaacat atccacactt cgggatcgaa ttcgccgaga gtcgtcaccg
                                                                       3660
tcacctgctc ctcttcggcc tgcctgacgg acaagtccga cggcgtatcg gccgaacgat
                                                                       3720
actgatgaag atctctacga aacgatagag ctgccagtat cggcctcgct cttggattgt
                                                                       3780
atatagctgt gacgaagtcc gcgnaggctg ctgccactat gccttttcga tgatcggcca
                                                                       3840
aggggtcatc agatcgctca gcgagatcag gagaggtcgt gaccgatggg agcacccagc
                                                                       3900
agcgaagccg ctttctgaaa gcactgatac cgggcagcac ttcgatgtcc atctccacgc
                                                                       3960
ctttggctct ttcatttcat atataagagg agccataccg tagatgccgg catcgccgag
                                                                       4020
ctgatcacgc agaccgtctt gccgctgagg gcatacccga atgcttctcg gcacgctgcc
                                                                       4080
gctccttctt catgccggta tccacgcagt gggtatcgga cggagataag gttcgataaa
                                                                       4140
acggaaatag tatttatagc cgacgctacg tcggaccggc cgatagccga tagcactgca
                                                                       4200
ggagtaatat ccgagctcct cccggaccga tgccggctac gatgattcgt gctcgattca
                                                                       4260
tttactgaaa acaaatgaag gtattggaag aatggagatg gcgggcgaat aggtttgcct
                                                                       4320
gcgctcccca caaaagtaaa gaaataagac atgcagccat acgccccgac atcgatccga
                                                                       4380
tcgcgccaat gtctatagcc tgctgtcatg aaacacgaac caaaaatgcg ccgattgcgg
                                                                       4440
cgcgtgtttt ctgaaaaaag gcgcgagaaa ttgtttcgtt gtggcgtgag aatttttcat
                                                                       4500
tttcccgaca gaagcaaaaa attacgcgcc acgttttgag gaacgacgaa caccaaattc
                                                                       4560
cggcgcgtaa ccgatccctg tataagccga tgtgtcaatg ctttttgttt gagttcggta
                                                                       4620
tcggaagaga gtaatagtag tatcggatga ggtaagcttc ggatcgtcga tggggtgctg
                                                                       4680
aaaggatgag attcggggaa gggcaaaaaa ttgctctatc ggatgacaga ttccggtttg
                                                                       4740
ttctgcgtct cgtaataaag acctttgcaa cggaggtcct gtcccgatta cttaagcatg
                                                                      4800
gagtagaagc attcgcccat agcgtagccc ctttggcccc tcgactcaaa cagtggcata
                                                                      4860
tagcatcctc gacgacgagg aagctgcggc cgacgtgtcg aagaggctct gatgcgtctg
                                                                      4920
tggatcaacc gagagcggct gggcggatag acagcatcga agcagtggct gtgaccactg
                                                                      4980
ctcggcgaat agccttggta tgctccgcaa agaaggacgg atggaaccgc taccggacga
                                                                      5040
totgoottot cogatoatgo coctacacco caaggtgtac tggagcaatc cgagacatgo
                                                                      5100
gtctggtgga agctgctatc gaagcactgc ctccgttgca gcgaagactt tccggctgaa
                                                                      5160
agagatcgaa ggctacgaaa gcgaggtaat cgccggctcg taggcgtgaa agtcgaagcc
                                                                      5220
gtttatacca acttgagccg cgccgacgcg cactgcgtac agcactggct ctccaactca
                                                                      5280
aacgatgatg aacgaatagg gttcaacaaa aaagctgttc cgaccgaagc ggaaatcggc
                                                                      5340
cattgttaga taagtacttc gacgggctta cctccggagc agaagaggat gcctgcgtcg
                                                                      5400
ctattttgct acggccaagc tgcccgagca gtgggagcat tgcgcccct cttcggttat
                                                                      5460
gtcagttgca ggcgtgccgt ggatgggctt tcctttccta cactcggaaa cttgctaccc
                                                                      5520
gcaacttgct ctcaagagta tcctgtggag tgtaggagga gcctccgtag cagcagccat
                                                                      5580
cgctctacga tcgctctccg atcgcctcat gtggcggatc agccactgcc gactagggtt
                                                                      5640
ccttcgccgt ggtgaacggc gagcgtgtga acgatcccga tctgtgcgac tgtatgcaca
                                                                      5700
ggaagcette gatgetgtat ceategatag ggagagttgg cacaggaget tttegacett
                                                                      5760
tgacagatag atgagcgaat actaaatca
                                                                      5789
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1058 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...1058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282

actcatggaa a	ntaccaacta	tttooogata	gggcagggac	tcgacgtcat	actctaacag	60
cccgattgaa	atguigatig	++00000000	ttatotacag	tctatcatgt	agttcggctg	120
cccgattgaa (ccaatacatc	teegcagga	artectare	acatacgcac	ctaacaaggg	180
tagcagatte	aactattaga	tegettgaga	agccccgaco	ccatttattt	AGAAGGCCCC	240
attctcggct	ttcttagagg	aagcagagcc	acccaatatg	cegeceacee	ctctgactgt	300
1 - 1	~~~~++++	gaatatttac	cttattctt	acaccacaac	CCCCBGCCBC	360
++++000000	atattactat	catccattat	caatactaat	LCCLEBACAC	5 ca c c c 6 a a a	420
*+a++c3	a+++ac++a0	cgaccctgca	Ctaacattat	BECCCA CEE	~~66~66~~	
+	tacactacca	acaacaccat	tataagcagu	CCgataacaa	Caaaaaacgg	480
tggctgccta	nantaccoga	aaaaggagtt	ttgcatttta	ctaataatgg	ctccatacag	540
tcatgtccgg	aaacaccgga	rasataggra	atcappctaa	aatatccgag	agaccggtgc	600
tcatgtccgg	aggaactetg	gaaacaggca	tagtettega	ttaacaagca	ggtagagata	660
taaccccacc	tttattaccg	ttlacggcga	eggetteggt	catacccaaa	tttcatttt	720
gacaatatag	accgacttaa	cttgtttcta	cgcatteggt	tatgeteada	acataaacaa	780
acact at as	attracagte	ccccecteta	tacaacgaac	igialigigg	agacaagcaa	840
++ 00001+++	ccaatcgaag	tgacattatt	tcaaagaatt	gigacciaag	Cgcgaaaaca	
atatattaa	cagttcgggg	ataacggtat	tcaagcctat	ggiacaagii	CCaccaccac	900
-++-+-+	2220022202	ttaccgacaa	tcttttttg	cgacaggaaa	CCCCCCCC	960
catatcacaa	acaccaccac	ttaacagcaa	cctccaatgc	tgccatcaag	ttagacaata	1020
catatcacaa	acaceccage	ccaccagoat	agtraato		_	1058
ttcctgagtt	taccatticc	ggaataaaat	agreausg			

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 609 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...609
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283

ggccaacctg cagtgttaactttttctttt ttggaggattgccaacctgc agtgttaactacatcgtttt ggcgcagatgattgccgacagcga ttacttcacccgctcactgt ttttcttctgatgttcatt gcccgcaatgccctcttatgt gcccgcaat	attgtctctt tgttctgttt atatattttt ctcctgcttt cttgagaggt gctgcagccg tgttattgtt ttttatgtca	ttttgtttg caccctccag gagcaccatc ttctctttgg gcttacaagt agttgattgt atagctatac	ggggtttcct cccattagat ctctatttca tcttcgtctt ccgatccgga acgcggtctg ttgcctgtac caatgccgat	gattgccaag gtgccggcat tcgtccgttc ataatgatcc ccaatggttt aaatgggaag ttcctgacta	60 120 180 240 300 360 420 480 540
gatgiticati gitgcitiggi cctcttatgt gctccgcaat ttcctgtcgg aatgtgctta cgtgcagaa	. ttttatgtca	atagctatac	caatgeegat	LLCCLgacta	540 600 609

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 530 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...530
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284

		ccaatacggc				60
acgatacgca	gctgtcggta	agtctgtcgt	ctcagttgtc	ggtgatcaga	cggaatccgt	120
cttcgttgtg	tccggtatcg	catacgaccg	tggctgctcg	gccaactgct	gccaacggcc	180
aaacagccct	gacattccgt	aacgtgggca	aatccttcac	ggacgtgttc	cgaagaaaga	240
ttcagccgca	tcgtttggaa	aggacctcca	cggcacagag	aatcgtacgc	gcgtctcctc	300
ctgagccaag	ccggtcagtt	cgccacgaac	cgatccatag	tccgtgtttg	gtatgtatag	360
caaccgtttt	ctaatgtcga	ggaaatgatt	accccgattc	ttgagcaaag	acaatatccg	420
ttctttcctc	atcggctttg	tctgaaaggc	atggcgcaca	cctcctcggc	tcggccgacc	480
acaacgggga	tccggacttg	atgatcccgg	ccttttcgaa	gctatcttct		530

- (2) INFORMATION FOR SEQ ID NO:1285
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 712 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...712
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285

ggcggcaggc	atccccacgg	gcgcatcgct	cggcaggacg	atagtcccgc	attcgacgag	60
cctacaccga	tttccacttc	ggagcaaatc	attccgaact	ctccactccg	cgaatcttgg	120
atttcttgat	ggcaaactct	tcttctcgtg	atagagcgtg	gtgcccaccg	ttgccactac	180
caccttttgt	cctgcaccac	attgggcgca	ccgcagacga	tttgcaaagg	cgcatccgcc	240
cccactctac	cgtggtgata	tgcaaatgat	ccgaattcgg	gtgttcctca	caagcagaac	300
atggccgatg	accaaacctc	gcaagcctcc	ccgaatcgtt	tcgtctcttc	tacaccgccg	360
gtctccagac	cgatggaagt	gagcgtgtcg	gcatctcttg	cggagagagg	gtgcagggca	420

		ttgagatatt	catctttgtt	actccttagt	tgtatatgtg	480
ggtactccaa	gagecatteg	ctgagacacc	casttattat	atotaagccc	acaaatttac	540
cttcagagac	catgggtcag	gicicaaacg	cgactactac	teatttaccc	ctccgagtgc	600
gtttttctcg	gggagtgttt	gttttatgtt	Cglcllgcgc	cggtttgccc	ctccgagtgc	660
tctgcttttc	gttctcccaa	agattctggc	tttcctttcc	ggtttggaaa	aaattcggtt	712
gtatttcngg	cctgtaaaac	gtggttttga	ggaaatattt	tttggttttg	gc	112

- (2) INFORMATION FOR SEQ ID NO:1286
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...527
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286

tgctttctcc	tetgaaaaca	cagttagagc	aacaagtcaa	ttggagttca	ccgtcttcgg	60
ctcttatggc	natagogagt	tetttateaa	cottttctcg	gattcctcat	attggcaggg	120
ctcttatggc	agragegage	t t = = = t t = =	******	atcongcagt	ttgatgcttt	180
atcatcctgg	accgcatggg	cgtgcgttca	Cigocaliti	accegeage	costoccoto	240
tgggtgccct	tattaagtat	atgccttgag	tgaagtcttc	aatggcggcg	getteggeta	
cgatagetea	attccttttc	tatgggtttc	ccgccatctg	ccaagctggc	ctgttcggtt	300
ttgctatttt	caastataac	totoaaatee	ccggcgtaac	cgttcccgtg	ctatcgtgaa	360
Ligitatici	CBBacacac	+ a c c t t t c c c	cannactta	agatogrtat	tecccettte	420
gtggttccat	ggcaaagagt	rggctttggc	Cagggacce	agacggccac	tgcccgtttg	480
ggagtcttcg	ccgtgttctg	gcttcaccta	tcatttcaaa	gcagttcgaa	ggtacgcttc	
agagcgttca	gtaccggtta	tttccgttac	ggcactcctt	tcatcgg		527

- (2) INFORMATION FOR SEQ ID NO:1287
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1613 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287

gcaaaagtct	cggtctgtaa	aatcaattct	atcaactcga	cacccatcaa	cgaaatgcaa	60
tgaaatatgc	acttcatccc	ctgtatgaat	caggttttt	catcttcttt	attgaaaagc	120
aagaatcaaa	attcgatcgc	cgtctctctt	gatcattcaa	gttcttcttt	ctacggcaat	180
			gaaaatgagt			240
ctcttctttg	ttcttgcatg	ccgaaaatga	cagaggttgg	caagcaaaac	ccgtcgacac	300
tgtaaattaa	atacttacct	ttgcaatagt	gacattaaaa	acataaagca	cagaaacaaa	360
tagcaaatct	gaaatgaaag	aatttttcaa	aagtttttcg	cctcgatcct	cggggttata	420
acggcaggaa	tcatcttgtt	cgtatctttc	tatttatctt	tttcggcatc	gtagccggta	480
ttgcctccaa	gcaacgggag	gaaccattcc	gaagatcgaa	gcaaactcca	tcctacataa	540
gacaattctt	ctttccctga	gatcgtatcg	gccaatccct	ggagcatgtc	acaggcaaag	600
acgagtccgt	atcgctctca	caggcagtcg	aagccatggc	caagccaaaa	ataatcccaa	660
cataaccggt	atcttcctcg	atctggcaac	ctttccgtcg	gtatggcatc	ggcagaggaa	720
ttgcgtcgcg	cgttgaggat	ttcaagatgt	cgggcaagtt	cgtcgtatcc	tatgccgaca	780
			tattgcagac			840
			caaacaatgt			900
			tggcacctac			960
			gaacaaatca			1020
			cgcgcaagac			1080
			tgccgagaaa			1140
			aaagaatcaa			1200
			tcaggttctg			1260
			gccgaaggtg			1320
ataaangccg	ttcgacactg	acggtagctc	catcacacaa	gaactcgcca	aaaaatcaag	1380
			gtagtacttc			1440
			ggtagccgat			1500
			ggcggatact			1560
agtatcgtgc	agagcatacg	actctgaccg	gcttcatcgg	catattcggc	atg	1613

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 747 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...7\overline{47}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288

taatcaccgg	agccacatcc	ggcatcggtg	cagcttcggc	tcgccgcttg	catcgctcga	60
ttataacctt	atcatcacgg	gacgacgctc	cgaacgttgc	aaaacattgc	cgatgaaatc	120
agagctgaat	accctgtcga	aatcctccgc	tctctttcga	tgtccgcaat	cgcgaagaag	180
tagaagccca	tttgggaatt	tgcctgatcc	ttggcaggcc	gtttccgtcc	tcgtgaataa	240
tgccgcttgg	cagcgggact	cgaccccata	cagtccggtg	acattgaaga	ctggaacgta	300
tgatagacac	caatatcaaa	ggactcctct	acgtaactcg	cacatcagcc	cgggtatgat	360
agcccgaagc	gccggccata	tcatcaatat	cggtctattg	ccggcaagga	agtttactct	420
aacggcaatg	tctattgtgc	ccgaagcatg	ccgtagatgc	tctttcgaaa	gcgatgcgta	480

tagatatact	ccttatooca	tcaaagtcac	acagatttgt	cccggagcag	tggagacggg	540
tagatatget	tanacttana	toatoatcao	оссановсей	atecceteac	aagggcttca	600
ttetegetgg	tereseases	atancagant	gtattgcgcc	gtactgaacc	tgcctgataa	660
ctcctctctg	tgcgaacgac	atageggage	gracegegee	Personense	acttttcaaa	720
			aagegeagee	ggcagcagac	acttttcaaa	747
caagttgatc	acaaaaggcc	aaacgat				, 4,

- (2) INFORMATION FOR SEQ ID NO:1289
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 670 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...670
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289

atoatoraoo	aceceattet	cggctgtttc	ttgctccctg	catgatgcag	acgcgattgt	60
acgatatttc	ttactcccta	catoatocao	paceceatet	cggctgtttc	ttgcttcctg	120
Cggctgtttt	Ligities	targatette	ttacttccta	cacoatocao	pacocoatto	180
cacgatgcag	gacgcgattg	Cagolgile	Ligiticity	cacgatgcag	attactteet	240
tcagctgatt	cttgctcctg	cacgatgcag	gacgcgattg	tcagttgatt	Citgottect	7 3 3
gcacgtgcag	gacgcgattg	tcggctgatt	cttgcttcct	gcacgatgca	ggaccgattg	300
tcagctgatt	ctgctcccat	caatgcgcta	actatcagct	attgcaacta	ttttatagga	360
cttttattga	agtettttge	cgcagagctg	atcttaagtg	tttttcagat	tacttgaggt	420
tteesesses	atcacatasa	atrtcctttc	ttcgtcaaat	caatgcttgt	gtctgtcttg	480
ttgcagagag	accecaceaa	gettettete	caacagtete	aaaatotoaa	gacgctcgga	540
atcgatatga	gaggtgggaa	ggitatigig	Caacageeee	aaaatgtgaa	64666666	600
tcggtcaaat	gtttcgacac	gattactgat	ttttgacctt	tctgagtaca	actitities	
gtacacatca	gaaatgatgg	tgtacagatc	ggatgaaagc	cgtttgccga	ttgtggtagc	660
tttcagccgt						670
CCCCGGCCG						

- (2) INFORMATION FOR SEQ ID NO:1290
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2736 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...2736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290

```
aaaagagacg acaaaaatta ctgcaatacg cataattgat ttatggctta aaaaggggtt
                                                                         60
gttgatgtac attccgtact atgggcgcaa agataatcca atcccaattt tgccgacctc
                                                                        120
taaaacgctt tgagaatgat atttattatg acgttttgga agcttcttcg atcaggagag
                                                                        180
gattgcggtc aggcgtttgc gaggttgtgt ttgacgggcg gaaaatgccg agtggttttt
                                                                        240
gttaatttgt tcatcctcaa tcattaacag cttcgcttat gaaaaagata ttatgacggt
                                                                        300
gatcctcatt tgtattttat cctctttcgg tgtggcgcaa gtggagtgcc acgaatcgat
                                                                        360
gatatgagag gaatgcgtat ggacaccgtg tcaagaaaat aaaggattat gcacaacggc
                                                                        420
ggttctttta taaggtggtt ttgtggaaga taccctgaag cgagaaaaga aaaccgaggc
                                                                        480
gcagtgtgtg tggagatcgg acggcacggc agcagcttca aggatttgta tcagttagct
                                                                        540
gggattettt gaacgatgee gttaceegge gaaaaggtte gatgatggge tatteaetga
                                                                        600
gggtgccggg ttggtgaaaa agataaagtg gagaatatcc tgctgaaagg gtatcctgaa
                                                                        660
ggagcggacc ggcatcaaca agaggtccat tgacaggtcg gtatgagtat gaatgtccgt
                                                                        720
cgccgtcttt cgattgcaga tcggggaaga gaccgaagag atcatggaat acacttgccg
                                                                        780
aaagccacct gccaccacag cggacgggat tatacggctt ggtatacccg aggtattgcc
                                                                        840
ctctcggatg ggcncgtaca tttttcgggg attgcccggc ctattgtggc catcgcttcg
                                                                        900
gatgatgggg aatatgcatt cgaacttaat gaatgcaggg ggagattact ttcccctcac
                                                                       960
ctatatttct gtacgacaaa aggtgcaaaa gtattcgcgc gaagaagtac gcaagattat
                                                                      1020
ccgaaacatt cggagaatta ttccgagacc atcatcaatc agggaagatt caggcttaga
                                                                      1080
atccggagga tattcagcgt atcagaaatt tgccgtacaa tcccttgaga aagaatgaaa
                                                                      1140
acaaataaaa cactcagcat gaaaaggaca cttttgtcct cgcatcctgc ttttttatga
                                                                      1200
gtatgagctt catacaggca caggtccacg tatcgtgggc gcagaaggga tgccggtaga
                                                                      1260
tactgtgccc aagaggtgga ggactatacc aaacggcgat ttttttacaa agtctctttt
                                                                      1320
gtgaagatac cacgaggcga gacaaagaaa cccaagcaca gtgtgtattg gaatagggca
                                                                      1380
gcgagggagt tgcttcaaag acttttacga gtatgcagcg gctcggtgaa tgatgccgta
                                                                      1440
gctcggaaga aagggactgc tatggagatc tttcgaaagc ttatgattac gtcaagaaga
                                                                      1500
cccaatggcg gactcccgtc ttaaaggcta tccatcggga caagattatc atcaatacgg
                                                                      1560
agateegaag teggttetta tgaataeggt tgteegtege egtetttega ttggeagteg
                                                                      1620
gggaagagac caaggagatc atggaataca cttgccgaaa ggccactgcc accacaggg
                                                                      1680
acgggattat actgcttggt atgccgagga tattgcctct cggatgggcc gtacatttt
                                                                      1740
eggggattge eeggeetgat egteetateg gtteggatga eggagagtae gtattegaat
                                                                      1800
tgaacggaat gcagagatta catttccgtc tccgatttat ctcaagaaaa atgcctttac
                                                                      1860
gaagtoggot ogogtgaaga gatgogoaaa acgattogta atatooacga gattatgoog
                                                                      1920
aagtcgtggc caattcgccg gcttttgtca attccccgat ccggtagact tttctcatct
                                                                      1980
gccacctcag ccgtttaatc cattggaggg gaataaagca tgatgaatag ggctgtcact
                                                                      2040
tcgattttgg cgtatttggg ctgtgcgtgg cggggctgtt gcctgtcgtt gctcaggaag
                                                                      2100
cgaccggcaa atgcttgccg gtcgtgtgat agatgccgag agccaggagc ctcttgcggg
                                                                      2160
gcagtgtgcc aactcatgga tgcctccggc aaaccgcttg ccttctcctc tcgaaagccg
                                                                      2220
acggctcgtt ctctctggag aaaaaagccg gcggaaactc cttagcgtaa gatatatggg
                                                                      2280
gtataggaag atgagcaaag ccacgatgcg gctgctcctc cgctgctttt cgctttggtg
                                                                      2340
ccgtccgacg tcagctcaag gaagtggtgg tacgcgccga accggtacgc aagctgggag
                                                                      2400
aacgattgcc tattcggctg cggctttcgt ggggccggac gatcggtatc ggccgatctg
                                                                      2460
ctgcgcaaat tgccgggaat agaggtctcg gcaaacggct cgtcaaatat cagggcgaac
                                                                      2520
ctatcacaca tatgtatatc gaaggcgtga catgctgcaa aaccgctaca atctggcctc
                                                                      2580
ccggaacatg cctcaagggc ggtgaaaaca gtggaggtgt tggaggggca tcagcacatc
                                                                      2640
aaaacgtgcg ggagacagtg ccggagaaaa gggctgcact caatatcaaa ctccaagaac
                                                                      2700
gcttccaagg tgcgtccctt ccngaanaag ttaacg
                                                                      2736
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 830 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...830
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291

```
gtggtcgatg ataacaaaca tgtactgacg gctttgaaat tgctcctgag gggagtttcg
                                                                        60
agaccgtgac gctcctacct tcccccaaga cactgcttcc acgatcgtag aggtgcatcc
                                                                       120
ggatgtactc ctgctggata tgaattttct accggcatca atacgggtaa tgaaggatta
                                                                       180
tattggctgg atcaggccgt agccgtttcc ctgacctccc tgtggtactc tttaccgctt
                                                                       240
atgcgacatt cgtctggcag tggaagcctt gaagcgtgga gcaagcgatt tcgtgtcaag
                                                                       300
ccgtggaaca acaccgagct gttggagtcg cttcgcatgg cgagaataag gccgcaagca
                                                                       360
ctcaagtgac ggctacacct aaagaaggcg atcggtattt ctcagcaaaa gcaaggccat
                                                                       420
gtgtgaggtg ttggagctgg cggtcgtatc ggcgatactg cagcccatgt cctcattacg
                                                                       480
                                                                       540
ggtgagaatg taccggcaag ggcgttttag ccgagtatat ccatgcccgt tctcctcgtg
ccggcagccg atgctgactg tggatatggg agctttgagc gagacgcttt cgagagcgaa
                                                                       600
ctgttcggcc atgtgaaagg agcctttacc gatgccaaag cgatcgcgcc ggcaagttcg
                                                                       660
agacggcgtc cggcggcacg atcttctgga cgagattggc aatctgagcc ttgccttgca
                                                                       720
agccaagttg ttggcgtact acagcaaaaa gtggtgaccc gtgtgggcag caatacaccg
                                                                       780
                                                                       830
atcctgtgga tgttcgtgtc atctctgcca cgaatagcga tttgcccttc
```

- (2) INFORMATION FOR SEQ ID NO:1292
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2389
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292

acggatcgta ag	равассара	tttgaaagaa	ttgatcatca	accgacttgt	accgaaacct	60
cttcgtccgt to	atececcac	atatctcggg	tgacaaaaga	atcattcggt	tatccggatg	120
gaccaccgct g	aaaaagccc	ttatcgtctt	tttctctttc	tcgtcaatgc	tctctttcaa	180
tacaaatcaa t	gagttaata	ccgttggtaa	atcaatgtcc	ggcatatctc	accccaagga	240
gattgcgaag a	aagaggaaa	aaagcagcag	atctgtaagc	cgggttctgt	actccggcca	300
cacgtagcca g	agcgtctgt	catttatctt	ggccgtgcgt	cacgcatggc	tccagcgatc	360
tacccccgg c	atcgggcga	gccaccctac	atcgccggta	tacatgatct	tacaacccat	420
cagacgtacg g	catgcagcg	taccgctgca	tccggtaggc	tcttacccca	ccttctcacc	480
cttaccctcc c	gtagtccgt	accgaagcac	agacaactca	tggaaaatgg	cggtcattcc	540

```
ttctacgctc ctttaccctc acgagtaact tcctgttagg aaggatgggc tctgcgttgc
                                                                       600
coggacetto otoccactot ogaaagagte agogacaaco gatoteote taatottito
                                                                       660
tttcgtcttc tatatcttat ctatgtccac ctctacgacc ttggtcggat caagatgttc
                                                                       720
attgcgatag tccactgctc taccactcgg gcagccaatt cgcggaaagc aattcccatc
                                                                       780
atogatoato cogaacagoa acgggtatto ottogtocco gotttggcat atacotgcac
                                                                       840
cagoggaato tgtoogagca agggaatatt caactootog gcaaattott acogcoatoa
                                                                       900
cgcccgaaga tgtagtattt gttctgtggc attcggccgg tgtgaaccac gacatgtttt
                                                                       960
ccaccaaacc gagtaccggc cattgatctt ctctccgaca aacatactga ttcctttccg
                                                                      1020
agcatcagca aggctacgtc ctgcggtgtc gtcactacaa cggctccggt aatagccacg
                                                                      1080
tctgtacaag tgtcaggtgg atgtcgctcg ttcccggagg catatcgtca ggaagtagtc
                                                                      1140
caactetece caattggcat cgcggataag ctgtgtaggg cattgcctge catacttecg
                                                                      1200
cgccagagaa cagcattgtc cggatcacga agaatccgat agagaggatt ttcacgccca
                                                                      1260
tcacctcttc gggacgatca attcgcgtcc gtccacttct tcaagtacgg gacgtgactc
                                                                      1320
ttccagtgga acatcttagg catagatggg ccgaatatgt cggcgtccaa aatcctaccc
                                                                      1380
gatagccgga tttggccaga gagacggcca gattagccgt acggtactct tcccgacacc
                                                                      1440
gcctttgcct gagaaaacag caatgatatt ttcaccccgg gcagaagttt ggccggagga
                                                                      1500
gcaggtattg cctgtttgcc ttgacagaga tattgccttt gatattgacg tcttcgctga
                                                                      1560
tatatgtcgg atggctgatt cagctgcttt gaccactgat ttgatgaatg gatcgttgct
                                                                      1620
ttgtcgaata tgagtgaaaa cgatacctta ttgccatcga ttctgaatcg tcctctacca
                                                                      1680
ttccggccga aaccaaatct tttcctgtcc ccggaagcga actttaccaa gggcttcgag
                                                                      1740
aataagattg ggatataatg ttactatgcc atgttctgag taggttattt attaggaagg
                                                                      1800
aactgcctga cttttctgga gcgattgtaa ctgcggtagc tgtcaggttc gatttcaata
                                                                      1860
toggttotog atactogoag toaggttoto coaagcoaaa gotgatgtac tgatogtoag
                                                                      1920
acctcgttcc agccactgtt gttcgtaata tgttcggatg cgaggatttc attctctacg
                                                                      1980
catcetttge egtacagate atcegttatt egtgtaeggg eaggeegttg agttegacea
                                                                      2040
acgcettegt ataggtatga ggaaaggget ateegtttte agatggatae gteeceeet
                                                                      2100
ttcgagtctt tgtcatagag cgagaggaac cgcgttccgg tcagtcgctt gcctacttct
                                                                      2160
                                                                      2220
tcatctgcgg atcggggaaa gtgatccata tttcggctac ctctcttcgg caaagaaccg
atccaaaagc tctatatccg tccgaaggaa agctcgttgg acatcccttc ttgaagagac
                                                                      2280
tetttggeac eggeceacat geggeteett tgatgtegat geegataaaa ttttteteeg
                                                                      2340
gaaaccgttt gccagaacct accgtatatt cttccttctt ccggaaccc
                                                                      2389
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 738 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...738
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293

```
cttatgggaa tcctccgaa tcatagttc cgaggagaaa agaacattat cattgccggg 60 gattaatacc tgcgatttat agcgagtctg ccggcattca atcttcctct ttaggatctt 120 acatcacatg tcacgttgca gaaattttgc atttgtggtt tctaaaaacg tggcgcgtaa 180 acttttcat tttggccgag aagtaaaaaa atctcgagcc aaaacgaaaa aaatcatgcg 240 ccacttattc cataaaatcg aaccgaaatc aaagtgtttt aggctcgtac tccgagacag 300 tagttcacaa gcatacagga gaatagcatt gatgtggaat caagtatctc aatattgaga 360
```

gcgttcgatc	ggtcaaaaga	aacactctat	ctccaaaatt	caaatttaca	tcggtttatt	420
				agcaaattgc		480
aaaaggataa	aggattagtc	tggttgcatt	tttttattta	gttttgtggc	tgtccgtata	540
tagagcagtt	gtggaagttt	cgtgacttgt	gtctaaggcc	ggtagcggtt	tttgagactt	600
				atancagtaa		660
tttaacgcat	aagaaaagtc	tatgaaagaa	tgacgctatt	cttcctttgc	ttgctgacga	720
catteeteee		, ,				738

- (2) INFORMATION FOR SEQ ID NO:1294
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...386
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294

atcgtatcat	tcctaatcta	ccggatagga	atacttttct	tctgaaccga	taagcccata	60
gatatgatac	agaatatcct	cacagccata	acgggtatgt	cgtcctcggc	ctgattattt	120
atcgtttggt	tcgtctctgg	aagcgaaaga	ttcgggtgga	gcatgctccg	gttgttcatc	180
		ttccaaggcg				240
		aggacggcaa				300
tctctatcct	cattattta	ttgatagtct	ttgctctaat	accgcttggt	acaacggcat	360
gtgggttttg	gtagctgcct	tgtggg				386

- (2) INFORMATION FOR SEQ ID NO:1295
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 943 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295

```
aattggagaa tagtgctgca gcagcagtga agcctttacg gacagatcca tggaagggca
                                                                        60
gattcaatta caaaagacca agcgcgaatt caaaggaccc tgactttggt ggttttccct
                                                                       120
tttgtcaaga agtctcgaaa aagtcccaag cgactgccac ggaaatagga gaatggttgc
                                                                       180
ttgcaaacga gtcggcgtat ctgccatcga agtggtaaag ggctttctca atctgaccat
                                                                       240
tgctcgaggg tatggttgga gctgctgaac gagatccgag cggatatcaa cttcgacata
                                                                       300
aggtcgctac agaggatagc ccgctggtaa tggtggagta ttctctccga ataccaataa
                                                                       360
gccgttacac cttggacacg tacgtaacaa ccattgggtt atagtctttc cgagatcatg
                                                                       420
aaagccaatg gctatcgtgt gtgaagacta atatcgtaaa tgaccgaggc attcatatct
                                                                       480
gtaagtccat ctcgcttggc aaaagtgggg agatggtgtg acgccggaga aggccggtag
                                                                       540
aaaggcgatc atctgatcgg agacttctat gtccttttcg ataagcacac aaagccgaac
                                                                       600
tcaattccct tatggctgaa ggtaagagca aagaagagcc gaagccgcaa gcaccctcat
                                                                       660
ggctgaagct cgtgagatgc tacgatgtgg gaggcaggag acgaaaaggt cgtcgatctc
                                                                       720
tggcgtacta tgaatagtgg gtatacgacg gattcgatgc cacatacaag atgatgggtg
                                                                       780
tagattcgac aagatatact atgaatccga gacctatctc gtcggcaagg aagagtgctg
                                                                       840
aggggtttgg aggaaggctt tgtttgtcaa gcattccgat ggttctgtat gggcggatct
                                                                       900
tgacaaagga tggcttggat gaaaaatgct ttgcgtgccg atg
                                                                       943
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2483
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296

```
tgagttgagc ggagagaatc acccgatcaa actccgnacg tgtctggtat tatacccgat
                                                                        60
cttccattcc gtggatgccc gtagccgccg gcgcgtttgt cagaaatgaa tgggaagagg
                                                                       120
agacgaggga aacggagcga gctttccccc catattccat gaagctgtgc gaacccttgc
                                                                       180
gaatggette gtaageceet tgagtttgat attgaacate teegeceeae gaaacaaatt
                                                                       240
gcgatggtga aaccgagaga caaagccgcc ccgaagtctc cagcggaatt ggtgcgagga
                                                                       300
cttcggcttc gaacgatttg ctcttggccg gaacggtaag aattagcagt ccacaaggcg
                                                                       360
agagetatee gecagageaa teteateett acattgtget ecacaaateg gatatteaeg
                                                                       420
ttccgaacga tagggagcgc atcagcttga tataagagcg ttccacatca tcctcgcaga
                                                                       480
aaaaagctcc ggtgtaacgg acaccgaccg cgtgagagcc gatgcccgga tataacgtcc
                                                                       540
ctactcccat agtaaacagt gtaatcgcca cgcgaaatcg aatcgatagt ggcagctcct
                                                                       600
gaactctgaa gtccgattcg agaggatcat aatcgggatg aaagaatacc ctgccgatcc
                                                                       660
gatatggata acgcccgatg ccattgccac taatttcaga tcggcagatt tcgtacccga
                                                                       720
tcctcctgaa acggtgtatc tgcttcataa taaacatcct cggcggagaa cttccagaag
                                                                       780
ccgtgttgcg catatgacga gctatcgcct ttctcttc atcgagtacg atggcgacaa
                                                                       840
gggagaaccc tcgctgatcc cgaccttgta tgccgaagga aggaattgcc aagcgcaacg
                                                                       900
ggaggaagga gtggattctt cacatccaaa gcatattgcg tatataataa cggcttccgg
                                                                       960
gctgaatcag ataagtaatg gagctttctt gtacaagccg gtgtctacca cggcacgagc
                                                                      1020
agtagcatca gaaagccatc gccggccatc gcctttgcca gacggttggc agtacgatgg
                                                                      1080
tgaggacaga atcgatgagg acaggcggtt cgcccatttt ccggagcaac ggttccacca
                                                                      1140
```

agtotgtaat cogtttcgct gacgagcagg cggaatgcga acgccaactg tgtgcttgag gatgctctca cccaccggag aatatgcata cttcttcaga gtatgccacg aacgacgaga gtcaattccg atgtcacg	tgggttgctg tgcgtcgtta aggaagcaag ggacatagga cacaacgcct cgcgatgcag cctataccct tggcattgac cacaccggga gcgcgcatca gcttcggatc tgggacgac tcgggacgac cctacccgtg	gagggatagic coctgtctaa catgaggagc aaacggatat gtatgagcag aagatcgttt cgaacggaat gatcagcttg gccgaaggct agctccaggc gaaagcgct atccgatca agagggag agaggggag	tagtctgcta aagcagccgg acggggagag atctccaatc cctgcggatt agacggacat tgccgttcga tgcgatgacc gcccacccg tatcggcaaa acgttctacc agatagcgca gagcgaaagc ttgattccct	agactcttca ccgtcttgaa	cataacgggt taataccgaa cgttccagat agaagccc tcataacaga gtggataata gtcagatccg ctattcccat gagagcttgc tcggtattat tacggctccg ttgtacggcg gttgggagag tttggcgttg	1200 1260 1320 1380 1440 1500 1560 1620 1680 1740 1800 1920 1980 2040 2100 2160
aatatgcata cttcttcaga gtatgccacg aacgacgaga gtcaattccg atgtcacgtt cgactccaga aagaattggc agtcccatat cgacagagag aagataggta gaagcataga tatcagagga	cacaccggga gcgcgcatca gcttcggatc tggggacgac cttcctcgtc gaacccctga gggaaaagtc agacagcgaa aaacggttgc catcaggtcc	gccgaaggcg cagcagagct agctccaggc gaaagcgcgc tatccgatcc agagagggag gtagacggca tgagccagtc cacctccaac gccagttctt catctgtgac tgagcacacg	gccccacccg tatcggcaaa acgttctacc agatagcgca gagcgaaagc ttgattccct gatagccgat gaaaggctac cccgtgaggc aggaaacgac	atcccaagac gcctttcaca cgaatcgtat cacctccact agactcttca ccgtcttgaa cagaccgtac gataaacgct atggctgcta cgacaaccgg	gagagettge teggtattat taeggeteeg ttgtaeggeg	1800 1860 1920 1980 2040

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...187
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297

ggcgatgatt tgtgccggac gtcggtgtga gttcgcttgc tcagcaactt ggcttgctga ctataga	accostooto	CEEECATCLL	gacticgicg	accacguate	
--	------------	------------	------------	------------	--

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 915 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...915
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298

```
agcgcaatct gaatacggac atcaaggtag accccaacgc cgtagtgata tatcgaaaga
                                                                        60
cacggettte gtagacgaaa geggeaatat cateagegaa ceattaegeg teegettage
                                                                       120
agcgaatacg attitctcaa cacatactcg taccgatcta tcccgatgag acctgctggg
                                                                       180
taaatgattt ccccaagctc gtaccgagat ttatacgaga atgtatttca atcacccggg
                                                                       240
ctacgtgatt atcccgtagt aggtatttca tgggaacagg ctcaggcgtt ctgtcgtggc
                                                                       300
ggtcggaatt cttccgcaaa ggtattcgct tgcctgaagg acaatcatgg acgacttccg
                                                                       360
tctgcccact gaagccgaat gggaatatgc tgccgaatgg gcgattccaa caataaatat
                                                                       420
ccctggagta ccgaagactt gggacaggac ggggttgttt cttgggcaac ttcaagcccg
                                                                       480
gggagggaga tatacggctg acggtcattt gataccgtcc cgcgtatcca gtttttcgcc
                                                                       540
aatgacttcg gcttgtacga tatggcgggc aatgtggccg aatggaccgc acggcatttt
                                                                       600
cggagtccgg actcaaacaa atgtcggaca tcaatccgaa ctggaataca aagctgcgct
                                                                       660
cacggatccg tacatcctga agcaaaggta gtacgcggtg gttcgtggaa agatgtggcc
                                                                       720
cgcttcatcc gctcgctact cgtagccatg aataccagaa cgtaggtcgt tcctatatcg
                                                                       780
gattcgttgt gtaccgtact tccattgcct tctcttccgg aaaggctcct taaagttcgc
                                                                       840
gtcgcaagca caaaggaaat aagtattcgc ccaatctata ttaaaacaag gaaaaacaag
                                                                       900
tattatgggt catta
                                                                       915
```

- (2) INFORMATION FOR SEQ ID NO:1299
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 969 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...969
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299

ggtcatactc	cagtttcgac	cactacaaaa	accetetana	attttanaat	caggttggtc	60
						60
					tgctgaagcc	120
ggctcccaca	ctggtcagta	cgacgagatg	aagatacccc	aaaatacacc	gaaggctgtg	180
gccagactgc	gtctgcattg	ctgtagatcg	tatgccagat	ctctatccaa	cgatctctat	240
cgaaaatctc	atagtctcct	ttctcctcct	tcgtttagtt	tçtcatcgcc	tccacgcggg	300
gattcgtacg	gctttgcggg	cgggttggta	tcctgctatg	gcacgcttac	taccatgact	360

atcagagcta	a+ accesst	actenanten	atctcggatc	gcggaagagt	gtcagcgtta	420
atcagagcta	atagggtagt	gcccaggccg	accessare	6-666-6-		480
ttccttctac	ctgtctgctc	cgacaccggt	ggtctgtacc	caatgcgata	cgaactccat	
cagaccaacg	cggccaccaa	gcctatcagt	ccggaaaaca	gtgtgaccac	taccgcctcg	540
tcagaatcat	gttgatgata	gctcttggct	tggctcccag	tgctttgcaa	tgcctatttc	600
gcgctgtctt	tcattgacgg	tcacttgcat	gatattgcca	ctccgataat	tccgatgaca	660
agggtgctca	acccgataat	ccaaagaaaa	catccatgcc	attgaatatc	ttgtccatca	720
+++++atatc	cotcacopto	catcgacata	gggcacttcc	atatcggtag	gatcatagcc	780
cttaggaagg	ccagttggcg	attoactact	actttgagtc	tctcacgttc	tctagttcgc	840
CLIEBRAARE	CCABCCBBCB	4006-60-6-		0++00000000	atacctanat	900
acagacggca	gttcatgaca	gtgtgcagtc	cagacigaac	CCCggcgaaa	atacctggat	
aggtgggaa	aggattagtt	gggctgaatg	cctgtcgcct	tgcaacgcta	cacgaggaac	960
	4664554655	88880	0 0	•		969
ggatttgga						,,,,

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1267
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300

```
aagtootoog gagooactto atatatgott aagtootooa tottgtogag togaatgota
                                                                        60
                                                                       120
taatagcctt gagcaaatac tccggataga tgtccatcgg aaaacgcggt catactcgtt
                                                                       180
gctcatgatc atagcacgtt cgccaccttg atccgggcat cgagtacgta ctctttgttt
                                                                       240
ttcccctgca accaaggaaa taagctctgc tcatgctgta ctgatcgaga cggggtgcag
                                                                       300
cccaccgaag agttcgtcca catcgtcgcc ttcggggatc accgtgatct ggtccaccgg
                                                                       360
gctgacagga aaggctcctt ctcgcagagc ttcttaccgg tcacacattg ccatcgatca
                                                                       420
cacgctcgtg agattccttt attgtcagtc ggcggggaag gaagcaaaga cattgcaacc
cggcataata cggacgtatc ctgagctgca gcgtctgagc cggtcatggc aatcattctg
                                                                       480
                                                                       540
gtaaaatcgg tttgcccgta agcaggaaac gtccgatcac gatcaggtcg gtagccttgg
                                                                       600
cgtccacacc gtttcgcccc gattgattgg cttcgtatga ttgatcagac gcccacgtta
                                                                       660
cctgccggat gaggtccgtg tacttctacg atttctgatt gtgcaagccc anagatgaac
                                                                       720
coggetteag geceacatae acetteetgt egtgagtttg gecaaggeat egatggeagt
                                                                       780
ctgcagggcg cgttctctcc tcgaacgatg aaatcgaagt ccggagccaa tggtgcagta
                                                                       840
aagtggcagt aatataaatg tcgcgtggag ctatatccgg tgtagccact atgcgtaagg
                                                                       900
acgttgctta ataaaacccc acataccgct cgacagtaaa agtccttgat ctgttcggca
                                                                       960
gagagggcag acggatcccc gacagggaat gctcgtattc gttcagtccg tccggtttca
                                                                      1020
cctcgatgct caacaccttg gcttggcacc gcgattcacc gcgatcactt cgccgctaac
cggacttgta acttcatctc cggatatgcc ttgtggtgca tcaagtgctg agccggcagc
                                                                      1080
accttatccc ccggacgagc cgtcaccttg gggataacac cttcaaatcg tcgggcacga
                                                                      1140
ccgcgtaagt aggactttgg gcccggttcg gncagctctc gggcagcggt tttcctttca
                                                                      1200
gattaagtgc aagggctttt tttggtttta taacttttgn catgacacag aattattatt
                                                                      1260
                                                                      1267
tccattt
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 793 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...793
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301

cgacaaagaa	ttaagaaggc	gattgactac	aaagttgatt	gcctttttt	tgatgactgg	60
ctcaggcgtc	aaatcacgaa	agcaaaagag	gctgtcccat	agagtcaggg	ggcagcctct	120
tcaggatcag	tatattttgt	gtctctgtta	ttcgggacga	gagcaacggc	tatagaatgt	180
gagttcttcc	ggacggaagc	gcgcacgtag	ctgtcgatct	tctcctgctc	agcctgaccg	240
taacgagata	tacctctgcc	gactgacgga	atgaatcgtc	gtcattggca	gccacatcag	300
cagatggccg	aagactgcat	gagcagtcat	ctctacaagc	cgagtgcttg	gaaatcgagc	360
agctcctggt	ctttctgttc	tgttacgaat	gcatcagtgc	ttcggcacgg	tcggtcatac	420
gagccagagc	ctctttcatc	gttgcaactc	tggcttaact	tctgtctgct	ggtactcttc	480
acggatacga	cgatataagt	gcctgtcgtg	atatggcgaa	tggctgctac	gacctgcaat	540
gtgtggtacc	ttcgtagatg	tttgtgatac	gtacatcgcg	gtagagactt	cgcaggtgta	600
gtccttcatg	aagccgctac	caccgtggat	ctgaacaagt	catagacatt	ctgattggca	660
aactcggagg	tcattccttt	gcccatgggg	tataggcatc	tgccagacgg	ctgaaatgct	720
tcattttccg	cacgtcttcg	gaagtcaatt	tgcgctcgtg	gctgatatcc	tccagcactt	780
tgtaatatcg	aca					793

- (2) INFORMATION FOR SEQ ID NO:1302
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1150 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1150
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302

agatgcagcg gttttttaag actgctccgg gcgaatatgc tgagggagac ttttcctcgg aatatccgtt cccgacattc gcgcttatga gaagacacta ggccttggag ggtggaaatc

ctcgctcttt	tgctgcaaca	gccttatacg	aggtgcggca	tctcgcactt	atcggcatga	180
ccgaactata	cagacggctc	ggtcggaagc	agtacgggag	gggctattag	cctcctatct	240
gagcctacga	ctatgatcaa	taactgggat	ttggttgatg	tatccgcacc	cggatagtag	300
gcgaatatgt	ccatgctcat	cccatcgagg	gcaatgcctt	gctgatagat	tggccgattc	360
atecttette	tgggaacaac	gaatagcgat	ggagccaatt	ggcgactgat	ccgatacgga	420
gagtacgaag	ctaccattcg	cttgccgagc	gattgctcca	ccacccacac	gatctcattc	480
ataaagcagt	ggctggatgc	tgcgtgagat	gggtaaaaag	caagaacggc	tcctgcttgt	540
ttccttgaca	aacatgccgc	cactatgcca	cggacagctc	tccgctatcc	atggaaaagc	600
tcccgtccga	tctgcgctct	tactacctga	ccaaaggaaa	taatctacct	ataatttta	660
tatatcattt	ataggcggag	ctgcgaaaaa	gaataagccg	agcaaaataa	cagacggaat	720
aaatcaaaaa	taaaagcaaa	tattgagtca	atatctgcct	ttttctcttt	ttccagtcgg	780
potectegat	togaaccago	gaccacacgc	ccccagacg	cgtactctaa	ccggctgagc	840
tacaccccgc	ttgcttattg	cgttgcaaag	gtagttttt	tttttaccct	ccaagagttt	900
cgcgataaaa	atcgaaacat	tcgtgcaaca	tttctccgtt	atctcacatg	gttctgccgg	960
taagcctatc	cctttaagtg	aataagcctg	attttgctcc	ccagattctt	cttgtctttc	1020
atgcaaaaac	cgtcagagac	ggatattgct	tgcaggtgaa	aaagaagggt	gagtagtatc	1080
tttggaccat	gcgaccagcg	agtagaggat	ctctcgaggg	aaaccattgc	caccaccgaa	1140
taatagagtt		5 5 00		_		1150

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 548 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...548
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303

ggcgaaatag	atgcggagct	tatcgccgat	cttgagatga	agtttgtcgc	agtaacttgt	60
				gctcggataa		120
				tcccccatca		180
				tcgtgggcac		240
				agcattgaaa		300
				tatccagact		360
				catcaagctg		420
				tctttccctc		480
				taccctattc		540
ggagaaaa					· ·	548
<u> </u>						

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 707 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...707
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304

gcccggtgaa	gtttccaagc	cttttattct	caaaacggac	aaaggtaata	ggaggttgtc	60
atcgtgaaga	tcaaaaatct	gatcgaagga	caccgagcaa	catgaactcc	gatttccaaa	120
cgatcaaggc	cttagcccta	aacaaaagaa	agaaggagtt	gtcgatgcat	ggataaggaa	180
gaagcaaaaa	gaaactatat	ccacatcgaa	cctgcctacc	gcaactgtca	gttccgctat	240
ccgggtggct	tgaagacaga	caataattcg	gggtggaaag	aaaatctctt	tggaagagag	300
tttctttctg	tctcgagtac	aaatagatga	gaaaggaga	aaacgagaat	ctcggctcgg	
tagccgacaa	ctgggggcga	taattctgat	cgcactctct	ctttttctac	ccttgcctct	360 420
ctccaaggtc	cccctcccaa	aggagtaagg	ggaaaacgca	tgtcatcctc	gaacatgccg	480
atgaactccg	tacgacagac	tctacaaccc	cgatgtacap	cetctectte	gcaatgtcag	540
atcaagcatg	aaggagctgt	gatgcgctgc	gacagogoto	atcttaatag	Penareces	600
ctttcgaagc	attcggccaa	gtttccatgc	agcaggcaca	ccetatcate	tcacccatat	
ctcatatgat	ggaacatcaa	atacgccgtc	ttcgccatga	gtgcactacg	reguergial	660
_		Ç -8	064	9-9-9-1		707

- (2) INFORMATION FOR SEQ ID NO:1305
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...397
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305

cataagagca	aaaacgattc	gtcaattttc	ctcaacccaa	acatctcatc	ggggaacgga	60
ttcggggatc	aaaaaaagaa	aaccatggca	totogactac	ttcctgccac	aagagaaaaa	120
tcaaggggga	gccgcaaatg	aaatactgcg	actoccott	acttagttta	agagaaatat	
cagatactga	aagctatgta	tggaagaaca	acagteetat	actoggittg	gcatcatctt	180
cttcaattat	tagttgacta	caactttcct	tacattecta	ctcctcccc	gacttgcaga	240
ctgacaacgt	agactccatc	gaccaatggt	tocatostas	cccgcggcag	ggttttacgt	300
ccaatcgaat	cagaagtttt	ccgtcagttg	daaaaca	actactteeg	ggttttacgt	360
_	0 - 0	066	Buuaaca			307

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- (2) INFORMATION FOR SEQ ID NO:1306
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1121
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306

```
gtatccaata cgctcatttc catgattgta atcttcctgc tactcaaaac gccggtatga
                                                                        60
aagacgggtc ggccaatctg atcggttata tagcaggatc atcaacagct tcatttggaa
                                                                       120
togtaaatgg acattoogga googgactot tggaggcaaa cattogtaco attoatootg
                                                                       180
atgttcgtaa tatgcttgca ctccaatacg gacttttgat gtggctcaac gaatactcca
                                                                       240
cctccacgac aagtattaca accacctgat aggaatggcc tttttcacca ttataatttc
                                                                       300
cttgccaata agttcattac attcggcaaa gaacggtagt gcgtatttgg acaatagaga
                                                                       360
aaactettta tetttgeage geaataaace aaggggtatt ageteatetg getagagege
                                                                       420
gacactggca gtgtcgaggt ggcggttcga gtccgctata ctccacccaa aaagaaggtg
                                                                       480
                                                                       540
caaaccggca tcgatgcagt ttgcaccttt ttcttttgtc cccatcggat gcttttcctc
                                                                       600
cgtccctatc tcgacaatct tccaaaagaa aagccgaaag accaataacc ctatcagcat
aattacgaaa gacagaagtg attgttttag aggcactaga aggaaattgt atcgtttccc
                                                                       660
caactccctt ttggacattg acacagggct gaaaaccatg gccaaaccaa agtatatagt
                                                                       720
ttggctttat caaagatata gtttggttcg accaaagtat atagtttagt tcaaccaaac
                                                                       780
                                                                       840
tataagttta gtttcaccaa agtatatagt ttggtttgac cgaactatat agttgtttca
ggagcatttt gagctttctt tcctcaagat ataatgcact ataatcaacc tcttatttct
                                                                       900
tettteetgt aggatgteat ttttgactge geatacaett ttgeetteeg ceatetteec
                                                                       960
gcaaagggaa togtacogga agcaatttta cooggaaact ctataaacto acaatgtgta
                                                                      1020
ctataatctg ggtagatttc ccgataggca tgatccaata gaatggttaa acattccctt
                                                                      1080
                                                                      1121
tcgttggggt tttcttctcc ccaaatacct gtcaaaacgg a
```

- (2) INFORMATION FOR SEQ ID NO:1307
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 772 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307

gaatttgtgg	gcctaagaac	cgcaatcatt	ttcataagaa	atacctccgc	ctttattaga	60
-	-	ccattcctga				120
acgaaggaaa	caatcaaatg	atatcattcc	caaaaggttt	ttcaaaccct	cgaaagagga	180
aataatataa	tcggtgaggg	gttggaaagg	tattcctttc	tgaccatcag	gacggttgta	240
aatccagttc	ccgtcctgct	tttatttcgg	aagcgggatc	atcgcctgcc	acatggcttt	300
tcggtctatt	aagttcggtt	ctctatgctg	actgtgataa	agatatccgg	acaaaataga	360
gttctatcct	cctgtagaat	gtataaagga	ttggagaacg	actaggctgc	tttgcaggaa	420
tcttttattt	acggaaacaa	atttctttcg	gacaactttt	gcttcgcatt	aaagaattac	480
agcagcgatt	cgaagtatcg	gcacaacggg	caagtagaaa	gtttttgcaa	aatattctat	540
tcctaagggc	gtaatcgttt	tccatattat	ctctcaaaag	gtctctcagc	cctcgaaaga	600
ggaaataata	taatcggtgt	aggagttgga	aaggtatcct	ttctgaccat	caggacngtt	660
gtaaatccca	attcccgtcc	tgctttattt	cggaagccgg	gatcatcgcc	taccacatac	720
gtctttcggt	cttttggtcc	aattccctgc	ttaattcacg	gaagatatcc	ag	772

(2) INFORMATION FOR SEQ ID NO:1308

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 781 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...781
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308

```
60
ttttaatcat gaaatctgca agtttcttgc cataaagata agaaaacttc agattcatca
                                                                       120
taggttttcg caaactaatt tgctcaatat cagagagtaa aggattctta agggacgact
                                                                       180
acatagtett acacagetat ttetegaatt gggaagtteg agteegtage etttetteae
                                                                       240
atcggcacct ttcagggaat accgaggata aaggcgagga taccgaacga agcaaaaacc
                                                                       300
agcatgccaa agtatagttc ttcggttcgc cggctgcaac acccttattc gtgggtcgag
                                                                       360
gatggctccg atcacgatgg gaacaaccat caagccgata ttcgaataaa gaaaatggcc
                                                                       420
gaataagccg agccaagtac tttggggtcg atatcttggg taccgacggc cagagagcag
                                                                       480
caggtaccaa agagaaagaa aacccagtac gacgatggct gcaatggcta tggcaagaga
                                                                       540
agaagtggtg cgctctcaaa ggggaaaatg gcgaatgtca ggtggcagat aaacatcaga
ctgctccgac aataagcatg gtggctcctt tcccgacttt atccaagatg cgccgaggaa
                                                                       600
aggegteage accatggete ceaaggggaa catactgaga taegggeage teetteggee
                                                                       660
                                                                       720
gtcagaccga tatttggact gaagcacttc ggtggcaaaa cttcttgaaa ggggaaaatg
                                                                       780
gcttgaatag taaagacgca caggagggca acattccaga catgctattg ccgaaccctg
                                                                       781
```

(2) INFORMATION FOR SEQ ID NO:1309

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...630
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309

cctctgcttc atagacattg gacaatccga gttctccttc gcatgtactt tagctgcatg atgacgagag tctgctccac gcagctttgt acggtagctt	ggcagggaag gcgactcgaa gatctcttgc tgtgcccgag ttcgggatcg ataccgttga aggtcggaat ccggggatgg actgtgcttc	tetgcatect tccttgcgca tttctccttc gtagaatttg ataccgttga agaaagaagc cctttgttct gtggaataaa gcccgagtaa	cggggcgacg gtattctacc attccttctt gtatttccgg gactccattc gtagagcttc cgtctccgaa tgccgatgat	tcccacactc gtaacagctc tttcatagtg cagatctcca cgatcactcc acggtttgtc ccggtacata	atcaggatac cgttgcgaac agcggtagca ccacgtgcac accaccgatg caatactctg gtagcaggtg	60 120 180 240 300 360 420 480 540 600 630
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- (2) INFORMATION FOR SEQ ID NO:1310
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1371
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310

gatcgattt gt ctgtttatcg gt tgtcagcaat ct ggtattcctc ga aacaactgcg ct	tgatcttat tatcaaggc aactgaaac	gcagcttccg gttttctttt catataccgg	tcattccatg cagacagatg	gtgattcgtc tacgctttac	agcatccgcc gtccttgctg gatctgtgaa	60 120 180 240 300 360
--	-------------------------------------	--	--------------------------	--------------------------	--	---------------------------------------

```
gccgatcaga tcaatcgacg cgctttggaa gcttacctgc actgccccat tcctaccaag
                                                                        420
cgatcatcaa gggcgatttt cggaacatct gtatcctttg gagccgacga tgacgttgaa
                                                                        480
agaaggtgcc gagtgatgtt cgttcgcaat gatactcgcc aacctagacg ctactacaag
                                                                       540
ggaaaatagc cgtagtccac tccctttctc cttcctcggt ggtcgttcga ctgacggcgg
                                                                       600
agagettata gaggtagage cacaegagtg gaccaactee getacteegt gaacceegag
                                                                       660
accaatgccc ccgaacagga agtaatggca gcttccgcct ttttccgctt cgagccgctt
                                                                       720
gggctatcac cgtgccaaga gccaaggact gactttcgaa cacgccgcca tagatctgga
aggttetteg tteeeggtea ggeetaegta geeetgteae gtatgaeggg eeegaaggaa
                                                                       780
tgatactgct ctcccctccc gatctgcgtg ggttggaaac tcccaagaac tggtcgaata
                                                                       840
                                                                       900
tgcacagacg aagcccgacg aaaaagaact cggacttctt tgcaggaaaa cagtcttatc
                                                                       960
tattggaagc agcaatccga gaggctttcg actggcagag cttgttgaat atatggcaca
                                                                      1020
aacacagtcc agctatcggg aggagagcga gctgagcagc aaaagccatt acagcgatga
                                                                      1080
gcagccgaac aatcggccaa gatagatgcg atcacggaag tagccggcgt tttcgccggc
                                                                      1140
aacttgccgg cctttggggg cagtctccgc ttggatcggt gccgtcaaag agcgaatcga
                                                                      1200
caaagccgtg gactatttcc tgccaaactt tctgccatag caggcgaact ttcctccacg
                                                                      1260
atccaagaag toggatgotg aaaaaagcca aacagtttgo gaaagaactg ctogagctac
                                                                      1320
aggcaatett catacegeeg tgtacegeet gettegetta egageegttt t
                                                                      1371
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 714 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...714
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311

```
acgtttttag gagcatgaaa caaaaaattt cacgaacgta aatgggacga tcgaagtttt
acttcggtct cgttttcat ctctattcgc ctatgaaatc ctaaggctct cttttagaca
                                                                        60
aaaaatcttt ggccaaaatc cttctatggg agcatcgagg aaatgaagtt gcagtcctcg
                                                                       120
gtcatatacc taatgaatag gggagtggat cggatcggtt tgctccctct cgaagagagg
                                                                       180
tttcttcccg tttcggtctg ccttatgaga attattcgaa gcagtcgttg gcggtttaag
                                                                       240
gtgtttcata tacctttgcg ctgcaatgca atcataaaga ctgtttctcc atgttggaaa
                                                                       300
agotoattat totggattto ggttotoaaa occacagoto atogocagao gaattogoga
                                                                       360
gctgaacacc tactgcgagg ttatccctac aacaaactgc cggaagacct ctaaggagtg
                                                                       420
cgaggcatca cctgtcgggg agcccttatt ccgtgtatga cagcaaggct ttcgtatcga
                                                                       480
ctgagccgaa ttacgggcca agttgcctct ctttgggtat ctgttacgtg cacagagcct
                                                                       540
tgtccatcaa gcccggtgca aagtagaagc cgtgcgaagt cgcgaatacg ggcgaacaca
                                                                       600
totgaccotc ggcagcotga tgatgcotgo tgacaggcot gcaatcoggo ctac
                                                                       660
                                                                       714
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 690 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...690
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312

			coccasata	cacotoaaga	eccetcetea	60
gccgaaggat	tcgacgggct	gatecteect	gcggaaaacg	cacgtgaaga	beentagaa	120
acaacctcaa	totctatogc	gtgaagcata	ttgcagaatg	attagttatt	CCaacggggg	
	carccacta	tagtogaacg	cgcagggaat	ttttcgacca	tcagcagcag	180
cgattagtta	Cagcccacta		agagaagt	CAARCECECE	ctcgaagtgg	240
gtgtctttcg	acttttggag	gtgaaggggc	aggagaagge	caagcgcgcc	antcatanta	300
CGGCCCAGGC	ogacacaatc	tgatcatggt	cgggagiccc	ggcagcggga	44664646	
00000	tacccagaat	tottoctccg	tttacactta	gcgatcgctc	gaaacgacca	360
gctaagcgaa	CECCEBAA		trattroato	ctcctgaccc	aacgcccttt	420
agatatactc	cgtggccggt	aagctgggag	Caccagaca		aacgcccttt	480
ccgctcgccc	caccattcca	ttcttccgcg	gcactcgtgg	geggeggeac	ttatccacag	
000000000	caagtetgge	gcacaategc	gtgctctttt	tggacgagct	ggccgagtta	540
CCCggagaga	tanger eggs	8	ctttggaaga	toggoagaca	ccgttttcga	600
accgctccgt	tctcgaggtg	argeggeage	C C C C G G G G G	at agot acca	ttgaattrct	660
gagccagaat	gacggtggat	tatcctgccg	gattcatctc	grageracea	ttgaattcct	
atacttacaa	ctactacaac	cattcccacg				690
giccitgegg	Cedecaca				•	

- (2) INFORMATION FOR SEQ ID NO:1313
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...524
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313

agactataca	cacacaccaa	atocactoat	caatgtattg	gataccatag	accactggca	60
ggactatgeg	cacacaccac	actortagga	ослорардаа	tcgggacaaa	ggcaaacgtc	120
aaatcgcaca	aggigaticat	ageggeagga	coascottto	atcctgacat	cggacaatcc	180
cgatcatggc	aaaggaggca	gcccgcaaag	gaatgata	tragactttc	gacagaagac	240
gcgtgatgaa	gagcctaaga	aataatccaa	gaaacggcca	CCECECGGCC	gacagaagac tecagcteec	300
aggaaaaaac	actgctcatt	actgatcggg	cggaagccac	cogcacage	tgcagctggc	360
agagaaggga	gactttgttt	tgatagccgg	caaaggicat	gaacctatca	ggaaatcaga	420
ggtgtcaagc	accattttga	tgatcgcgaa	gtgtctgcga	tgccatgtcg	aaagatcgta	480
tcgttcaata	aactctatag	acccatgttg	tactatctgt	ttgattattt	cgaaaagcta	400

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 539 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...539
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314

gcaccggcga	cgatgacgcc	cgagcaggct	ccgatggatt	ggatgatcaa	ttctgcccca	60
gcatatttcg	gcgtcccgaa	atggtgccga	tacctacgcc	aggatggcaa	tgggaatggc	120
ggcttcgaat	acttgcccga	ccttcagccc	agataagctg	cggcagcaga	gaaaataact	180
gtcatcacca	aacccacagg	acagaatagg	aggtaatctc	gcgcggcgta	ctgccggcag	240
gcatcccggt	tcgtactctt	cgcccggctt	cagctcccga	tatgcatttt	cgggagcttg	300
ctcgttgtct	gtttgttttc	catataatat	atgtgtttga	ttgatcgttt	tttgcaccgc	360
cctccgatcg	caataagagg	gcggagaatc	gtctgaaaca	aagcgctcaa	atatatacaa	420
cttcgttgaa	aaccggtcct	tcgatcggac	aggaagcccg	atcattcccg	gcagtatatc	480
cgtgcgatgc	cttcggagtc	gatagactac	agaccgccgc	tttcgccgcc	gccttgctc	539

- (2) INFORMATION FOR SEQ ID NO:1315
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 626 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...626
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315

+000+0000+		cacttatata	gcaggtcttc	tgacttattc	aaggcttcgc	180
CCCCLgagac	teagaaagaa	chartesett	totogtagea	aaacccttac	atctgaactt	240
tgccttccca	tacgatctgt	atagiggett	cccgcgcc	ttcattctac	actcatoaac	300
acagcgaggg	tacagtccca	gaatttcact	gggtttttt	ttcattctac	tacaanaaat	360
cggtgtagaa	aaccattgac	acggcaaaga	tattcattat	atcatactag	LgLggaaaaL	420
+ 0 2 2 0 2 2 2 2 2	aatatggatt	tettteagga	tactttcagt	atacgtcatt	aaggctaatc	
aaatataaaa	teccecteat	atttatgtgt	tcgtgtgtaa	ataaaaactg	aggetgtete	480
666 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	acctcaactt	catttattee	taggaatatt	tgggatattc	cgctgcagta	540
gicatgagat	ccattccaa	acattetett	catagatttg	ctctgatggc	ccttccttca	600
ttactacaat	Cigatticaa	gegeeeeee	Cacabas8	0 00		626
atggtatgcg	atccgcagaa	Caccat				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 967 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...967
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316

```
ggcttatgct catttatagt atagtgcatg caactctctg aacaaaagga ttgaaatagg
                                                                        60
                                                                       120
aatcaggagt acttttgaca gataagccca agtatgcatg ggatgatcaa gtctcgatca
acaataaatc agtgtaagca tgctgtcgga ttcagcactt cggccgcaat ctcacggagc
                                                                       180
                                                                       240
cgatcggagg taatggatcg atacgatgga aaatatccga aaggggatcg tatttgccat
                                                                       300
agagggcata ctcttgccca atgaaaggaa tgtggactcc ttattgtcag ccgaacgatg
                                                                       360
agctgtcctt tgaactgtcg cttggcagat tccagttcta tcgagaaaga gggtgttcga
                                                                       420
tcaaatagcg caactctttt ctgacaagct cctggctgct tccgcatatc ggggagcgca
                                                                       480
gccgaggtag atattgaaga ccccgtatcg gaatagggcg tgtaattgct ctctacgtta
                                                                       540
tagacatage atgetettea egeagtgaga gattgageeg ggagtteata eceggeeete
                                                                       600
gaggatatta ttaagcagac ttagcggaat gcgtctgtcg tcgtggagga atacgccgga
                                                                       660
ccgcccatga ggatgtgatg ctggtaggta tccttgtccg tctgatggta cgcggcagaa
                                                                       720
agccttctct gagggtatgg agaggatacc atcggtatta cggatggaga ccttctcggc
                                                                       780
cggattaagg ggccatcgga caggtctgct tctccggcca ggaagaagat catattgtcc
                                                                       840
ggccgtagtg gcgacggagg aagttacgac ctatttgtcc cgtgatgcgt gatcagaagc
                                                                       900
ctctgtgccg agaatgttat gtccgagagg atgatgaccg gaaaggatat tctcgaattc
                                                                       960
gtcgaatata agttccgagg gattggtctt cataagaaat cgattttcgt cgaataacaa
                                                                        967
ccggttt
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317

```
ccggacgctc cgaatagaga tacgtgcagg cggctgaaag aaatcttgtc tgcaggaagc
                                                                        60
tgtagcaatc ctcgaagaat tccggtttct cacctctctt cctacaatga catctatccc
                                                                       120
gatgaaggcg tggggcaatg ccctgcgata tgctccactc gctcccgaaa gagagccgta
                                                                       180
togtacogac ggogcagago ttgagcacat ogtoggatoc gototgaago ggoatatgga
                                                                       240
aatgtgagca atacggtgtg ccgaggcaca gaagtcaata agttcgtcgg agagagattt
                                                                       300
ggttcgatag aaccgattcg gtatcgctcg ataccttcca cttgtccaga gcacgcaaga
                                                                       360
gatcgaggaa tgtctccccc gtactgcgcc cgagtcacct atattgactc ccgtaagtac
                                                                       420
gatctccttt cctcctctg cgctacggcc tcagcctgtc ggacgagaga ctctatcgac
                                                                       480
ccgtttcggc gcgtccgcga gctttgggta tcgtgcagta agagcagtgg tagtcgcatc
                                                                       540
gtcctgcact ttgaggaaat ggcgtgtgcg gtcgtccgcc gaacagccgg ttgaaatttg
                                                                       600
cgaatatcct ttgtgggggt cgtgagaata gtctgctggc aaagccctgt atcggtcttt
                                                                       660
ggctgagaat acttacgagg tcgagctctc atcggctccc agtacgatgt ctactccgtc
                                                                       720
tattcgagct atttctccgg tttgagctgg gcatagcagc cggtgacgat catcaacgca
                                                                       780
ccggatgctc tttatgtaac ttgcggatgg cattgcggca tttcttatcg gccgctccgt
                                                                       840
tacggagcat gtattgatca cgcatatatc ggccttttcg cctctcgcac agggcgcaca
                                                                       900
ccctgctcgg cgagagcttt tccgatggtc gagtctctgc gaaattcagt ttgcagccaa
                                                                       960
gagtcaggaa agccgctttt tgttttcaaa gatgaaagca tctgtcatac cgcgcaaatt
                                                                      1020
tactgctttt gagactgtgg gacagatatt tcagggcaac tcacagggca atcgcattga
                                                                      1080
actgtcaaca cacttataaa cctaactaac gattgctaca ctcggtttca aacaagtacg
                                                                      1140
aattaatggg acctttgcac aacaagcagg cncctttggt tattcttctt at
                                                                      1192
```

- (2) INFORMATION FOR SEQ ID NO:1318
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1855 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1855
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318

gagatcgacc gtaagco	ccac tataagtaat	caccccgata	gcaggtcgga	agcatagtag	60
egggetatet getett	gtog cogttotgog	gagaagaggt	gcgcttctgt	tcattgatgc	120
cgatagcgat gatcaco	ctca tcgaataggc	cagcgagcgt	tegacgatgt	cggcgtggcc	180

```
gcgtgtgaaa gggtcgacga accggcaaag agggcgatat tctttttcat atttgattct
                                                                       240
tgagaatcgg gaggatcgct taaagcacat cctcatccac gactaagttg tcaagataaa
                                                                       300
ctcctgacgc tcgctcgtat tctttcccat atagaaagtg agcgttcctt gatcttatcc
                                                                       360
tegegettga ggetgacegg etegagaegg attteteete gtegateaaa teettgaatt
                                                                       420
gctccggaga gatttctccc atcctttgaa gcgcgtgaca tcggctttct tgcccagctg
                                                                       480
cttcagcgcg cttgcttctc ggcctcacta tagcagtata tatccgtcac cggcttagga
                                                                       540
tatcggactc ctgtttcttg cgtccgcgtt tgggggtggc tccgaaggtt gttttttgga
                                                                       600
ttcgggcgga aggaaaacgc ggaagagtgg cgtttcggga catagacatg ccccttgcgc
                                                                       660
acaaggtcag ggaagaactg aagaaaaaag tgatgatcag caagcgaata tgcataccat
                                                                       720
catcategge atcagggeaa tgatcacaeg attgtagege aggeegteea accetteete
                                                                       780
gatatcagag ctgcctgcaa gaggttgaac tcctcgttct catagactac cttttggtca
                                                                       840
ggccgaaaca gttgagcggc ttaccacgca ggctgaacac ggctgatagt tggcatcccg
                                                                       900
acacgtagta atagagccgc tggccgaatt acctcggtga tgaaaatgct ggtacgctcc
                                                                       960
ggttccttcg ccttgggatc ttgaggtgga cggtgcagtc acgcagtttt ttgttgtgca
                                                                      1020
gattggattc ttagctcgtt cgcgtgccaa tttggtgatg ccgctcattg ctttgcgccg
                                                                      1080
cgttcgctct gctggatctt gcgcagcatc tcctccgccg tttcggttgg atatgcagat
                                                                      1140
agtcgtccag ttctttcttc aggaagtcgc ccacgatttt tgtatcgtag gcccatccgg
                                                                      1200
cccatgtca cggctaccga gtttgtcttg gtctgactct cgaagacagg ctcttccact
                                                                      1260
ttgatactga tagcgcggcc atgccgctac gaatgtcgct gtattcgaaa ttcttggagt
                                                                      1320
agactetttg ategtaeggg ctaeggeete aeggaaagea eteagatgeg teeceettgt
                                                                      1380
gtcgtattct gaccgttcac aaagctgtag aactcatcgc ctactgctgc gtatgggtga
                                                                      1440
cgacgatete aatateegta tegeteaggt aatgategga tacagtgeat egecegteat
                                                                      1500
attctcagcc aaaaggtctc caaacctttg cgactgagga atttcttccc gttgtagaag
                                                                       1560
aatgacaacc cgtattcagg aaagtatagt tcttgatcat cgaaacgacg aactcctctg
                                                                       1620
ataccgatag ttgcggaaga gactgtcgtc gggcgtaaac cgcactcagt accggaaggc
                                                                       1680
tcaccggaag ggacaggatc ggtctcctcc aagagtcggc acgactgtac cgtacgcgtt
                                                                       1740
tggtttgtcc atcgcgccat accgaacgac aaattcggtg gagagagcat tgacagcttt
                                                                       1800
gatgccgaca ccgtcagtcc gacggatttc ttgaaagctt tggaatcgat tttgc
                                                                       1855
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3755 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...3755
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319

```
60
ggcgcccatt tagtcacgag cagtagacgc gaaaccaagt gatctaccct ggtcaggttg
aaggttaggt aacactaact ggaggaccga atcggtaacg ttgaaaagct ttcgaatgaa
                                                                       120
ctgagggtag gggtgaaagg ctaatcaact tggagatagc tcgtactccc cgaaatgcat
                                                                       180
ttaggtgcag cctgttgatg ttatcatgag gtagagcgac tgattggatg cgagggtttc
                                                                       240
accectatca agtocagata aactocgaat goatgataat tgaccgatgg agtggggcat
                                                                       300
gggtgctaag gtccatgtcc gagaggagaa gaatccggac cacggctaag gtcccgaaat
                                                                       360
                                                                       420
aattgctaag ttgtaaaaac gaagtcaaga tgagagacag ctaggatgtt ggcttggaag
                                                                       480
cagccattca tttaaagagt ggtaacagct cactagtcga ggattttggc atggataata
cacgggcata gcaatttacc gaagccgtgg gatatagtaa tatatcggta ggggagcatc
                                                                       540
```

```
cagcgacgta gaagggaaaa gggcgacttt ttctggagtt tctggaaagc aaatgtaggt
                                                                        600
ataagtaacg ataaaggggg cgagaacccc cctcgccaaa gaccaaggtt tcctgatcaa
                                                                        660
cgctaatcgg atcagggtta gtcgggccta aggataagcc gaatggcgat tccgatggaa
                                                                        720
gaaccggtta atattcggta ctgatacaga gagcgatgtg gtgacggaga agtgacagtc
                                                                        780
cggcgtctga cggaataggc ggttaaaggg tgtagatgtt gatcggggta ggcaatccgc
                                                                        840
cctgagagtc gaacctgaca gtacccggag tacaagtacg aaggataagg acgtaaaccg
                                                                        900
gctcccaaga aaacccgcta agcatatttc ttgttacccg taccgtaaac cgacacaggt
                                                                        960
                                                                       1020
ggttgggttg agtatactaa gcgctcgaga gattcgcggt taaggaacta ggcaaaatgg
teetgtaact egggagaaag gaegeetgte teeggacagg eegcagaaac eaggeecage
                                                                       1080
gactgtttaa caaaaacaca aggctatgca aaaaagcaat ttgaggttat agtctgacac
                                                                       1140
ctgcccggtg ctggaaggtt aagaggagga gtcatctcaa gagaagctct gaattgaagc
                                                                       1200
cccagtaaac ggcggccgta actatacggt cctaaggtag cgaaattcct tgtcgggtaa
                                                                       1260
gttccgacct gcacaatggt gtaacgatct gggcactgtc tcaaccgcga tctcggtgaa
                                                                       1320
atttagtatc ggtgaagatg ccgattaccc gcaacgggac gaaaagaccc cggaaccttt
                                                                       1380
actatagett tacattgtat ttgggcatca gatgtgtagg aaggeeggag geagagaage
                                                                      1440
gggtacgcca gtattcgtgg agtcgatgtt aaatacggcc cttttgatgt ttggatacta
                                                                       1500
actogoggeg tgogaggacg tgtatggtgg gtagtttgac tggggtggtc gcctccaaaa
                                                                       1560
                                                                       1620
gcgtaacgag gcttctaaag gtaccctcag gccgattggt aaccggtcgc agagtgtatg
                                                                      1680
gcacaagggt gcttgactgg gagacaaaca agtcgcacag gtaggaacta gagcatagtg
atccggtggt tccgcatgga agggccatcg ctcaaggata aaaggtactc cggggataac
                                                                      1740
aggetgatea eteccaagag eteaategae ggagtggttt ggeacetega tgteggeteg
                                                                       1800
tcacatcctg gggtggagaa ggtcccaagg gttgggctgt tcgcccatta aagtggcacg
                                                                       1860
cggctgggtt cagaacgtcg tgagacagtt cggtctctat ctgttgtggg ccaggaaatt
                                                                      1920
tgcgagggtc tgacactagt acgagaggac cgtgttggac gacccctggt ttaccggttg
                                                                      1980
                                                                      2040
taccgccagg tgcaccgcgg gtatccacgc tggtaaggat aagtgctgaa agcatctaag
                                                                      2100
cacgaagccg gcctcaagta agatttccat aaatagggtg gttaaagact atgaccttga
taggctgagg tgtatgattg gtaacaatta agccgagcag tactaatagc ccgaactttg
                                                                      2160
tgcatcccga aggatgcggt ataggttggt ttgttgccgc aaagctgagg aattatttgt
                                                                      2220
tggcctttcg atatgtcgat tgccttttcg aagtttcagg tggttataac gttggggatc
                                                                      2280
cacctcttcc cattccgaac agaaagttaa gcccaacggt gccgatggta ctgcgtcaca
                                                                      2340
gtgggagagt agacgccgcc gttttttaag aagcgtgaga gagaggggg gataggatct
                                                                      2400
caccctcctc cccggaaaaa aaggtgaagg agagagtctc gaatccgagg tctctccttt
                                                                      2460
tttattttct ctctcccaa aaatcatttt gcttttctcc tattcctctt tctccttttc
                                                                      2520
cttccttcct ttcctcccc ttgctgcggt tattcctcta acagatcgta cgccaactat
                                                                      2580
ctcattgttc ggtaggtcca taggtagccg cggacggatg gatagcccat cgagacgagc
                                                                      2640
agcoggtata attotocato tgtgcatgat gaactttgcg aactgotocg aattttagto
                                                                      2700
tacgatgtct gtgtgatcgt cgtagagaat gatccgatcg ggacacgctg ttccccttcc
                                                                      2760
gggaggagaa tatcctgttc attaagaact cgtcgctacc atcgaaccaa cgagacaatc
                                                                      2820
                                                                      2880
gactgtccga agtgacaaca gaaggcgatc gaccaattcg atcgcctcat ctctcgtgac
                                                                      2940
gattcctccc gcacataacg ctcaagagca ggctcgatgt ccttggcgag aacgatgtcg
                                                                      3000
caaggattct gtgcattaca tgtccgtggt aaagcggttt gtgcctgcgt aaaattcact
                                                                      3060
gccttcaggc cggatagcca agcggtcggc tacggccgga gacttccttt gggcagggta
aaaggtaagc cagaagaggg gtgatcttcg ttttttgtct cgcggatatg accggacttc
                                                                      3120
                                                                      3180
cccagcagta catatcgact ctgtcttatt ctcgtccaag gaagcaagag ctaaatgtat
aagatteeca eggtagagag egatteggge ttttgggaag gatgtaacea eagageatet
                                                                      3240
cgtccttcgc tcgtgtcgta gccacataaa gaagattgag gtttcaagga gaatatcggc
                                                                      3300
tettetegg aaataatetg tggcaaacat tgttgtgeca teteettett atatetgate
                                                                      3360
ggcactacgg gcaggatatt gaaggactgc gggcaggatc gatcttgcac cagaggatgt
                                                                      3420
gtcgatgtgc gcttcgtcgt ccagattcca gtccaagaaa ggaataagaa caacgcggag
                                                                      3480
cctagacctt tcgccttgtg aatggtcatt agcgtgacgg cctgactgtg ggagcggagg
                                                                      3540
                                                                      3600
aaatacggct tttggcatgc cccgtttcgt cccaccatgc aggaaagagt gcagatcggc
agatogttog tgacogaaat cattgataaa tooagcoaag caattagata gggcatotot
                                                                      3660
ctttcaggta ggtataatgg aaaaaagaga ccaatccttc tgccaattcg tataaggagc
                                                                      3720
gacgcgaagg ttggcaaatt ctgcaagctc tgcgg
                                                                      3755
```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...295
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320

	teatetteac	taagtgggtC	tacctgatct	tcaggagcag	taccagttcc	60
cggcgaacci	ccatccctc	tttacaaatc	ggacaattoo	attctcgggg	tctatcaaac	120
tgatgagtag	gaatggcttg	LLLacgaacc	tactttaagg	gattettta	ctcctcttc	180
tcaaataata	aggtgtgata	gccattcgag	Lactingage	gacteteet	togattgagg	240
ttcttcagcg	gtgagttaac	gtactttttc	agctggtcga	gegeeteaat	tcgattgagg	295
acctgcaatg	ccagtcgttc	cattgctcat	cggtgaacat	cagggaaata	atact	293

- (2) INFORMATION FOR SEQ ID NO:1321
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1353
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321

toggcatttt	coottcoaaa	atccaagttt	ccaaccaanc	cacagacttg	atcgctcccc	60
Leggeatett	castotataa	ctaccaattc	atccopaaca	ggaaactttt	ttcttgttat	120
tttgcatage	aaatetgtga	tegeoggee	**********	teetteeegg	cctettagag	180
cgttcaagaa	cgnaaagtct	gtgccgacga	Liggiacaag	tccttcccgg	occase statt	240
attgaggact	gtcagcaatc	ggactttcgc	atcggtcatt	atgacagacg	aggaagtatt	
gaacaccgcc	aaacggtcat	tgttatgctt	aaagggataa	atccgaatcg	tgcgcacgat	300
aattocaata	cotaottaga	gatggcatac	gactttacac	aaaattccgc	aacagcctgg	360
aattgcaata	+000000000	accentetes	grtrgtagcc	gtgacgcaag	atatgctcgt	420
agtacagcia	Caggaagca	accegeeeeg	Secret Cases	testacaacs	ctatoppatc	480
actcggtatc	attcgcgacg	ggacaatggt	gcgaccgaca	tcatgcggca	ttacctactc	540
aacttgtacg	actcaaacgg	ttgatcgagt	tggaagccat	cgccgagagt	Ligitingett	600
occtoaggga	tcgcccatct	tcaccccttc	ggctcgggag	gctatcgaga	tgccacagac	
atctgtgccg	acatggagga	cgaggccgtc	agcccggcca	tctgttgctg	agtatcctca	660
accegegees	agagagetta	gtacaaagat	atttatgaaa	caaggtataa	aatacgacac	720
actogacaca	ggagageeea	Penenagas	ccctccgaag	ggaagtetee	ctccgaaatg	780
catcctgtcg	gattattegg	acagegeaac	teereegaag	Peraeces	ctccgaaatg	840
gagacctcga	cgggtaccaa	gacaacgact	tegaegaega	agaggacgaa	tccctccgcc	900
ttccgggaat	agcgggacag	gcggaggctc	cggcgacgcc	ccgaacagaa	taccggcgga	900

ggcgatacta ccac	cacgac acggagtgga	gcgacacgcc	tgcactggac	accttcggca	960
ccgacatcac tgcc	atggcg cagcaggcaa	gctcgacccg	gtagtgggtc	gggagcagga	1020
gatcgaaagg tgat	acagat actcagccgg	cgcaaaaaga	acaatccggt	gctcatcgcg	1080
aacccggtgt atgg	caagag tgccatcgtg	gaaggactgg	ccgaacgatc	gtgaacagga	1140
aggtgagccg tatte	cttttc gacaagcgga	tcatcacctc	gattttggct	cagatggtag	1200
ccggcaccaa atat	cgcgga cagttgaaga	gcggttgaaa	gccgtgctcg	atgagctgaa	1260
gaagaatccg caga	catnot ottoatogac	gagatacata	ccatcgtggg	gaagcaggct	1320
ctgagccgga tcga	tggata ccgtcaatat	gct			1353

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 625 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{2}5$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322

toagotggca gotcaccott ttogtottoa tootootaco gatagooggg ggotgatggg	60
taaggtgggc aaaactctca agcgcaagag tctggaaggc agaatcagtg gggaagcctg	120
atgagccaga tagaagaaac gcttggcgcc tgcgtatcat caaggcattc aatgccgaga	180
aaaagatgca ggatcgttcc atcgtgccaa cgagcagttt cgccgtacga cgatgaaggt	
cttccccgcc agcagttggc acatccgatg agcgaatttc tcggcacagc tacctagcca	240
togtactgtg gtatgggggt accettatee tgaacaatae gaggagateg atgetteeae	300
Cttatatat tatotogra tottotogra togatografic gaggagatcg atgcttccac	360
ctttatatat tatctggtga tcttctacag tcgatcaatc cggtcaagga gctgagcaag	420
gcatcctacg ccattgaaaa gggttggcct ccatgtcgcg cgtggacaag atcctgatgg	480
ccgagaacga atcaaagatc ccgaacagcc ccaccccgtg gtgttcgaag aggaggtcgt	540
tacgaccatg tgtggttccg ctacggcgaa gactgggtgc tgcgcgattc tgtctgacaa	600
tcccgaaggc aagacggtgg cattg	625

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1221 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1221
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323

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aatgactgtg ctacgggcgt cagacggtct ttctaacaga ttctactatt tccgcaagct
                                                                    60
gctggttatc tcgtttgttg ttgctgcggt aggccaacgc tgggctttgc catcggagcg
                                                                   120
atatggettt tetgtggtat tteetattgt atgetattge teaaaagaaa ttetatetge
                                                                   180
cggtaggtat tcttgtctat tggtagctta ctatctgttt cagatgacgg ggcttatcgg
                                                                   240
                                                                   300
agctgagaga ctaaagacgc tctgcataca cttaagcagc gacttccctt attgctttgc
cgttagcttt gtgctgttgg cgtccgacaa gaacggaatg ggggtatttc tttcttttc
                                                                   360
tttccgcctt gtattggtgt acttatcctg cacattgttg tctctttgct tctgaatcag
                                                                   420
tactatggcc aatccatttt gctccgtttt cttttgataa attctatctg aagactcata
                                                                    480
ttccgacatt gcatcgagtt tctgtatgct ccattggacg cattttgccc atcccacttt
                                                                    540
atcttcttgg gcatattcgc tatttttatg gcagtcgccg tacgtcagat ttctatcggg
                                                                    600
660
tattacccaa agccgcttgg ccatgccttc attcccctgt ccatcatgtt ctttttttg
                                                                    720
gtgcgagcct ttttctatct cagaagaaaa aacttttgtt cacctctttc atgcttatca
                                                                    780
tcgtggcggt tttatcttca acggcctctt gtctcatcgt ttttttgcgg acgagagcgc
                                                                    840
atgcagatgc gtgatatagc catggatgcc atcaatcggc atcatggaca ggtattcggt
                                                                    900
taggcactat ggacaatata ttgcaggcgc aatcgatacg gatattttgt tgaagcatcc
                                                                    960
gcacaaccag cttctggccg tggtatgcag cttggtattc ccgggatggt tgttttggtt
                                                                   1020
gtattcgtag cggtttgttt tattttgcct atcgcgatcg ccgatatgat ttcctccttt
                                                                   1080
cctacctgct atcctcctga caatggcagt cgaatcccct ctgatctcgt tcgaggtgcc
                                                                   1140
                                                                   1200
tatttgttgg cattttggtt ctcggtattt gccgttctcc gactcgaaag aaagactttg
                                                                   1221
cttgaaagaa tttttaagt t
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 655 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...655
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324

cccgcagagg agctttgtta acgctgcgca cacaatttac gcctgttcga	gatgtagcgt ttgctacagc tggattcatc gcaattcatt agttattaga ctgctcagaa	tcttaacata	ccgaatcgaa atcaaagaca attgtaatcc tttttttac ttgcttgcat ttccatgcaa	gagacagact atggaaagag cgatagattc gcgccggtgc tttatttgaa aagagggcct	tagcaacagc attttactgc acatctacga tctagtacgt ctgtgaagaa	60 120 180 240 300 360 420
aaaaacaact	ctgctcagaa aaggctgttt	tcttaacata taatattgag	ttccatgcaa caccttaaga	tgttactcga	ctgtgaagaa	420 480 540

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1064 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1064
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325

tgtgtgccgc atcggtatgc cngtatttga tagcacgctt ataggaggag ggaaaaaaag 60 tgcactaccc tctcctccga gttgctccaa atcggagaga gatagccggc ttcttccata 120 tccgaagcaa tgcaaaggac agggcgacgg attcgtgcag cagtttcact ataagagctg 180 ccgacgaccc gcaaagccgt cgagagctac gcacttctct cggtcgaggg ctttcatcaa 240 agcctcacac cattgtgccg gcgaaagagg gaaagaatat cgattggttg gggaatttga 300 tcatgagaca aaaataagcg gtctgtacca attattttag cgaacgatat tacgatccat 360 cctaaagttc cggccaaatc agattgcacg ggtggtttat gcgcaagatt tttctctttt 420 gtccttcttg aaaacgtgac ggcaccgaaa aagttgatgc tcggaatcgg tcaaatgttt 480 cgacataatt acatcagcac gatagtccat ttagagccgg tgccatagag tggagcagtt 540 ttgtagttaa tacagtgtac atttgtgtcg ataaaaggcg aacaaccctt tcgaccgcat 600 caacatgctg ataatgaata aaataaaaaa gtgaaagaat ataatgaaca agcaaaaaaa 660 caatcgcgaa cgaacgcctc agcccgacag gataccgaaa gagacgaaca actgacaaac 720 agtcacgaaa atgattagat agtgcccccg cagccgaaga gaacgacaag gtggcagacc 780 cggtgagcag ctcacggctc agttggctgc tcttaacgac acccactgcg tttatggcag 840 aatatgacaa ctaccgcaag cggacactca aggaaaagag cgacttatcc gcaatggagg 900 agaaaaggtg ctcgtgggat ctgctgcccg tatcgacgac ttcgagcgcg ccctcagcaa 960 tctgggcgac atgtcggagc tgctgccatc aagaaggagt ggaactgatc tacngcaagt 1020 tcatggactt ctgcagagca tggtgtcaaa aagatagaac cgca 1064

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 631 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326

atattcctcg gaatccgccg gattatactg ccatacgatc tggggtgtac gcgtgctttg attccccac	gtatcgtcgg tgtagtggga atgacatggc tttgcgacat ttatttgcag cgtgtgcctc gtgtcccta	tccacgacag tttcctgcct caaggtgttt atgctgctga cgaccgaagc tccttattat	gagcgtattc gcggccgtag cctctcggcc tggtttttct taccgcagcg atatagcagc	agtagaggta tacgaaacgg caggactcct	tcggcgaggg acgtcatgtt tttgtcggat ttcccgtact gatgggatcc ccgtatcgta gccctttgc	60 120 180 240 300 360 420 480 540
attcccccac gtacaaccga gtcaggcctt	gttctcccta ccgtccggtc tgtttgcagt	tccttattat	ggagccgaaa gaaaagagac	caggactcct	ccgtatcgta gcccctttgc tcataatagg	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...3385
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327

					gtragrtgat	60
ggacgcgatt	gtcaactgat	tcttgcttcc	tgcacgatgc	aggacgcgat	Becageegae	120
+ a + + a a + + c c	tararatar	aggacgcgat	tgtcggctat	LULLEUGE	-660-	
accessat	tatcaactaa	ttattgataa	tgcacgatgc	aggacgcgac	CECCAMO CB-	180
aggacgcgat	cgccaaccga	aactatcagc	tatttgcaac	tattttatag	ggctttcatt	240
ttctgctccc	atcaatcgct	aactattage	tatttttaa	attacttoso	gttccagaga	300
gaagtttttg	ccgcagagct	gattettaag	Lguillicag	attacttgag	togatatogo	360
+cacataaaa	captectete	ttcgtcaaat	caatgettgt	gicgcccga	cceaca see	420
accetege 200	aattattata	CAAAPPICIC	ttaattagat	acgacgccac	CCCCB	
84666664	ctososccat	cctgaatcca	tcgcagcgat	gcacttgata	ccggaatagg	480
grigitatac	ccgagaccat	acctattata	ctacagactg	caaagggata	tatatttgcg	540
caaaacaaat	ccggcaaaat	aggiaciaca	-tacagaces	causacacsa	atootaagaa	600
ctgtaacttt	ttttttcgac	agaaccaatt	ataaagagat	cggagcgcag	constants	660
	actacterss	ragarctaca	gcatggcgca	agcaaacacg	CCaugacas	720
otateagata	ttttggttgg	gcatcaggcc	ggagcataca	LIBULALUES	aggerees-8	
gcaccagaca	+000+0000	tttcccgaga	teecceaago	caatccgggg	ttggccaaac	780
tecetgings	LUBBLAABBL	coccocctt	gattettata	gtgctcaccg	gagcgagtta	840
tgctagtggg	gcgatgttcc	CCECCEECC	gaccccccc	gtgctcaccg		900
ttcaccagca	ataatgccgt	actgattcct	geegetatea	aagtcgcatt	<u> </u>	960
+000000+000	actitagata	gtggtctatg	tgccaacttt	atcggtgctt	CCCCCCCC	
	atcastttgg	røøcttegee	gatgcggatc	Cttggcatag	CECCACCEC	1020
CLACLUCULU	6000000000	tocctacett	ttcacgtage	atttcttagg	ggaatcgggc	1080
catctgtcga	agacaaaacc	CCCCCECCCC				

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caactggttg ggtttgtctg gccgtctggc tgggactttc ggctcatact ttacgggcaa
                                                                       1140
aatgttcggt atctggtggc cggtgatggc attcgtgcta tgggattcga acactccatt
                                                                      1200
gccaatatgt tctatattcc actcgcatac tgcaaggggc ctccgtcagc tggggcagct
                                                                      1260
tegtgatega caattgetge cegteaceat eggaaatate gteggeggtg caetetttgt
                                                                      1320
cggttcttcc acgtccatat attcgataga ggaggaaagt agaaaaaagg cttgctccaa
                                                                      1380
gtggcatatc agacaccatc ttgcctgatg tttcaagaga gattggctga aaaaaagctg
                                                                      1440
acggettace ggagetatte tecacegata gaaaacgaat egeteeggae teategatea
                                                                      1500
gcaggagttc taattcggcg atggtaccga tgggcggcaa gtttcccaag atcgttcggc
                                                                      1560
aatettteta geagtegate getgteetee geacteggea tagteeatag etcaegacea
                                                                      1620
aattcaggct gtctattatg gcatggatgt cttccgaaca acctgctgac gagccagttc
                                                                      1680
gtgcaggaaa tcccgattca tcactacctt tttacgtgcg tatccagata gccttcggcg
                                                                      1740
agtttcactg ctttgccgag catgttccta ccgttaccga acggacagaa gggaaggaag
                                                                      1800
ctacacaact gaggattcgc cgacgaaatt gccatactgc acaaaggcct gtggaatgag
                                                                      1860
tgcggatagg ctccttttac ataacgctca ctcttggctc ccgaattgag gcgatatgat
                                                                      1920
tggctcccaa ggcggtggca atacccactt gcttacggat gcaccaacga acgcttcggc
                                                                      1980
cgaaaaaggt ttcacgactc ccgatgttcg ataatagaga tgccgtcccg tatgccgagt
                                                                      2040
cggggattga atgtctggta gcagcctctc ggccttcggg tacgctaatc gtaatatcca
                                                                      2100
cacctcctgc gcatagagtc ggcgtacctc tgctgtcatc attcgtcgag gtacgagttg
                                                                      2160
atagccggac ctccgacctc cagaccgagg ccggggagcg tcactcccc accccttcac
                                                                      2220
cctgcaggaa gcggacttcc tcatgttcgg gattagcctg atcgtagcgc ataccgccat
                                                                      2280
gccattggtc acatccggat catacctgca tctttcagga ctgcggatac gacagcatct
                                                                      2340
tetteetete gattteeget atgggeagae tgaetattte geeegaagge aattetaegg
                                                                      2400
ggcttcggcg agagagccaa gccccatcaa tcggtacatg gctgctacta tgcagcggta
                                                                      2460
gctgtggtgc cggtagtgaa tccgcttcgg agtgaaaaga tcccggcacg aggcgttcta
                                                                      2520
ccgcccgtct caaaccgaca ggcccgccac gggaatgaat gaaggaggca aaggggggac
                                                                      2580
gtacgacggc atatatagga tgcccatccg tcgggcagct tctatctttt ctcggaagta
                                                                      2640
accgcttctc cgctttcttt tgtgataatg gcatcggggc gaacggcttg catcactcct
                                                                      2700
cgtccgcatg cggttcgaag aaaacgatgc gctccgcagg aaagcgttct tctctgccaa
                                                                      2760
agcaaccgat tcgtctcgct tcaatatgcg gcaaaggtgg tgcgctcttt ccagaaagca
                                                                      2820
gccagcttgg ggatcgtatt catcctgtga gcatcagcag acgctgcacg ccatcgccaa
                                                                      2880
gcatccgctc gcagccgtat cgtagtttgc acaccagacg ataccttctt cgcgtggagg
                                                                      2940
tattgtctct cgtatcttac tacggggata cctgtttgtt cagaggcttt gccactgaag
                                                                      3000
cgtgcaattc ttcggcgaaa ggatgagcgg cgtccacgtc agtcggatct cttctttccg
                                                                      3060
acaaaacgaa accatgtcgg caaccgtatg gctcctgtca gacgatggcc gtggctactc
                                                                      3120
tggatctctt gcagatgcct ttggtggagt agaaaaacgg acttcccgct tcatccagca
                                                                      3180
cgcgactgcg gcacggcctt ccgtagtacc gccgaagagt aggatcatgt gcggagaggt
                                                                      3240
gtttgaattc gtcggcatac aaccgtgaca gcccttcccg atttctatgg cttctcccac
                                                                      3300
gactatcatc gttgtcaggg tcaggttgtt ccttttacga tttctgccaa atgccggagc
                                                                      3360
gtacctcgga agatttttc accgg
                                                                      3385
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 614 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328

```
agcttgcgac tgatattgag agccaagcgt atcaagcagc ttattcagat atcctttttg
                                                                        60
attgctttga ccggatccgc ttgaaatcga agtacagaga aagtaaggag ccgttatggc
                                                                       120
cacgggctct cccgtctgta gcgtataatt gccgcgaata ggtgccagat ccaccggttc
                                                                       180
                                                                       240
ggggcgatga agagttetee gatggtacge caettgteee etteaacaaa aattgtette
agaatttacc gaataccacg agcaagaata caatcatcaa cgctcccacg atgcgtagcg
                                                                       300
gcgtacggcc ttgatggtca ccggattgtt tgtctcttcc tgttcatatc ggtgtttat
                                                                       360
ttcttgcgcc gatcagtatc gacaggacgg taagaatgta tggcggagtc tgcgagagtg
                                                                       420
tcagctcgag gttttgcgat tgatggcttt ctctacattc agtttctgac tcatagcagt
                                                                       480
aacttcagaa ctttgaacag ggcacgatag cgataatctt tcacttgttc ctccagacgc
                                                                       540
ctatttcgcg cacctgctcg atggcttggt agccgttcca aatgttaaga cggacatcac
                                                                       600
                                                                        614
gacgatgacc agtc
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1408
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329

```
tgcaggggat gccttatgat gcaggtctgt ttaccggatt tatctttatc tcggtattac
                                                                        60
gatggtggca nctccgggag tgccgggtgg agccatcagg cggctttagg tgttttgcag
                                                                       120
agtatgeteg gtttegatga gteettaagg cacteatgat agcattgtat ataaccatgg
                                                                       180
acaacttegg taeggetgta atgteacagg egaeggtget atetegetga tegtggacaa
                                                                       240
actcagatgo gcaagaggoa ggcagtogoa aggtagacaa gaggttagga agaaaagaaa
                                                                       300
ggagaggaga ctgtcggcat gtacagatct cctctcttt gttatttgtt ggaggcttta
                                                                       360
cgtccacagg atggcgcagt atatgtctgc ccttttcagc cgcggatcat ggtgaggagc
                                                                       420
atcttgaagc gtttcgtagc aggagtgcat ggctgacgtt ggccggcatg atgacggacc
                                                                       480
ggccggcttt aggagaagag gttggcctcc gattcttatt tccgcttccc cttccaatac
                                                                       540
tgtacgaagg catcgaaagg tgctgtgtgt tcgctcaatc cctgccctgg tcgaaggaga
                                                                       600
agagagtaat gttgcctact tcgttcttaa gtacttgttg ctgatgattc cgccgtcgga
                                                                       660
atactctact gatgccgata tgtcgagaca gtagctttgg ggtatgtttc ttttgtcatt
                                                                       720
gtttgttttc gattgttagt ctgatctcat gtcttgtaaa cgggcatggg cattaccctt
                                                                        780
attggtcgga gagagcctat acgagaagag ggtgtgccaa acgaaaatac ttctggcaca
                                                                        840
ctctctctt cttgcattcg gaaagcctgt atctccctct cccagcgtaa ggaatcagcg
                                                                        900
ggagaagegg ggttegttag aaageatatt eegaaegaae teegtggetg eetgtatetg
                                                                        960
tttgtacatg actacatcgt ctccaccttg ggagctacct tgcgcagctc gccgagcatc
                                                                       1020
ttctccaaga cggagacgtc ttggtcggac ggcggaattc gaaggcttgg gccgcatcag
                                                                       1080
gagttcgatg gcgaagatca tctccaggtt ttctatgatc ggaagcactt cgttgctgcg
                                                                       1140
ttagctccca tagaaaccgt ggtcttcctg cccgttctgc tgacgatact atcgctggct
                                                                       1200
gcggagaaac agtacattct tgttctgctc accatagctg cggctgcata ctggcggtat
                                                                       1260
catgaatccc gctgtcagac cggggattgg ctacgaggaa ctcaggcaga ttgcgcaacc
                                                                       1320
 cgatatgage tgaacetgee nacgtteget gatatgeeca gtteageeag geatageega
                                                                       1380
                                                                       1408
 aaatcatata cgatgcaaga agttggcc
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1378
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330

```
tggggattgt agccgaactg gtattgccat aacgctcgat attgaccata ctttctcata
                                                                        60
tgggactccc atacgtcggg caacggcatc gatgattcga ggttggcctg atgaggtact
                                                                       120
acccaagtaa tatcatcgtg cgaaagatgt tgcgctccat gatctccaca cagctgttgc
                                                                       180
acatatctac gacagetgtt tgaagactac etgecettee tgatacacat aatgecaacg
                                                                       240
attatcaccg tttcgtgcgt agcaggacat gccgatccac cggccttcat gatcaatgat
                                                                       300
ctttgccgat gccattggag tgcagcacag catccataac gccacttctt cttcggtagc
                                                                       360
ctcgagcaaa acacaaccgg cgccatcccc gatagcggac aagtggctcg atcggtataa
                                                                       420
tccgtaaaag ctgtcatctt cccgtagcga tcacaaggat cttggaataa cgccccgaac
                                                                       480
ggataaaatt gctcccactt caagggcata aataaacgtg ggacaggctg cctgcatatg
                                                                       540
aaagaaaaga tgtcgccaca accgatttca tgagcaacga tgctggcctg gaagggaaat
                                                                       600
gatagtcgct cgagttggtt gcaaggatca agccgtcata ctcttgggat cgataccatg
                                                                       660
acgttcgaag aggtcttgtg ccgcacgatg gccaaatagg aagctccttt attcttgtct
                                                                       720
cgaaggatcc gacgcctttg atccccacac gggtcatgat ccattcgtca ttggtatcaa
                                                                       780
ccatttttcc agatcgtcat tggtaataac atcttcaggg agataggccc caaggctgtt
                                                                       840
atagccgcgt ttatttatt cataatcgaa tttgttgcat aaggacgggc accggccctt
                                                                       900
tttaaagacc atatcccgcc ggaaaagatt attgtggccg ctaaaataaa aaaaaagtcc
                                                                       960
caaagaacag gtctaaggga tcttttgctc gttcttgccg cctaagcgac gaccggcatc
                                                                      1020
gaccgaggga agcaattttt acactgccac ttctttttcg attgccaact taccgcggag
                                                                      1080
tagccacaat caccacatac tgtgtgatag atgtgccatg ctccacatta ggacacttgg
                                                                      1140
ccaaagtcgg cataacggct ttgtcatgag ttctcccttg gcggttctcg ttttggactg
                                                                      1200
tottotttta ggatgtgcca tttttttat ttaaattgtt ctttttgttc caatagtttt
                                                                      1260
ccaagagaat cccactcgaa tcgtgagcgg tcataccgga ttcttctgtt gcttcatcgg
                                                                      1320
cattatcgcc agcagatcgg acattcgatt catcatctcg gggtcgcact ctatccga
                                                                      1378
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1000 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{000}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331

		atcasattct	gtcagcagat	tggcaaagcg	tcgaaagcag	60
agaccgtttg	ctttggacag	allgagitte	Beer Beer Beer	tagtcccctg	cagaagaacc	120
tcaggccggt	acaattgcta	atatctataa	aggtagcaca	ttattatct	gaactcaaca	180
	+++ 00000	+++tocctay	aceateecce	CCECCEC	0	240
			CCCEdates	accepce -	0 0 00	300
		tagecateet	CEECTICAL	CCCE GCC GCC	•	
		taatococtc	PCCalceace	KK CCG BBGGG		360
ggcttcactt	aguccatga	caaceeec.a	gaaggattac	aagggctgag	aatagcggtt	420
gaggccgggt	gaaccgattt	gaagaageeg	tassastoo	tragtatttg	tactgatctc	480
ttcttttcat	aactggttag	ttttggtttg	tgaaaaatgg	tagctgccat	tatccgaggt	540
atgttttcaa	atctcattgc	caattcggcc	ggagggccg	cagoogcouc	tatccgaggt	600
	a a a t a t c t t c	cattttcatt	CCECCELARA	gcaacgaaga	~~6~6600	660
	~+++a+acac	- ctttctctpp	ataguguuu	g c c c g a a c c c		720
	++ ~ ~ ~ + + >	aataaacaaa	ratatagagt	atticates		
		tttataaaga	BCCCTIFFFF	gattgtutg.		780
ttttttttt	aaatageeta	totastates	taactttgac	ttnctaaacg	gtaaaaattg cttgtcggtn	840
gcctgcacgg	atgtaactgc	Letatecca	angetegae	otatotctgc	cttgtcggtn	900
ttttcgatgg	caaataatac	tettetggeg	aagactegae	agtcactato	cttgtcggtn	960
ttctattagc	tcatggcgat	gatgcacctc	ttgggcagga	agicactucg	tggggggaca	1000
gccatggagt	ggcgccgaac	aagtgcgccg	aacgctggtg			2000

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 755 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...755
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332

cctgtcagaa aataaaaagg cttgccatac agcco	ctccc ccgaatacac gacgctgaat 600
aagcttgtcg ccaatagcaa cggcaagcct tcctg	togta cocgaataga gtaggggcte
agtgaagtac agagatcagg agatagcaat aatca	gtate deegaataga gtaggggeta 660 gtate agageaagat gaetgagtat 720
aggccaatct ttaaaaganc ctttttcntt gctta	755

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...2\overline{3}51$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333

```
gggcccactg ataaagcagg agtatggaga ctgcgaatct atttcggccc acgittataa
                                                                       60
 gcctcgtgca tgttgtgtac gagctttgtc ttgtccaaac gatgaccagg tattccgaaa
                                                                      120
 taaaaaacat ggctcgcttc tgtatcgctg atccacccat acacatccgt tctcgcacac
                                                                      180
 ccctatttca ccttcgtaat agccaagtcc gtaccgttca tgtcgcccgg attctctact
                                                                      240
 300
gggatatgcg gctctgatca cttcgttaat gtcctgtccg ggcgaagctc tatggcatcg
                                                                      360
ccacccactg cacgcgatat ttcgatgaag cggccacctt gtccggatag gtaatgggag
                                                                      420
taaagttcat ctccggtttc gctcacgctg cttggtgtgc tgtttgattc tgtctaatat
                                                                      480
gattigtotg tgtccatgat gattacttct tgatattctt cttccaccaa ttattgaaca
                                                                      540
agtagaggca aagcgaggca attcgcgccc cttgccccat gcgttcagcc gttgtacagc
                                                                      600
aggaaccgag gcagactgtt ggccatggga gccatttcag agccgtattg aaacgccacg
                                                                      660
gactatecat caggtattte atacegeega cateagettt ttetettgge tggcaegeee
                                                                      720
caaatgatcc aaatctgacg ccaacgatag atctgctcac cgaggtcgat tttcacaggg
                                                                      780
cacaattcga acaggagaga cagagcgagc aggccgatac attatcgcta tacgacgcgg
                                                                      840
atccttgagc atccccagat tgatcccgat aggcccgggg ataaataagt gtaggaataa
                                                                      900
ccgccggagc gacgatagac gggacacgta tcatacatgc accgcatctt atgcagttga
                                                                     960
gcgtttttac gtgctcctca tttcgatgat gtccgtcctt ccgttgtcca cgatgatata
                                                                    1020
gtgtagctcc caccttcatg aggcttgcgg tagtgtgccg tataggtggt agagggcttc
                                                                    1080
ctgtacccga acgcgccaga agtcgggtga atacccctac ggcatccagt cgggtaccaa
                                                                    1140
tttctccagc ccgaaagagc aaatgttcaa tttctgcaag ccatacccat atcggcattg
                                                                    1200
ccctcattgg tgcaaacgac cacttgcctg tagaggcaac ggcaaagttg ccgccgtca
                                                                    1260
ttgctgcatc cgcgtgataa agtcttcgcg caggcttttg cgtgctgcac gtgtcagata
                                                                    1320
cgtgggtcgt aattgccctt ctccgtaccc aacttgtcat ggaatagatc gctacagcct
                                                                    1380
cgcgtttgat atggatagcc ggcatcacga tgtggctcgg tgctcttcca taagctggag
                                                                    1440
gatacgeteg eegaggteeg tttegateae tttataceet tttetataag atattegtte
                                                                    1500
aggtggcact cctccgtaac atggatttgc tcttcacgaa ttttttgacg ccatgatcac
                                                                    1560
gcagaatgca tacaggatct cgttgtgctc cttggcgtcc ttagcccaat ggacgataca
                                                                    1620
ccgttgcgac gagcattttc ttcaaatcgc agcagcagct catccagtgt gtcacattga
                                                                    1680
gcgtttgatt tcatgagcca gttggcgcag atcttcccca ctcggggcac cgtatcacgc
                                                                    1740
tggatgtcgc gtttgtggcg caccttccag agcgtctcgt catgccactt gggctccgga
                                                                    1800
cttattctcc aaaagcgggc agccgcttcg ctatgcttcg tactcataag tttgctgcta
                                                                    1860
aatttctact gcatgaattg tcttgatcgg caatttctct ctgtctatca cccctgcata
                                                                    1920
tgcatgaggc acgagetgte eggeeetgtg atgtacteeg acetgtggat atgtgateca
                                                                    1980
```

		coastagato	ctccpgctcc	tccaccgagt	acataccgcc	2040
gcaccttgtc	atgeceeata	Caggiggaic	teenstacct	ctatecccte	acataccgcc caccatctcc	2100
						2160
		+ ~ ~ + ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	UUIVLACEE	~~~nnooo-o	0	2220
	~~~+~~~~~~	+0++0+0(20	DI. I. L. al C C C C C	~666~~~~~	00 0000 00	
						2280
ctggtgatct	Caggicacc	gracadado	atcatagttt	totttcacga	aagcaacgca	2340
tgcagacatg	tcctgtcggt	ctgggatatg	accacagece		aagcaacgca	2351
actgaccggg						

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 908 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...908
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334

```
taatgtottt totoccoago aggatagaga cootcaogga ogcacoggoo otaccagoat
                                                                        60
accgaaggcc atcaggaaga tcaggattgg gaaggtgaag ccaagcccga caaggcatat
                                                                       120
tegeteacee egtteegat gaagatgggt ctacgatgtt gtatagegaa ttgactgetg
                                                                       180
tacccaccac cgccggagag catagtgaaa caacagtttg ggtatctttt ccgattctaa
                                                                       240
tgcttgatct gttgggatga cataaattac ctctttatgc tccggatcgt tatcatccgg
                                                                       300
gagtgaaaaa gccggcagca tatactgcag agcttcccct ccttacaaaa tagaccgaaa
                                                                       360
accetetegg acttteggte ttgtteggtt geetteetet tggaettgaa ceaaggaece
                                                                       420
totgattaac agtoagatgo ttaaccaact gagotaagga agaatagaaa aacggottgt
                                                                       480
gacagogott otottoggot ogaaccaagg accototgat taacagtoag atgototaac
                                                                       540
gactgagcta agaaagcctt tcgtttttcg tgatgcaaag gtagtgcata tcccaaacat
                                                                       600
gcaagaggtt ccgcaaaaaa aatacattca gatattaaac cttctcgcca ccacatccgt
                                                                       660
tggggcatct catccatatt catgacgaga aagggctgcc gcctccagac ggtttaggct
                                                                       720
cgtgaatttt ccattcgatg ctccgaaaaa cgtggcgcga gaattttttc gtattggttc
                                                                       780
cacagttttt atttcccgag ccaaacgaaa atttacgcgc gtgttttcag gattacgaac
                                                                       840
catgacgtgt actgaaaaag ttgacagttg ggtggatagt tcacaatggt tactaggtct
                                                                        900
                                                                        908
tctataat
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 967 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...967
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335

```
ttctttgccg atgggcatct gatcggacgc aaggcttcag cttgggcgat aagttttttg
                                                                        60
attgcgaacg tattcccttt gcccgaaaat agtaatttgt gccttgtttg ggtgggactt
                                                                       120
gttctcattc gccaaccgga aataattgga aacaggaata atataatggt ggaaatatcc
                                                                       180
gccttcggtc aattgacgac ccggcacttt caccatagca taatacaaga aaatgactga
                                                                       240
tcgagagaca gaattattaa catcagcatc gaggaggaaa tgaagaccgc ctactcgact
                                                                       300
attogatgto ggtgatogto tocagagott tgcotgatgt coggacggat toaagcoggt
                                                                       360
tcatcgccgt gtgctgtatg ccatgaacga aacggcaatg tgtacaccat cccactcgca
                                                                       420
aatgcgccaa tgctgtcggc gggtgctggg acactatcac ccgcatggcg actcttccgt
                                                                       480
ttatatggcc tggtgcgtat ggcacagccg tggagcctgc gctatccgtt ggtggacggc
                                                                       540
agggcaactt cggttcggtg gatggcgatt cgcctgctgc catgcgttta ccgagtcgcg
                                                                       600
cctcagcagg attgccggtg agatgcttca ggacataata aggaaacggt agacttccag
                                                                       660
aacaatttcg atgatacacg tcaggaccta cggttctgcc gacacgcatt ccgaacctcc
                                                                       720
tcataaacgg ggcttcggta ttgctgtcgg tatggctacc aatatgcctc cccacaattt
                                                                       780
gtccaagcta ttgacggatg tgtggcgtac atcgaagcag atggcgacat agagtggagg
                                                                       840
gcttgatgca gtatgtcaag gctccggatt tccccacagg agattcatat acggctattc
                                                                       900
cggagtgaag gaagccttcg agacgggacg agccgtgtcg ttatcagaag tcgtgccgag
                                                                       960
atcgagc
                                                                       967
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 658 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...658
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336

taaaggtgca	tggatgatct	ctatgcaccc	ttcgttttga	tccgatacgt	cgaactcgat	60
tgtcagtcga	gcgatcgagc	cactgacggc	taatgtgctc	gagccaatta	gctcccacgc	120
			gggcatcacg			180
gcatacgaga	agcattcgat	gcgttggaag	aggcaaatag	cttgccaaat	cgaggaaatg	240
aaaagcgttc	gtagagctta	aaatgatgcc	gatatccttc	actacataat	ctgttgcatt	300
			tccgaaattt			360
			cgtttgattt			420
aggagcagcc	cagtgtccgt	ggtaaagctc	ctgatgcacc	ggccgaatcg	acagaaaaga	480
			aacaagcagt			540

- (2) INFORMATION FOR SEQ ID NO:1337
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 687 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...687
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337

catatacaac	gtacatgtct	ccggtgcagt	acctttctct	ccaaggatct	ggaatagtag	60
taccaga	gcagttcgtt	ctcttgccac	caaagacgag	aggcgccatg	tcgtgcgtag	120
tgccggcgag	taccgaacaa	taggggggg	actcatatog	gcaaagtcct	gtcccggctc	180
aggtggtaca	taccgaacaa	sassastass	anttocaact	gttccattac	gacaggcact	240
tttggatatt	Ctttccaaac	gaggatage	ageegeaace	atccatagag	gacaggcact	300
gcaggggtat	cattcccaga	tectetacae	agacgagcac	tterettete	gaaacagcgg	360
tatcagccgc	gacagtgcct	cttgcttcca	caggicalcg	ttegettgeg	gaagtagtcg	420
tccgacagac	gctgccaagc	tttcttttcc	tcaagctcag	acgagcacag	cgaaaagact	480
tttcgaaatg	gatgcgtgga	tgaaggcccc	gggcttgcct	gattctatta	cgaaacatac	540
ttctgtggct	cacgcatcaa	acctctgatc	gtgtcctctc	ctccgacaac	ggccgcaggc	
ctaacgctgc	tatatcggtc	tgatagaaat	tcttcgtcgc	cagcgtatat	aatccgaatc	600
gaacggacga	aggtatcgac	agcatacttc	gcttgcaagc	gtccgaaaat	ctgcttgagg	660
	gaacgaagcg					687

- (2) INFORMATION FOR SEQ ID NO:1338
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2996 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...2996

```
ccaggcgaag tgcatggcat ctggcgtatg aaggagacca aatgatgtcg gcctttcgtg
                                                                        60
 gcacaggett tegtegatgg agategggta gtagtggtga gggtttegta tateatecea
                                                                       120
 atgagaagaa acgcgatctg atgcggcgat ggaagcggca ctatacagca tgcgtccgaa
                                                                       180
 ggccgagaaa gagttcatcc gtccattatc aggaaagctc gctggactac actcaaataa
                                                                       240
 atatcgaaac ggcttaccga caacacacga agattcaatg caatggagaa taaaagctga
                                                                       300
 aagtggccat ttcccatggc gacatcaatg gtattgggta tgaattctgc ttaagacctt
                                                                       360
 tgccgaagcc tcgatactgg atctcttcac gctgtcatat acggatccgc caaggtggca
                                                                       420
 gcctattaca ggaagacctt gagttggatt tggaaagttg gaaccaagta tcctcggcaa
                                                                       480
 ccgaagcggt gagggcagag tgaatctggt aaactgcata cccgaagacg ccaaagtggg
                                                                       540
 atgggcgttt gctctcctca ggccggagcc tatgcgataa aagctctgac atggccatcc
                                                                       600
 aagccgtgaa gcaaggcgat gcggatgtgc tggtgacatg ccgatcaaca aagcagccat
                                                                       660
 gccgcaggac atctttccat acaaagccat acggaatacc tgcaggccca agccggcata
                                                                       720
 gagggcgaag atgcgtgatg atcctggcgc aggataagct ccgcacagct ttggtaacga
                                                                       780
 tgcagagccg atagcacgcg tgccatcgct tatcactcgg gagcaaatcc tggcaagctg
                                                                       840
 aaggettteg ategeageet eegeatggat tteggtatag tagteegegg atageegtea
                                                                       900
 tggctctgaa tccgcatgcc ggcgacagcg gctgatcggc accgaggaaa gcgacacgat
                                                                       960
 ccggccggcg gtgcaagagg agaagaacag ggattgttag tgttcggccc ttatgccgct
                                                                      1020
 gacggttttg ggggtcggat atggctctgc atttcgatgg cattctgtcc atgtatcaga
                                                                      1080
 tcaggggctg atccctttca agactctctg catggacaga ggggtcatgt gacggcaggg
                                                                      1140
 ctttccatcg tacgcacttc gccggatcat ggtacagctt cgacatcgtc ggcaagggcg
                                                                      1200
 aggettegee egattette egegegeeat etateaggeg ategacattt ategttegeg
                                                                      1260
 ggcatcgtgg cgatggctac gcgcaatcct ctccgaaaga gttatttcga gcggggcaat
                                                                     1320
 gacatgagaa attgccgcaa acagaagatg agcattaatt ttaataccct atgactctat
                                                                     1380
 gtttaaggat aagactatcg tttacacatc cgggacattc gtatgttcca ctacaaccat
                                                                     1440
ttgcgcatga tcaactatgc gcgcagtttg cagacatcct tatcgttggc gtcagcacgg
                                                                     1500
acgaactggt cgcttcataa aggcgccgcc cattattcct tttatcgagc gcttgcaaat
                                                                     1560
ccttgaagcc tgaagacacc ggacatcgtg attccgcagc atacattgga tcacacgaga
                                                                     1620
tcgtcaagaa gctgaatata gacgctttcg tagtggggga cgactgaatg gcaaatacga
                                                                     1680
1740
accaaaatca aggagactat acacatagct atgccaagac gctgaatgaa gagcgtcagc
                                                                     1800
acaagcccaa gtcgtccaaa acatgtagga attatggcgg tcggatacgc gttgattacg
                                                                     1860
ggggaaccaa ggggatcggt ctcgcagtag cccgtctctt ggcaagcaga gatactccct
                                                                     1920
cgttcttacc tacggacatg atcaggagac ggcgcgagca tggcggccga attggcagag
                                                                     1980
agogotocat cogtagagot gotgoaagog atgotacoga tgogaaaggt atogacotga
                                                                     2040
tagcggaagc ccttgagcga gggatattac tctgcaagct cttatcatga atgccggcat
                                                                     2100
cacatgegea egeetttega ggagatgaet ategaegaat ggeagegegt attettgeea
                                                                     2160
atgtccattt ccccaccttc ctgatccaac gccttctgcc gcgtacgagc gcaacaacgg
                                                                     2220
atgtatcatc tttaccggat cgctcatggg aataaaccgc acggcatggc tctgccttat
                                                                     2280
ggagtgagca aatccgctgt acagctctga cccgcaatct ggtgaagcat ctggagcctt
                                                                     2340
atggcatccg aggaatgccg tggcaccggg atttgtagat acggaatggc agaagaacaa
                                                                     2400
acggccgaaa tacgccgaaa tatcgagaat aaggttgctt tgcatcgctt gcgacaccgg
                                                                     2460
atgaagtagc cgaagctttt ttatttttgc tcgccaacgt tattgcaatg gtgaggtctt
                                                                     2520
gactettgat ggaggetaca getteegega acageteaga catgaacgaa aacgacaagg
                                                                     2580
agtaccaage eteteteaat caetggagae ggaaaatata attgacegga aattetaeeg
                                                                     2640
tocgatggtt tttactttgc caagettete agtegtacaa gggtaaegee caataggtta
                                                                     2700
cgatcctgtc catctttgtc ggattaggcg gcgggctgtg cttctgcata ctccttatga
                                                                     2760
tctccgttgg gctgtggccg gtattctatg tatgtagtgg ctaatatcat ggactgcatc
                                                                     2820
gacggacagc tggctcgtct gacgggatca agagtgagat cgggcgtatt ctcgacggca
                                                                     2880
ttgccggaga ctttggttcg cctgcatcta tatctgcttc atcattcgct tgacagcaga
                                                                     2940
gtatcccgat gccttaagtt cgatgaccac cggtattcct gaattgccgc ggtctt
                                                                     2996
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 338 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...3\overline{38}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339

cccaacaaga	actcggtaaa	aattatcggt	gacaatacga	ataaatactt	caggettact	60 120
tcgcttacga	ctcgaagtaa	atcgggtgga	accegactto	gtggcttgcc	acgtgcctgc	180 240
-		700222005	стоянунана	aaggaactt	cctgctcaat cgtttttggc	300
taagaacaac	atccgattct	acacgattaa	cgctactg			338

- (2) INFORMATION FOR SEQ ID NO:1340
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 534 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...534
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340

attatgggac ccttgaaagt tccccctcgg ctatgtttga agtcctccct tataaaacgg	agtattcaga atatagagga gatttttcgg agaacaggct tttgtctcct agctttcgtc	agattitati gacggcaggt tttttccata ttctttcctc ttccaaatgt tatgtggtaa	tcttttggcc ngagtacaaa aatcaggatg ttcgctgggt aaccgttttt gtattgcatc	gaactgtgtg acatttcctn atgaactatt gcgagaccta	aaaaggggcg gcgatcgcta taaatggcca gcaatgcaga atgatgaatt cccggattgt	60 120 180 240 300 360 420 480 534
gagttatggg gctcgatgtg	gaggagcagc cattcactcg	cggattcatt	tcgtgctcag	cttttgtcga	taga	534

- (2) INFORMATION FOR SEQ ID NO:1341
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 877 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...877
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341

gccgaaagga	agacctatcg	gcagcggcat	atcggcgata	accagattgc	cggacctgtg	60
	tctccggatg					120
	gcaggtcgta					180
	ccggcatcag					240
	tgcggaagtt					300
	aaaggccatc					360
	gtattgagat					420
	cgaaaagata					480
	atatcttcca					540
	cggcaggaag					600
	tttcgctgta					660
	ataggacgtt					720
	accataaagt					780
	agcaaaggta					840
	cgcattaaat					877

- (2) INFORMATION FOR SEQ ID NO:1342
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 803 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...803
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342

tcccagtggc aaatcgtcgt	ggtttgccat	cttcgtcttg	gcgtgctcgt	tgagtgtacc	60
gaagaaaaga ttctgcagta					120
aaatccttga ggatggtctt					180
tttgcttgat gaaccaacaa	acataatacg	cgtaattagg	cggattatct	tcgtttctag	240

			anctuatato	PACCCAPASE	300
catcttcact	tgtactagta	tcattaggga	aactgatatt	66000685	360
a+ aa+ accac	trossosost	CCLLETagaa	CCECCECC	0-00	
CCGGCCCCC	ottt anatte	mantcttggC	gttgtttctt	gtcgattaac	420
tcctcaatat	CLLEGARILL	gageeeegg	GCCGaGCAAG	aaggtgaaac	480
+ a + c + a c + a c	t t a c o a c a o t	DCLECTCARR	FCCBCBC	00 0	540
ataatatcaa	actooctcct	CCCCTLRIAR	Cagaaggcaa		
Beautebeeks	atagaatata	ataaaagcac	tcgaatagtg	tcatgatacg	600
tgtcctcgta	guggaatatt	acadage	tastctaact	agataccete	660
ttctggatgc	caaccttatt	gcgagcccc	Lgattegget	Lastatata	720
+ ~++ ~ ~ + ~ ~ ~ ~	attgaatcca	TATCEALALL	KCCE GCC GC	56	
	testestass	troogtacat	ctctaggata	gatcaccatg	780
gcttggctgc	LEGICELAGE	0066600000	- 00		803
atagctctga	cca				
	ctggtaccac tcctcaatat tgtctgctgc gtaatgtcgg tgtcctcgta ttctggatgc tgttgatagg gcttggctgc	ctggtaccac tcgaagagat tcctcaatat ctttgagttc tgtctgctgc ttacgacagt gtaatgtcgg actggctcct tgtcctcgta gtggaatatc ttctggatgc caaccttatt	tcctcaatat cttgaggagat ccttgtagaa tcctcaatat ctttgagttc gagtcttggc tgtctgctgc ttacgacagt gctgcccagg gtaatgtcgg actggctcct ccccttgtgg tgtcctcgta gtggaatatc ataaaagcac ttctggatgc caaccttatt gcgagcctct tgttgatagg attgaatcca tatcgatatt gcttggctgc tggtcgtagg tcgggtacat	tcctcaatat ctttgagttc gagtcttggc gttgtttctt tgtctgctgc ttacgacagt gctgcccagg gccgagcaag gtaatgtcgg actggctcct ccccttgtgg cagaaggtaa tgtcctcgta gtggaatatc ataaaagcac tcgaatagtg ttctggatgc caaccttatt gcgagcctct tgatctggct tgttgatagg attgaatcca tatcgatatt gccgatatgc gcttggctgc tggtcgtagg tcgggtacat ctctaggata	catcttcact tgtactagta tcattaggga aactgatatc ggcccgggag ctggtaccac tcgaaggat ccttgtagaa ctgttcgtca gtgcctcgac tcctcaatat ctttgagttc gagtcttggc gttgtttctt gtcgattaac tgtctgctgc ttacgacagt gctgcccagg gccgagcaag aaggtgaaac gtaatgtcgg actggctcct ccccttgtgg cagaaggtaa accgccattc tgtcctcgta gtggaatatc ataaaagcac tcgaatagtg tcatgatacg ttctggatgc caaccttatt gcgagcctct tgatctggct agataccgtg tgtgatagg attgaatcca tatcgatatt gccgatatgc tgatctcag gctgctgacg tcgggtacat ctctaggata gatcaccatg atagctctga cca

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 540 base pairs
  - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...540
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343

tctttggttt ttcattttca tcaaaattat tttttgttgc atttgcataa tttcttttga 60 ttcatgcgct gcaaaggtag cagcaataag aagaaaagga ataaattcag tataaacgaa 120 ttgaagccga acaggaggaa tagacaaggc cgaatcttcg gatttctttg ctttcccgat 180 attggaagta tccgtacttc gtgctcggct gtggccgaca ggcccatgca gcgaattaag 240 aaacgttgta ggctgtttct tgctccctgc acgatgctgg aagccgttgt cacggacaat 300 cactccgtgc atgatgcagg aagccgttgt cacgtgacaa tcatccgtgc acgatgcagg 360 aagccgtcgt cacgtgacaa tcacgtcctg cagatgcagg aaacgattgt cagccgacaa 420 tegtttegeg caeggetgtt tgacettteg tegeetgaca atgettatat aaaagetgtt 480 tcagggggca tgtcacttga cactgctacc aataacagat taataatcaa tcaaatacac 540

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 777 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:

#### (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...777
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344

gct cggattgcta	cgattgcttc	gaaggcgcgt	ctcaaagtgc	60
ccc gactatatcg	atcctaagat	caccgccttg	catgcggaac	120
atg ctttcatatg	agtcgggagc	atatcgcccg	actctatgat	180
gat gtttctattg	tggagggagt	gatgggcttc	ttcgacgggt	240
gca gtgccctttt	ggccgaaaat	ctgcgcattc	ccgtttgctt	300
cac ggcctattcc	gtggctccga	tacgtatggc	ttcaaacact	360
ccg gtgggtgtcg	tttcaataag	gttggctccg	cttcgcatta	420
cag cgcggatgcc	ggtgtggcca	gcctcggtta	cttgccgaag	480
ccg tcgcggcatt	tgggcttgtc	tgtggaggat	ttagtccgta	540
				600
cga tgtcgatccg	gttatcgaga	agagagcttt	acggagtctt	660
tgc attgcgtggc	ggatgacgaa	gcatttaact	tcacctatcg	720
				777
	ccc gactatatcg atg ctttcatatg gat gtttctattg gca gtgccctttt cac ggcctattcc ccg gtgggtgtcg cag cgcggatgcc ccg tcgcggcatt ggg tggcagatgc cga tgtcgatccg tgcagatgcc	ccc gactatatcg atcctaagat atg ctttcatatg agtcgggagc gat gtttctattg tggagggagt gca gtgccctttt ggccgaaaat cac ggcctattcc gtggctcgaccg gtgggtgcc tttcaataag cac gcggatgcc ggtgtggccaccg tcgcggcatt tgggcttgtcggg tggcagatgc catcgagaag cga tgtcgatccg ggatgacgaa attgcgtggc ggatgacgaa	ccc gactatatcg atcctaagat caccgccttg atg ctttcatatg agtcgggagc atatcgccg gat gtttctattg tggagggagt gatgggcttc gca gtgccctttt ggccgaaaat ctgcgcattc cac ggcctattcc gtggctccga tacgtatggcccg gtgggtgcg tttcaataag gttggctccg cag cgcggatgcc ggtgtggcca gcctcggtta ccg tcgcgcatt tgggcttgtc tgtggaggat tggcagatgc catcgagaag tatgtgggt tgc attgcgtccg gtatcgaga gcatttaact atgcgtggc ggatgacgaa gcatttaact	gct cggattgcta cgattgcttc gaaggcgcgt ctcaaagtgc ccc gactatatcg atcctaagat caccgccttg catgcggaac atg ctttcatatg agtcgggagc atatcgccg actctatgat gat gtttctattg tggagggagt gatgggcttc ttcgacggt gca gtgccctttt ggccgaaaat ctgcgcattc ccgtttgctt cac ggcctattcc gtggctccga tacgtatggc ttcaaacact ccg gtgggtgcg tttcaataag gttggctccg cttcgcatta cag cgcggatgcc ggtggcca gcctcggtta cttgccgaag ccg tcgcggcatt tgggcttgtc tgtggaggat ttagtccgta ggg tggcagatgc catcgagaag tatgtggagt ggaggagttt acggagtctt atgcagaa agagagcttt acggagaa aagccgggaa gggtttgtc gattcagtcc tttgcgaa aagccgggaa gggtttgtc gattcagtcc tttgcga aagccggaa gggtttgtc gattcagtcc tttgcgaa

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 773 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...773
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345

ggaagcttcc	accggtaaga	atgaggctat	cgagcttcgc	gatcaggata	ggctcgctac	60
tgtgncaaag	gtgtcctcaa	ggctgtgaag	aacgtaaaga	agtgatagat	cccgcactct	120
gcggaatgtc	tgtattggaa	caaacagtat	tgaccgcaag	ctcatcgaat	tggatggcac	180
caaaacgaaa	agcaactcgg	agcaaatgcc	atgctgggcg	tatcactggc	cgtagccaaa	240
gcagcgcagc	ttatttggat	attcctctct	accgatatat	cggcggttcg	aacactatgt	300
cctgcctgtt	cctatgatga	atatcatcaa	cggcggttct	caccggacgc	tcctatcgca	360
ttccaggagt	tcatgatccg	ccctgtggga	gctgctgctt	ccgtgagggc	ttgcgcatgg	420
gtgcccgaaa	gttttccatg	cctcaaaaag	gtgcttcacg	atcgtggtct	gagtactgca	480
gtcggggatg	aggaggtttt	gctcctgccc	tgaatggtac	ggaagatgct	atcgaatcat	540
cctcaaggct	gtggaagctg	ccggatacgt	gcccggtaag	gatattacat	cgcaatggac	600
tgcgcctctt	ccgagttctt	caaggatggt	atttacgcta	cactaagttc	gaaggcgaaa	660
agggcaagaa	acgctctatc	gatgagaggt	ggcttatctg	accgaactgg	ttggcaagta	720
tcccatcgat	ctatcaagac	ggatgagcga	aaatgactgg	gaaggatgga	aga	773

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 893 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...893
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346

```
gcgcagtagc cgaagcatcc gattettetg cetgeaacaa tatataettg ceaegceate
                                                                        60
gaagetgaga geataceteg actgeeceaa agetttgtgt ttatggteag tagttegtet
                                                                       120
gtaccatata ggatatecte gateaactet teegggeaaa tegegeaaag gegttttgat
                                                                       180
cgtcacatcg tacttccgca caatgcctct atttgccaaa agaaaagatt gtttttgtat
                                                                       240
                                                                       300
ttgccaatgg ctcaatgcca ccttcgtata tactcttctc acgagatgga atgacttgtc
catatooggo agattoactt ogoccaagoo ottacagogo ggaaatagoo atgaggggaa
                                                                       360
ttgaaactga aattgtgcgg agccggatcg cttacgaaat tcccgtatca ggacacatca
                                                                       420
teatecgaet aaaatgteee attegtttt tteegaatee aacaccatea caagecette
                                                                       480
gccttcacgc tagccagtgc caagctctcc gctatacgtt tgctttgatt cgatgctacc
                                                                       540
acagettgte gatetgeact tegacgteat geattttata gegateaact teateceatg
                                                                       600
caaaatctcg cgaatctcac cattcacgcg tacgtgcgat agcctttctt acgaagcctt
                                                                       660
tegaataget cettataatg eccettegeg agegaaceae eggggetaae aaagetatet
                                                                       720
                                                                       780
tacggccatc atactttcca aaatgaggtg gaagatttgc tcctcggtgt atttcaccat
                                                                       840
cttcttcctc cggnataaga ataagcctna gcaacacgag catagagcaa acgaagaagt
                                                                       893
cgtacacctc tgtaacggta ccgacagtcg atctcggatt ccattggtcg tct
```

- (2) INFORMATION FOR SEQ ID NO:1347
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1284 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1284
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347,

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60
gggaatatgt cggcttttac agtcacttta atcatccgga acgtgattgg aaactcaatt
tgcaagggga agaaaccccg ccggagccta atctttttga tggaggctta ctaaagcgaa
                                                                       120
aaacgctcta aagcgaccta tttactgaat tacttgtcgt ttttatccct actctgaggt
                                                                       180
ttatcggaca gcaatgatct agacatatac cttcggtgtt gataagtttt tgttcgtatc
                                                                       240
                                                                       300
tccaaattat ttctctcgtt tatgcgttat tggctaactt tggagcgtgg tatatacaat
tactacaagt gaagatttag aagagaccaa ccagcatgca ttgcctgata aagagagtgt
                                                                       360
                                                                       420
ttatcacata ccggtgatgc tcggcgagtg ttggaaggat tgcgtattga tcctgacggg
                                                                       480
tgctatgtcg atgtcacgtt cgcggcggcg gacattcccg ggctatcgtg gaaaaattaa
gctccaaagg cggctgtacg ggttcgacca agatgccgat gcttgtcgaa acattctcca
                                                                       540
gatgagcgct tcacctttgt aacttccaac ttccgctacc tcgccaactc atggattatt
                                                                       600
                                                                       660
acggagagga tggagtcgac ggcatattgg cagacctggt gtatcgtcac atcatttcga
                                                                       720
cgaagaggag cgcggattca gtttccttcg gaaagtcctc ttttggacat gagaatgaac
                                                                       780
gctcgtgccg gccgcatgca gctgccatct tgaacgaata cgatgcctcg tccctgtccg
                                                                       840
ccctttctat cactatgggg aactgaaaca ggcacgtcgt tttgctgcat ccatgtccac
                                                                       900
tacagggagt ctctttccgg cggactgcaa actgtggggc aattctcgag gccgtgcgcg
                                                                       960
gtotoatoto toogogagaa gaaaagaaac attggcotgc atottocaag cottgogcat
                                                                      1020
cgaggtaaac gatgagttgg agctttgcag caaatgctcg aagcagccct cggctgtctg
agaagtggtg gcgacttgtg gtaatgacgt accattcgct tgaggacagg atggtcaaaa
                                                                      1080
                                                                      1140
cgtccttcgc tacggaactg taaaggcacc cgatgaagat tctttgctct gtacggagca
                                                                      1200
ccacagagte ettggcaaca gateactege aageegtgae agettegaea aaagagetgt
ccgacaaccc ccgttcaaga agtgcaaact acgaatagca gaaaaaatat aatggcagac
                                                                      1260
actgcgaaaa acaaatcagc gaag
                                                                      1284
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 710 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...710
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348

```
60
gacggaaaag aggctgatgg agacggcaga catgacgagg acgtcaccgg gaaaaagtag
                                                                       120
ttgaacagga agacgacaag gctgatgata gaggcattat cagggctacg acgacttcct
                                                                       180
tggctatgag actccagagt ttggcctctt cagactattg tttgccagcc cctgtaccac
                                                                       240
gatggccgaa gactggtgcc cacattgccg cctgtgccgc caatgagcgg aatgaagagg
                                                                       300
gccatttggg attggcggca aagagggaat cgaatcctcc caagaggatg gagtggccaa
                                                                       360
tecteegee atgeegatga gaageeaegg eaggegtget gegtetgeat atagaeetta
                                                                       420
tecgatgett etatatettg egaaataece gageaagetg atagtegege tegtgetgtt
                                                                       480
cgcgaatttc gtcgatcaca tgtcgatagt gatccggcct accaaacgac ccgatactgt
                                                                       540
ccactaccgg agagccacga ggtcgtactt ctctatcttc tccgcgactt cttcgatcgg
                                                                       600
tcattgtctt tgacggaaat aggctcggtc ttcatcacat acttgatctg gaagcggaag
                                                                       660
ggctggtgat cagtttcttc agcggcagca ctcctttagc cgtcttcatc gtcgatgaca
tagacgtagt atatctcgtc cacatctctg cctgcatacg catctctcga
                                                                       710
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...3\overline{40}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349

gtatgaaggt tgtgccttac	caaaactgct gcctcttcgg cacaccggct	ctgaagggcg tcagccgata gtaaacaaag	tccgtatgag gaacaacagc catttaatag	ggtggatctt tgacaacgat	tatatgcctc gtgtccttga catcctcgga aaatatctga cgacaaacag	60 120 180 240 300
acgtcttatt	cgacaataca	tccctaaaga	andtagaga	accgacacaa	cgasaaasag	340
atctccatta	tgagaccttt	gaaaaataat	aaguggagga			

- (2) INFORMATION FOR SEQ ID NO:1350
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 681 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...681
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350

tatggtgcag	accascatec	tggaagagaa	gaaaaaccgg	atcatggaat	aatggtgtcc	60
tacebacaac	cottcaacct	gatgatgggC	aaaatcatgg	tatcggtctc	gtaggcctta	120
cacacacage	ctantaggga	gtgctcaggn	actgctgctg	acggtagcac	agatcgcctt	180
ceteggeeat	ctgtacgccc	agaggccctg	agtcggatgc	aggcttccga	cataacgggc	240
ctccggcaac	catgaatgca	gaggacttcg	ccgagatgaa	ggaagtgatg	aacacatcgg	300
atggetegee	ttcagaacgea	tottcotoat	gtttctcatc	ttctcatcgg	cggctacctg	360
gggcaccaac	castcttcgc	cgttatcgga	tcategtatc	gaacgacgaa	gacaccagcc	420
t-setect	caatcttege	acctcctgat	gttcggcttc	tateccecct	acggcagcat	480
agticatgat	guilgigate	cacattctaa	tottcoctoa	tecetteac	ttcccccctg	540
gaacaatccc	aaggateget	CECACCCCE	-999-		•	

tgatgatggt	gcggttgccc	tacgacgttc	cgctgtggca	ggagttgcaa	gcatcggcct		600
gctgtacgga	tgcttcgtat	tgaagaggtg	gatcgggcga	agatttaccg	cgtaggcgtg	·	660
ctcatgtacg	gaagaaagcc	a					681

- (2) INFORMATION FOR SEQ ID NO:1351
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 669 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...669
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351

tcgttcctgt	cttacccgat	ttcaatgcag	ccgatgcagc	aagtatagta	cgcattccga	60
			atgggagaga			120
			atacggtctt			180
gcttgctcag	ccaggagtag	aaggattgag	tcgctctttc	tccgaacact	acccttccgg	240
cttcaggcag	aggatattcg	ctatgccgag	gtgtcgaacg	acgatctcat	cctgtgaact	300
atacctccgg	tacgaccgga	ttcagtaagg	gggttatgct	tcggccaaca	atctggccgg	360
caatgtaacc	tacgttaagg	atagagacat	tagttccgag	gcgagacgat	cctttgcttc	420
cttccattgg	cccatactta	tgctgtgcgt	tcaacttcct	tacgccattg	actataggtg	480
tgcatgtgta	atcttgggca	aaatcccctc	tcctctcact	ctgatcaaag	cctttgcagt	540
gtacgcccct	catttgtcat	catggtgcct	ctcatcatag	agaaattgat	cacaaggcaa	600
tagctccgaa	aatcaagaca	ccgttaatca	aattcctcta	agacttcctg	tgctgaaaaa	660
ggtgataca						669

- (2) INFORMATION FOR SEQ ID NO:1352
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2624 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...2624

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352

gtgaacgaaa	cegateette	ccgtctgatt	ctggccggag	atatggcacg	cttccgccgg	60
tragragtat	potgagtccg	gcattggatg	ccggggtatg	gaaacttcct	aceguiceee	120
+ n + n c a + q a a	totacactga	ccgaggtgta	cgtcagcaga	aagaacccgc	Cattetee	180
ctagccacga	gcctacccgt	ttactttcca	atggtatttc	ggaaaaaacc	aagiigaaca	240
taaggattCg	pgagatgtgt	cggctatttc	cggcactgaa	Ligalagaag	caccgacgee	300
togtttogga	ctetaggcat	ggacgagacc	attattgtca	gctttccaat	aaacgigiii	360
tageetataa	totogggcate	cgcagtcagg	tatgtactac	gaagaagagc	LEGICLESES	420
coatcoatto	otooteacec	gaataactat	cgttattgtg	acaggcgaga	Caagacagac	480
++cattacca	togagagatc	gtggagattt	tgcggttggg	Caaacgacac	gagetgtacg	540
atttagattt	gccgatgcta	ccatcagcct	tgtggagcaa	gggcgcgaac	agaagcaaga	600
ttactcctcg	atggactgac	agccgaaaca	gccggctgac	Calglacaa	agacaaaaac	660
tatataatac	agttgcttga	ggactaaatt	ctatggcaag	tateceggee	agacgcaaag	720
ccatcaaaga	ggatgtttct	tttcggcctt	ggaagtaaag	tatgeetatg	CCattactig	780
CCACAAGCGC	agggaggaca	gtggaaacat	gtctatgtag	acacgggcac	geengeenee	840
tacctcataa	cgagcaactc	tgtcgttggc	tgtatacggc	agractigag	CLLCEBABCE	900
actittticte	ptcaatactc	cgaaggatat	gtcccataag	aggggaaaaa	gcccccaca	960
actoccasota	gagacctata	tcaccaattc	gttcacctgc	caatacgttc	ctttaccgtc	1020
COOCAOCOAA	cectetcetc	atagcgcagg	tatagatata	tacgggtact	Cagcaging	1080
Seecases	ottgagggca	ttttcaaatt	ctgccaccgt	attatcgatg	tggtattggc	1140
atacaggcgc	gactgccaac	tcagacgact	atcgaattcc	atacgagicc	ggcttttatg	1200
gccgaaccca	attcgtgtac	gatggctttc	cttcgggaaa	gccgtggcga	gccaagicia	1260
tatogototg	atcgccattt	gaggatgtac	gagaggggag	ataggaacag	CCCCABCCCB	1320
gogacttgcc	atagactttt	ttgctttttg	tatccagtcg	tacticalac	Cgtactggaa	1380
ttgaagatca	toggagcaag	gaatgcagat	tgctttttag	grgttttag	Cicgatiggi	1440
aaatagetgt	gtacgcattt	ccgcatcgaa	gagtagtacc	actgcttgaa	agccttatag	1500
ccgaagttgg	aacgcaggcg	agcaaatcct	cggccactcg	atagegatig	accgigicit	1560
tooctocate	aagacactta	gtttgtttc	caactcattt	ttccagcgaa	Collecting	1620
coatatteec	ggacgatcag	attgccgaac	atgatattca	ggttgccgat	CCCCCCCE	1680
accaptitic	ggaaatgtag	ttctgtgaga	actgcgcatt	gtctccatgc	igaaaaacca	1740
otagogggt	ttgagttcga	ttcccggatt	ttttccggca	tgattattct	gccggacaag	1800
geteccccat	cgagagctga	atgtcttgtg	gttttatata	ggaataatcc	ggigigaaag	1860
gcccaattcc	gtacggctat	atgtgaaaag	atccaatcgg	cgatattgca	gicggicagg	1920
actotecete	ccaattccac	ttctgcaatc	: atgtcgctca	. atccggtacg	ggaagaggii	1980
ctgtccggcg	gacttgttgc	aaacgcgagg	tatctcaggc	atggtgattt	gecacattee	2040
toctoctaac	ggaccggaga	attttcggct	. acgagcggta	gttgcagata	gillallage	2100
aggcggcgga	gactatcgga	gatgtcggga	ı ggctgtctgt	gtcggctaac	ggaggarrig	2160
capttgggac	agtggaagca	caggettegt	: ggccatcgca	ceggigeiee	Cataaagtaa	2220
сараасарда	atatggagag	gagatatctt	: atctcattgt	. agtcaaaaac	agillilaca	2280
taaccatttt	atgccgggca	aagtatacta	l ttctttattt	. tcctttttg	gggaatttt	2340
cacaacagga	tagatcatat	tttacgctt	: tgtatcctgt	ttttgaaaa	agcaaacccc	2400
ggagtttta	tttgactctc	ggggttcgct	: ttcgtttatt	, accegeace	gigaagiiii	2460
tattgattgt	tgaaaacctc	acatgcgctg	g cagaggeteg	g aaccaaatt	gegeegeeat	2520 2580
agccgttgtc	gatacgggct	. acgttgagca	a gaacttatto	cacgcange	attccagcgg	2580
ataagctgcc	tttcgcggag	tacggatgc	g accagtcgtt	agcc		2024

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1299 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1299
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353

```
aaagaaacgt ttttatctga caccaatgat tctgatgatc acagtttgca agagagctgt
                                                                        60
ttcctaagga aattagtttg ccgatatgtt ttatttggac ctttgcgctg gcaaaaagat
                                                                       120
gcacctatgc atccaatgac tgcagaaaag aaaaattact taataactta acccacttaa
                                                                       180
acattgtttt ctcagagaag aagcacaatt tcaccgcagg accctgtatc ctcaatgact
                                                                       240
tagtttgaaa gatgctgcat cagcatgtct caattttgca ggaacgggtc tttcgttctt
                                                                       300
gaagtttctc accgcgacaa agagttcgat gctgtaatgc tcgagctcgc aatctcttca
                                                                       360
aagaacttct tgatgtgccc gaaggctatg aatacttttc ctcggtggtg gcgccagcct
                                                                       420
ccaattctac caagtaccgc taacctgcta aagaagaaag cagcctttat caacaccggt
                                                                       480
acatgggcaa caacgccatc aagcaggcca agatcatgac gcaggtatat ggtggagaat
                                                                       540
agaggttttg gcttcatctg aagacaagaa cttctcatac atccccaaga tttcgttatt
                                                                       600
cctgaggacg tagattattt ccacttcacg acaaacacac gatctacggt actgaaattc
                                                                       660
gtaaggactt cgacacgaag actcgcttgt agcagacatg tcttccgaca ttttctctcg
                                                                       720
tccgatagac gtttcaagta tgacctcatc tacggtggtg ctcagaagaa catcggtccg
                                                                       780
gccgagctac tttcgtattg gtaaaaacgg atgtgctcgg acaagtagat cgtctctacc
                                                                       840
cgatatgctg aactatcaga tccacatcaa gaaagactct atttcaacac tcctcccgta
                                                                       900
ttccccgttt atgtagcact ccagacgatg agtggtacaa agaactcggc ggtgtgaagg
                                                                       960
tgttggaaaa gatgaatctg acaaggcagc ccttatctac gatgccatcg acagcagcaa
                                                                      1020
gatcttccgg gcacggttaa tcctgaagac cgctctatca tgaacgcttg cttcgtgaga
                                                                      1080
aggatgagta caaagaactg gagaaagagt tcgctacgtt tgcagctcac gcggcatggt
                                                                      1140
aggtatcaag ggacaccgct ctgtaggcgg tttccggctt ctctctacaa cgcattgcct
                                                                      1200
atcgaaagcg tacaatcttt ggttacgtaa tgaaggaatt cgaagctaag cactaatcgt
                                                                      1260
gaataaattg aaaggataag atgattgccc gatttcgct
                                                                      1299
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 652 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...6\overline{52}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354

gaaaaatgct gtaaa	actgaa ataaacttac c	catatogttt t	tttataagc	agaatgcctt	60
ctgccggaaa ataac	gccgg ttccctattt t	gaaagacgt a	aatttcccgt	ttcttcccca 1	120
cctcaaagct gtttt	tgaaat gtattcgaaa a	tcctcgcta c	catcaaaagc	atcgtaatag 1	180
	tcaaa tttttctctg g				240
cgtttttgtt caata	aattcc attgtttcgc a	itataactga t	tataactctt	ggcctacggt 3	300

		-++-+	cancenatte	otttaagata	aatgctcttg	360
ctttgacgtc	gaccgtttgc	algaliciti	Cgaccagccc	But the sale by	ttattatat	420
ggcgtgaaap	acttcttttg	cgatttgtcc	cattccgtaa	gtttccgttt	ttctttgtct	,
660606000	tototoccc	gaacgtgca	tttccttttc	cctgtcccat	ccgaacagca	480
tccggagatt	tetetetet	gaaacgigca			CCGGCGGGC	540
tcaaaggtac	tccaacgggc	ttccatccct	tactttaagt	gcittacga	ccgacaaagc	•
conttotont	ctttctctat	pgagaggatg	gccgccgact	tgcgctgagt	tccgaaccga	600
ggattettat		66-6-66-66	anatagatac	acagataata	ca	652
tatgcccacg	cagtttaatc	Cgttcggaca	aaatggatat	acagataata		

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 972 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...972
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355

++	gtaagatttt	trataottaa	ggttttggtt	aatttgggag	gagtgagtcg	60
tgatggaaaa	toottttata	ttctgatact	cttotctace	tctcttgtct	gaatttatcg	120
tgagactcgc	atatatata	aananttoan	tactttcgcg	ggcaacaaag	ttaatcgatt	180
ttatttttcc	ciciatatga	adgageceag	otactatooc	tctaagattt	atcactgcag	240
tcaacaacaa	ccaactagca	ataacaacae	castotcooc	tttagcggtt	ttaccctgca	300
aagaacagcg	gagtitgigt	tacaacaata	CCCSSCCSSC	ctatgcagcg	catgaaaaag	360
ggcaacccta	aggraguace	etetteacen	gtcaagegag	ggtgctcggt	tggacggtgt	420
gcaatccctt	caagategge	tagetteet	actocatato	agtccaataa	ggatctgcgc	480
cttggcacag	gccgatgctg	nettectatt	treatritra	tctctctact	ttggctcaga	540
aatcttatca	caatggcagc	accicciaci	tataaccatc	atagaggtgc	agacgttacc	600
tctgcgctat	ggctttacg	gcaaggcgga	geggeeace	atagaggtgc	teccetctee	660
gaagacggta	agateetgee	attacagge	graggracer	gcctactatt	gtatgcacga	720
cagaccgaat	catcgtggag	cctaacacaa	gcaccccaaa	ctatctatac	gtatgcacga	780
cttgtgcgaa	cctctgatcc	geetgeeege	cgcgagctgc	agtcagtata	tccttcggat	840
cgtacggcaa	gccttatgta	caggtggatc	cggccaagac	atacacaaac	gtggtacgag	900
cgaacctaat	gacgagagcg	attttgcgcc	ccccgacccc	gracgcagge	tattggggac	960
_		gagcgaaatg	aagccggacg	aacacccaaa	gattttcttc	972
ccctgcaaag	cg					,,,

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 616 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...616
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356

```
ggacaacatc gtcaatacga tcaatagtct gcgcgatacg attgctattc gttcgtcatc
                                                                       60
gttattcttg tggttctgtt tttcctcgga cgatggcggc cacatttatc atcggtctga
                                                                      120
cgatccctat ttcactggtt gcctccttat ctacctgatg gctacaggca atacgttgaa
                                                                      180
tatcatttct ctcagcccct ctctatcgct atcggtatgg tagtgggacg atgccattgt
                                                                      240
                                                                      300
agtgccgaaa acgtaacgac acatattgaa cggggcagct atcccaagca ggctccatac
acggcacgaa cgaagtgggg atctccgtta tagcttccac gctacgatgc tggctgtatt
                                                                      360
cctcccattg acgatgattc aggggcttac ggtatccttt tccgtcagtt gggttggatc
                                                                      420
gtgagtatta tcatgattat cctacggtag ctgctctcag cctgacgccg atgctctgtt
                                                                      480
                                                                      540
cgcagttgct cagcgcgaca naaagcaagg acggctgcaa caaaagctct ttgtcccgac
gaacgettte ttgattetgt agaategage atatgageeg ttteetgatt gggaetgtga
                                                                      600
                                                                      616
gacacagaac cggtta
```

- (2) INFORMATION FOR SEQ ID NO:1357
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1347 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1347
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357

ttttggacga	actoatoago	cactaccca	aacattatta	tagagettet	cagaacacta	60
		cgctaccccg				
cactttcgct	ttccatcccg	cccctgaaaa	gagcttcacc	gtggcttcac	taatctcctt	120
ctaagtggta	agcgcgacac	aaatacctca	tcacacccga	atcgaacaaa	agcaaaggtg	180
cctatatcgg	ctgcgtacag	ctgtaaaccg	cgacaaggtc	agtatccggc	tgcgacccga	240
taatagggag	ccaagccctc	cctggccaat	ggcgatggcc	tttacctcct	gcacccgacg	300
gcaacatgag	cggtacgcgc	atcaatgtgg	ttttacccga	cggagcatac	aagtggacaa	360
tcctgccggc	atcgtatcgg	gaacaaacgt	atccgcaatt	acgacatccg	tttcgagaaa	420
gctctctcgc	aagacaactc	gccgttcgcc	tcattcccgt	atctcttacc	ttgacggatg	480
ttccggacgg	ttctctctct	cgatagaggc	cgactgctac	ccatctgcaa	aggctacgaa	540
acagctgctc	acgagcctgc	cacacggttc	gatgaagagc	agatccgcag	aatctgacca	600
aattaggtgg	tacaccgctt	gaagccgtat	cagtcgaatc	cggctcagtc	acgactattt	660
catcccgctt	tctctcattg	gccggtaagg	agagatgcag	tccaatcctt	catcgagaaa	720
gcctcctcta	tgcctaacgt	gaggaaaaac	cggtcgtaca	acgtcgcatt	tctcctgcgg	780
cgagagcttg	caggaggag	agcagagcct	ttccttctta	gccaatgtgg	cgacaaggaa	840
gcagaaacct	tctatcggca	aatgggatat	acatctatcg	ccccgccttc	gaacactcgc	900

			nonctatoto	coctateatt	tgggctattg	960
atccccaagg	cgttccgctt	atgttttcga	acactgicte	cetactast	tgggctattg tcatggcgaa	1020
	0000000000	atcoccotac	agagaaccgc	actace co-		1080
	anterestte.	gactgccaac	actettaaat	ACC860000		1140
	a a a a a a a t a a t	acgaggggaa	acayaytaay	ACE CE CE	- 000 0 0	1200
<b></b>	a a a a t a a t a a	tattccatpt.	tcatagccac	LLELUCUCA		
cattagaaac		gtcattcgca	aaatgccgtg	caatggtctc	taataagcct aggtattctt	1260
gacgtaagaa	aagaccaacg	gecaceegea	tacttactcc	popactacca	aggtattctt	1320
ctgggcgatg	ttgtcttctt	Citgatggea	Caccegooo	8888- 0 0	aggtattctt	1347
ccaaatgtga	agacgctcgg	aataggt				

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2473 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION  $1...2\overline{473}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358

```
cagtgtgatt cagcatgcct tggtatagcc attaccacga tcatggtcaa tcactgctac
                                                                        60
gcctcagccc caaagcagct ttggtgaaac ttgtagccta gagaagaaat agacgatacc
                                                                       120
atcattcttc gtgcagagat gcttgtcttt ctggatcggt gatatttacg ttgttgatcg
                                                                       180
taacatcaca catctcccat tcgtaagctt ttcgatctct tccattacag gcaccggctt
                                                                       240
cgttgatcgg cagagaatac atgatcgcag aaaccgagag ctttcaagcg atcctactct
                                                                       300
totgtgagtg gcaaagaccg attaccttac cggttacacc ggccgttttt tggcttcgta
                                                                       360
gcagcagagc ataccgctct tgccacctgc acgataataa gtaccgtatc tcccggcttc
                                                                       420
accaatttgg ctgtctgagc agagcacctg ccacatcaag tgccgataga gccagctttt
                                                                       480
caggcaaatc ttaggaatct tcgcatagat accgctttcg aagagaatag cctttccttg
                                                                       540
atgtccactt gatctacatc cggacgaatt tccttgattt tgtcgatggg agtggcgtta
                                                                       600
gagaaagcga cacgagcgtg gcaattttat cgcctacttc aagtcgattt tgtctttgag
                                                                       660
agcatcgccg atcitttcaa ctacgcgaga agcatcccgc ctgagcctgt aacagggtta
                                                                       720
cgatgettte ettgttgget acaatgecaa geatgattte ggegatttta geettatete
                                                                        780
caccggettg ttcatggate tgcgtgaaac ttgcagagte tatattcaaa gtctaacate
                                                                        840
gataagaatc tcattgtcgt agatttcatc catgttgttg tcactttttc agcgggctgg
                                                                        900
ggtagaacgc cctgaggggc taaaacacgg ttgtgccgta tttgtttcct ttcttttgca
                                                                        960
ttgtcgaaac gtattgagtg attttgtgag ttttggagtt gttatttgct aagccccaat
                                                                       1020
atccgacggc ttctgccgga gtggctatct cacgacccat ttccttggcc atacgaacac
                                                                       1080
tttttctacc aattctccat tagagcgagc taaaactcct ttggataata tacattgtct
                                                                       1140
 tegaaaceta caegeacatg teetecatea atgataceag tgeegegagg ggaaacteat
                                                                       1200
 agogtoccac acctgctaca gtatagtggc atotgcgggg atactttcgc gaaggaaaac
                                                                       1260
 gaaatcacgc attttccgct gataccgcca tttacaccca ttacgaagtc gaagtgcata
                                                                       1320
 gggattggat ataacctttg cggtgaagac gaagagccat gtncgatcat gccttgtcga
                                                                       1380
 agacttcaag ttcaggtttg atgccacgct cgatcatttt cccccgaaat atttgatcgt
                                                                       1440
 gttttccgta ttggtgaaca cttcatcacc ccgaagttaa gggtgccaca atccaaagta
                                                                       1500
 gccatttcgg gaaaaagctt gtcggttgca gacgttcatc attcgtcatg cccacagcac
                                                                       1560
 ctcctgtcaa ggctggatga ttacatcggg acataccgcc ttgatggctt ccatgactct
                                                                       1620
 ttgaagcgat ttctatcttg agtaggggta ccatcatcgt atctcaatgg agatgaatga
                                                                       1680
 tgctggcacc tgcatcatag gccgatttgg cttcagtaca cactcttcta ccgtgtaggg
                                                                       1740
```

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aacggccgga ttatgctctt tcagacctct gcaccgcaga tggctgccgt aatgatcatt
                                                                      1800
ttttccataa tttcagtcgg tataatggtt ttacttattt gttgcgctgg caattagccg
                                                                      1860
gtccacacaa gtgccggtag cacggcaaac aacaataggt tcgtcaagca ctcggctgcc
                                                                      1920
gactccgaaa tatccgtacg aggacgaatc accttacgag ttcgaatttc atctttcgac
                                                                      1980
tggtatttcc cacatgagtg atttcgcctc agcctctata taatctccgg caaataccgg
                                                                      2040
agccaaaaat tocacattto ataagcacag aagaggcott catcaccato ttgcatgata
                                                                      2100
aggagtttgt ggcaacgtct ccgaagagtt ggagcatgcg agccccatct actaagtacc
                                                                      2160
tccgtaatga gcatcatgcg cactcatccg aagacggatc attgagtctt tgtcatagtc
                                                                      2220
gtattggagt tattgtgagt agttgatttg tctagagcag ggagccgatt agcggaggat
                                                                      2280
                                                                      2340
atagtccacg aatatgccgc tggatggatt tgttccatgg ggatctgtcc gatggggtgg
atttcttcga ttctgccact acacagtctg ctgccattgc catcaggggc tggaagttct
                                                                      2400
ggttgtgcct ttatagatga gattcccaaa ttcatcgcca acacttccct gataaaggca
                                                                      2460
                                                                      2473
aagtcggcac gga
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 597 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...597
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359

tttcatcatt	tttggttcca	aaatcgggag	gcactcctat	cgaatcacct	aaaagagcct	60
coatattocc	catgaagtgt	aaagaatcct	tggcagataa	tattcagttg	gattaaactc	120
catotoaaao	cagatttaat	tototetttt	ttttgttggt	ttttatctaa	agtttatgtg	180
tacatttatt	tttcaaactt	caaaaatcaa	ttcgtatgga	ttttaaagac	atcttgaggc	240
aacttcagag	agaatcgaaa	aacttagaga	caatttgcaa	acagaggagg	caacaagaat	300
accettatea	taccatttat	traggraats	ggatatgacg	tettaatcce	ttggaagtta	360
ttccccatta	tacttgcgat	ataggcacaa	8820008080	aagattgatt	atgcaattat	420
cccggaact	gaacccatca	tttgattgag	tocaaacatt	ppcpcpatac	ccttactctt	480
gegegataat	gaacccacca	tactttcata	tttcatctac	aaaattcooo	atgctaacta	540
gccgataatc	actactaagg	attendent	gatesaget	221222102	toaaaac	597
cggtatcatc	tategettet	acacagacci	ggatcaagct	aacaaaacga	ceananc	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 657 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...657
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360

aaacaaaac	tectegaaca	actgatcttc	acctttggga	gtagggccga	aataatcaaa	60
gggcaaaaac	catantagat	caatacggaa	tecacetete	gactategee	tagttgtgct	120
ggagttcggg	Cglcalcgal	caacacggaa	cotattata	cacaaataat	сраярссраа	180
tacgctgcac	caagtcctta	ggactcgggc	Catatigues	teresease	at cognition	240
ttcgttattg	gtgccaatgt	aatatctgca	ttataggcct	tgcggcgggc	accegaaceg	
gactatactt	atctatgcaa	tccacggtta	aaccatggaa	catatacagt	ggcccatcca	300
ttccgagtca	cotttagaaa	ggtagtcatt	gaccgtcact	acagcacgcc	gttaccagtc	360
Licegageea	cacatacaa	tagggtagct	acaatgtett	tccctcaccg	gtagccattt	420
agagcattga	ggaatatggg	Laggerager	accatege	tassatat	agtgaatcat	480
cggcaatttt	tcctttgtgt	agactgtacc	accgacgage	Lgaacaccac	agtgaatcat	540
gtcccacaag	tttcattgcc	tcctgccacc	cagtggtttt	ggtagacggc	ggtatctcct	
cgatcgagac	gaaatcatgg	ttgattgcga	gatcacgatc	aagatcaggg	ctttgactcg	600
aataottoot	ttopgcgaat	ctgcgacagt	atctttgtaa	tagcaaagct	tcgggag	657
445465566	000-0	5 5 5	•			

- (2) INFORMATION FOR SEQ ID NO:1361
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1089 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1089
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361

ggacactaat	ootoaaaata	gcgaattgtc	ggtttgctgt	tgttataaaa	acaatatctt	60
tattcccatc	gtagtggtcc	ctgctcgtct	cgaacaagtg	agtggggtgt	aagagggaat	120
caaataaaaa	tecepageag	tcccgctctg	taagctttta	ccgccgtgtc	ggttttgaca	180
tacagactet	tatcacttcc	aaatgatgcc	actettcatt	ctccactatt	agaggtggag	240
ctusaduas	Geogeans	acagaaaaga	gatgaagtaa	gccagaatac	ctgctctacg	300
agttacctat	aaadtatooa	gagaagacct	Ceageaaage	agttccccgg	cactaagaga	360
ageegeetat	acascucscu	ttttacaata	actattacaa	tggaagaggt	aatccttcgc	420
atagatetea	ggaagtatta	ttgcagtcgt	togatoogga	aaaaatccgt	caggogataa	480
tongcatta	grgarggrea	gtgtgcacga	agaagctgca	cgtatcgaca	atattgtccg	540
totatescor	cacacacac	tcagagcggt	gagettetea	ccetegaaaa	atacaggatc	600
tetgeaaceg	accuractors	catttaaatc	ctttcatecc	aaaaaatata	ttatctatcg	660
gtgttgagga	ggaactgatg	gtgacagcgt	acatccatoa	agcatacgat	ggacggcatc	720
agagtggcgc	accgtagage	grantetaa	otaatoccas	cateagttce	catactcctg	780
gtaacgatag	agaagacgac	cttcaaaat	PeageBeege	tatoccaoca	aattctgctt	840
caggcaaatg	atgacttttg	cttcggaagt	aaccaaggac	afttcatgat	ttopactatt	900
tcgctacgct	atagcagagc	acacagggca	ggagatatat	acccacgac	ttggactatt	

atccgaccaa aacgactaca tgtgtccagt agatatagca gacctctacg aacgggggtt ccgtaccaaa aacggcagca ccgtacaccg cagaatatcc atagctatgc aacgctggct 1020 accatcatat ccagaccaat cagaacgaac agcatggcgg acangctatc ccggccttat ttcttcatg 1089

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2897 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...2897
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362

tgcgatttct	tgtatctgcc	cggtggttat	ccggagtttt	acctgccgga	ttgagtgcca	60
acgaatccat	gaagcggtcg	gtacgggact	atatcgagcg	ggaggttatg	ctctggccga	120
gtgtggaggt	atgatgtacc	tttgcgaacg	atacggggca	tggacggacg	ggactatccc	180
atgtgtggcg	tattgctgag	acggctacga	tggaaggaat	gcgcctgcac	ctcggctaca	240
ggcgatggta	tacaagggga	aagagctacg	aggacatgaa	ttccactact	cttcactatc	300
ggctctacgc	cgtccgtggc	acagcagtac	aatgtgcgag	gcgagccgtg	gagactccgc	360
tataccgata	caagaatctc	ttggccggat	atcgcatctc	tactggggtg	agcatgacga	420
tctgtggatg	tggttcgact	gtggaagcga	aacgatgtaa	tctatgatat	atacgaagac	480
aggagacaaa	gaaccaccgg	catattcggt	ggggagcgtg	tgccgaaaga	tgatgtacgg	540
tggaagccta	cggcacgatg	gatgagctga	atgctgccat	cggcatgacc	ggacattcct	600
gccggaggag	gatgagcgtc	agaccgtgct	gtacgatttc	agatgcggat	gatggcagcg	660
atgagtatag	tggccactcc	tgccggaagc	gtgagcagaa	tcccaatcat	ttccccgaag	720
aagcagcagc	caactcgagg	cttttatcga	caggcttttg	gccgaaacaa	ccgacaacgg	780
ctactcattc	ttccgggcgg	tacgccgctt	tctgctcatt	tgcagttggc	tcgacgatag	840
			tgcaccgatc			900
cttgaagtgg	atgaatcgcc	tgtccgatct	ttcttcgtga	tggctcggca	cgaaatgcag	960
cagcagggtt	ggagcgagga	aagtggcata	gattcgccta	taagagaaag	aagaaatgac	1020
ggaaggcgga	agctacggcc	gattatgttt	gtcggcacag	gcagcgatgt	aggcaagata	1080
ttatcgctac	gggtttctgt	cgcattttc	ggcaggacgg	ttatcatcgg	ccccgttcaa	1140
agcgcagaat	atggctttga	attcgttcgt	cacgccgaag	gtttggagat	cggacgagcg	1200
cagctgtgca	ggccgaagct	gccggatccc	atgtcatacg	gatatgaatc	ccgtgctgct	1260
			gtgctcaatg			1320
gatcttacga	atactttcga	cgagaggga	gggacgaact	gcgtacggag	gttacgccgc	1380
			cgttgtaatg			1440
			atatgccgat			1500
			aggcgtgttt			1560
catgttgcct	ctgccgaaga	gcgaaagtat	gtacgaggca	tcatgatcaa	taagtttggg	1620
			agatccttga			1680
			tcatacgagg			1740
tcggtcaagc	agtatgctgc	cggaagggac	gggtgaatgt	ggctgtagtc	ctgctgcgat	1800
			ggaacgcgat			1860
			gatattatca			1920
ccttggccga	tctctatgaa	ttgcggcgca	atggtgcggc	căagctatcg	tacaggcaca	1980

```
tegegaeggg acaaeggtat tggggatatt ggeggattee aacteatggg eatggaggtt
                                                                      2040
tgcgatcccg accatataag ggcgatatag aacgcctgcc cggtctcggt ctgctgcctg
                                                                      2100
                                                                      2160
taacgacgtg atgacaggcg agaaggttac acgtcgcacg gcatttcgct ttctggtcat
acggatgaat gcgagggata tgagattcat atggggcgga cgatgctgtc gaaggtgcag
                                                                      2220
catcttctcc actgaatcga ctctcggatg gaacgaggat ggatatttcg tggatgctac
                                                                      2280
ttgtatgggt acttatgtgc atgtatcctg gacaatccgg ccgtaataga ctatctgctt
                                                                      2340
tcaccgtatg caacaaaatg gaagagcgga aaagcttcga ctatgtccgc tataaggatg
                                                                      2400
acaatacgat aaattggccg accatctgag acgatatgcc gatgtcccgc gatttaccaa
                                                                      2460
ctgatgaaag acgatgatta aaggacacgg agatgacctt accgtcacgg ccccattcgg
                                                                      2520
gcaaatttca gttcgaatgt ttataacgca ccgagcgtca gggattgctg gatcaccttc
                                                                      2580
acaggagatt ggatageteg gtteetatee ggageeggag eettattett tggagaaagg
                                                                      2640
tttggcgatt atcacggtat agctgccgat tcaatcagtg tgaccagcgg tgccacgaag
                                                                      2700
ctatttatct catagogoag gotttcogtg gatottottc agoctagtag ttoccacttt
                                                                      2760
cagcgaatat gccgatgctt gccggctgca tggcatcgtg tggattttat ttccaagccc
                                                                      2820
gaagaggett ettetegata tgtatggtet ggetetgtaa teegaacaat eegaegggae
                                                                      2880
                                                                      2897
gtgtttggaa gcaagcg
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1215 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1215
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363

```
gtttggattt gcaaagggga ggtttacgag aaacgcgacc tcgcccccat tttgcagtgg
                                                                        60
ccaaaaacca aagccgtcgt cccaatgcac agggcggcac aaccgtggcg gtgatcgcaa
                                                                       120
ccgtagaaga aaaggtaatc gctaacatta gaaagacaga caaaatgtta caaccaaaaa
                                                                       180
aaacaaagtt tagaagcagc agaaaggtcg catgaagggt tttgcccaga gaggtaacca
                                                                       240
                                                                       300
gttgttttcg gttcttttgg aatcaagtct ttgcagagca agtggataac cggtgtcaga
                                                                       360
ttgaggccgc tcgtattgca gtgactcgct atatgcagcg tcaggacaag tatgggttcg
                                                                       420
tattttccct gacaagccta ttaccaagaa ggagaaggtg tccgtatggg taaaggtaag
ggtgctccgg aaggtttcgt tctcctatta ctcccggtcg aatcattttc gaagtggaag
                                                                       480
gtgtgcctta gaaatagcta aggaagctct tcgtttggct gctcagaagc tccccgtaag
                                                                       540
                                                                       600
actaagttcg tggttcgtca cgattatgat atccaaaatc aaaatgcgaa ttgtcatgaa
gattgccgaa attaaagagc ttgcaacaaa agagctcagg agcgattgga tgccgaagtg
                                                                       660
                                                                       720
gctgcttatg accaaatgcg aatcaacatg cggtttcgcc tttggatagt cctgctaaac
taaagcatca acgtctatga ttgcgcagat gaagacagtg ctgcgccaac gcgaactcaa
                                                                       780
taaaaaatag agtgcacaca tggaaagaaa tottagaaaa gaacgtgtgg gtgtgtotca
                                                                       840
                                                                       900
agcaacaaaa tggataagac tatcacggtt gctgtgaagt ggaagagaag catcctatat
atggtaagtt tgtcaataag acaaaaaat acacgcacat gacgagaaga atgaatgcgg
                                                                       960
tatcggtgat acggtacgta catggagacg cgtcctctga gtcgtacaaa gagatggaga
                                                                       1020
ctaactgaat aatcgaaagg gcaaaataag atgatacaac aagaatcaag actcgttgcg
                                                                       1080
ctgacaacag cggagcaaaa gaagctctct gtattcgtgt tttgggcgca cgcgcagacg
                                                                       1140
ttatgcctct gtgggtgata tcatcgtggt ttcggtaaga gtgttatccc ttcaagcgat
                                                                       1200
                                                                       1215
atcaagaaag gtgct
```

- (2) INFORMATION FOR SEQ ID NO:1364
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 693 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...693
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364

ctgcggatct	gtcgttgccg	aaagtcggtc	gatgcacatc	cgacttgctc	cggtgtagca	60
agcactcctc	aagacgttgg	atgaaatgga	aaagaccgta	tcgagcaagc	cttggcacga	120
aacggcagca	acctttcgaa	tgtggcaggg	aattaggcat	cagccgccag	actctgtata	180
ataagatgaa	acgctagggc	tgtagcccct	cttctatggg	aagacggaag	accggcagtt	240
tcggctgcat	ctgttattta	ccatcgtcat	ggcggtggtg	ggtacttggt	cggcgctgca	300
ggacattatg	ccatcactgt	ttttgcagcc	ggactcgtta	tctttccgcc	ttgcggttgc	360
gtttacttta	tcggcgccat	cttcaagatc	ttccctgctc	ttgaatgcta	tcgagaatgg	420
cgattattcc	gtgcgctttt	cgaaatggga	ggcaatgtct	cgcatcgaac	attcaaccgc	480
acgcttaatc	tatcaaggag	atcctcagcc	gttctcgtga	tgaggctata	gccggcgaga	540
gtttctcgta	catgtattgg	aacagattcc	tgtcggcatc	atgatggtgc	tccggaagga	600
tatgtctatt	ctaccaatac	agtgctgttg	cgcctcccgg	gttacccgtt	atcacacacc	660
ttcgatcagc	taaacgtgtg	tcgccgacat	gcc			693

- (2) INFORMATION FOR SEQ ID NO:1365
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 965 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...965
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365

```
acttcgaaat tgttatcggg tgaaggcaaa tggcgactcg aactgccctg caggctattg
                                                                        60
ccacgcatcg cggcggggaa tacaactggg cgcagcagat accgtgcata catgggtcaa
                                                                       120
tggagctgtc ggacttaagc tttcgtacgc cctcgtaccg acaaacccat gcagatttgg
                                                                       180
ggatctgctt atggtgggca gccttgtcaa gcggaggata cttcccttac gaaagagggt
                                                                       240
ggggcgttat ctttctctcg gaatggactt ggagcacttc gcttttcgta ccgatattgg
                                                                       300
tacggcagge attacgtttc tccctttgct gcacctttcg ccattccctg acgtatgaca
                                                                       360
aacagcctct tacgaacggt tggggcgatt atttcgtctc tatgccgact attcgtggcg
                                                                       420
gatggcacga agtgtttcgt tgcggctgtt gctcgggtat ggttccagcc ttcggatcgt
                                                                       480
tttgcgatga ccacgccttg gaactgacga tgcgtatcga tcccaaattc ccaatagctt
                                                                       540
totgaaaggo aatoattgat ottttogata tttgcgagtg gattootogt gatcatttag
                                                                       600
teeggtaagg ttgggtgaat gecaaaagaa agaggaegee aaagagetee aageteettt
                                                                       660
gacagtcctt ttcgtttata ttggaaggat gtcgcttaca gctatgcgat gtccatttcc
                                                                       720
ttcatgatct ctgccgtgat tccttggcat ctccgagttt gaggaataca cccgttgctc
                                                                       780
gtgttagagc ggattgtcca cacctgcata accgggtttc aggtcgaagt tgcaatgatt
                                                                       840
actteggage ategteeacg tteageacgg geatacegta taaggegtae ceteageatt
                                                                       900
gcgagcagca gggttcatta cgtcgttggc acgattacta ccacggcatc cgtctgagcg
                                                                       960
                                                                       965
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 592 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...592
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 634 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...634
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367

aatttcattc	acaatattac	acaatctgct	taaagaaaaa	agagaagaga	60
atttttata	tatttcctta	ссяарааара	gagaactcta	cattcgaaat	120
accitata	ot contttta	ggaatccgaa	garratatat	tatttttcac	180
acatectgtt	testtesses	ggaacccgaa	agcastttt	agectotage	240
atacagaagc	tgattaggaa	ggcgaattcg	ggcgacccc	acttttatca	300
cagtttttc	tttatttggc	atgtggtgtt	gagiceggat	toosetesse	360
gttccggcaa	gcccttacca	ctctcctccc	tcttctaatt	tecactaaaa	420
aaaaaagttt	tcaacaacga	agcgagtttg	gaatgattcc	aaataagcat	. — -
gaggcatcca	agtaaaaaag	gatagaaaac	tgtcttccca	acttcgaaat	480
agagtcgaat	aacgatttgt	atataaatga	ctttcaattt	atatataaag	540
tatatataaa	tcgttttcaa	taaatatata	gatcgtaatg	attcgtatat	600
ctcgaaaagg	ccttttccga	agcc			634
	atttttata acatcctgtt atacagaagc cagtttttc gttccggcaa aaaaaagttt gaggcatcca agagtcgaat tatataaa	atttttata tgtttccttg acatcctgtt ctgaatttta atacagaagc tgattaggaa cagtttttc tttatttggc gttccggcaa gcccttacca aaaaaagttt tcaacaacga gaggcatcca agtaaaaaag agagtcgaat aacgatttgt tatatataaa tcgtttcaa	atttttata tgtttccttg ccaagaaaga acatcctgtt ctgaatttta ggaatccgaa atacagaagc tgattaggaa ggcgaattcg cagtttttc tttatttggc atgtggtgtt gttccggcaa gcccttacca ctctcctcc aaaaaagttt tcaacaacga agcgagtttg gaggcatcca agtaaaaaag gatagaaaac agagtcgaat aacgatttgt atataaatga	atttttata tgtttccttg ccaagaaaga gagaactcta acatcctgtt ctgaatttta ggaatccgaa ggccgtgtat atacagaagc tgattaggaa ggcgaattcg ggcgattttt cagtttttc tttatttggc atgtggtgtt gagtccggat gttccggcaa gcccttacca ctctctccc tcttctaatt aaaaaagttt tcaacaacga agcgagtttg gaatgatcc gaggcatcca agtaaaaaag gatagaaaac tgtcttccca agagtcgaat aacgatttgt atataaatga ctttcaatt tatataaa tcgtttcaa taaatataa gatcgtaatg	aatttcattc acaatattac acaatctgct taaagaaaaa agagaagaga

- (2) INFORMATION FOR SEQ ID NO:1368
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 908 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...908
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368

gaatccanca	tctccctctg	gtcgagacag	tagtagaagg	cggtactctg	taatcaaaat	60
gaagccatcg	ctatctatct	ctatcaataa	aggtgtccga	tcaggataac	tactccccaa	120
ctgtcagaag	cagagetaca	cggaagcgtg	atattacatt	tgccggaaaa	ttccgtctgc	180
gatctcttag	gatcgactct	ccggaagcgg	tgacatcact	tttgccaatg	ccacgatagc	240
caatgtctga	acetcaecct	tagaggtagt	ggcgacatac	ggggcaatat	ccttccggca	300
ggaatgcaac	tctctcgctg	gccggttcgg	gcgacataga	ccttcgctcg	gtcatcctca	360
gagagtggaa	gccggtatca	gcggaagcgg	agtataaaga	taaagggaca	aacagccttt	420
grogracta	aatgcagcgg	agcggagacc	tcgaatgccg	taacctgtcg	gcccaacaag	480
ccascatasa	atcagtggca	gcggagatgg	caagctggct	gttaccgaaa	agctggatac	540
aacctatccg	patcagccgg	ctttgtctgc	tatggcaaac	ctgtcatcgt	acacacaaag	600
tcagccgttc	ttcctctttc	cgaatggttc	cttaaatcaa	cgacagcata	gattagaact	660

tttcatagac	ocoaotaeca	ataggggaga	cattccatca	gagagaatgt	actcgccctt	720
actecatagae	Population	ggaggtetta	teceeectcc	ataaatgaat	tttgaaacag	780
actacattig	atagaaacc	ctttcccca	actcaattte	tttgtatttc	atccggcata	840
cccccgatta	attgtggatt	atttatangt	accontators	aagcgcaatg	gtagtttcta	900
	ttttaattgc	acctatagge	agggegegea	4460606	80-80-00-	908
tgtttggg						,,,

- (2) INFORMATION FOR SEQ ID NO:1369
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 708 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...708
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369

gaagtgaccg	gctttggtta	tcgatcggga	tccgatattt	ggagcacaag	tcccaccttg	60
cttctcgaca	gccttgtcgt	tcagcagggt	gctaccctac	tttacctgcc	ggatgccgtc	120
tecteateec	caataaggcc	cacatcaggt	tcggggtcgc	ctaatggcgg	agggcaatcc	180
орссаарсра	gtgatgtaga	gaatctgcgc	cacgatetee	tcgtacagga	tgtaccttat	240
accetattee	cogacagtee	ggcggtattc	ttttctctga	agagagtcgt	ggcatgaact	300
tcattatact	actatoceca	aceetceate	gggaatcatt	gccaaggcgg	taaggatgtc	360
accaccccaa	aattecttt	ggagggctgt	atgtcaccaa	tacgaaaggc	tccggtctgg	420
ctacttccaa	tooctatato	ctattctcaa	cagtgagatc	agcaataccc	toggotatac	480
tatageeete	teggerates	atoroaatto	асссаваяса	ctgtttgcaa	tttctatagt	540
cgcagccccc	CCSSCAGGS	accttacact	acotoacooc	attcgctccg	ateteecage	600
gggacaaccg	notoctcato	gacagtest	taatttacac	agtattgtcg	atggcagtcg	660
cggatcctat	acticitati	ggacagccgc	cgacccgcac	castctst	2088008008	708
gtctgtggtc	aaacagggag	ataagaagtg	gaggagaat	Cagicugu		

- (2) INFORMATION FOR SEQ ID NO:1370
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 772 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...772

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370

```
gtgtgacttc cgacagaaca gttgtgagca atctgtacaa ggttgtctac tttactccgc
                                                                       60
gatgtatgat cgttgaatcc ataacagccc tgtcgataaa gtgttggcac cgatttcgac
                                                                       120
atcatcttca atgataacgt tccccagtgc ggaatcttgc tgtagccttc ggcattcgga
                                                                       180
gcaaaaccga atccatcgct ccgataacgg ctcccgaatg aatcacgcaa cgcgaaccga
                                                                       240
tggaaagcca tcatagaccg tcacatgggg gtagaggatc gtcccctctc caacgacaca
                                                                       300
ccgctaccta cataaacatg cggatacaag ctacagcctg taccagcgat gccccttccg
                                                                       360
acacgtaggc aaaagctcct acatagcaat caccggcagt atcaccgatg gatgaacgaa
                                                                       420
agccgtggaa tcgactccct tctttggggc ttcatgctgt ccaccaactg cattagttgc
                                                                       480
gccaatgctg ataggcattg ggaactcgta tcagggtcgt cttcaccgat tcgcgcggtc
                                                                       540
gaagtcctga ttgacgagta ctgcatcgga ttgtgtttgg tacaaatatg ttcgtactta
                                                                       600
gcattggcta aaaacgagag acagccacta cgaccttctc tatcttggca aaagtcgtgc
                                                                       660
agtogoacct tgggattgco ctccacgaac cgtggaggta gtcaagctat ctggtgggct
                                                                      720
gtaaattcca tgtgacgggt taattagggt acaatggatc ttaaaacatt tt
                                                                      772
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1455 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION  $1...1\overline{455}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371

ggcaattggc	ataattttt	ttgcagacaa	atccgcctct	ccaaagttcc	agaccggaaa	60
tgctctgatt	gcggagcgtg	ttttcgggaa	aagcggcgga	gaatttttc	cctgcggcgc	120
gagaatttt	cacttcccga	accaaaagaa	aaagttcccg	cgccacgttt	ttcagagcgt	180
ggaaatagaa	aattatgcgc	gtaaacccgt	ccttctctct	taatacgata	gcgcacgaaa	240
tgatggtctc	cacgcgaaat	gaactttggg	gagcttgatt	ccgagacaaa	taccctcatc	300
ccctgccaag	ctccatagat	gccaaaaccg	aaagttgcta	acttgttaag	taatcacggc	360
cgacaccggt	gtctgccgcc	ggtactaagg	aacattccaa	tgcaattcaa	ttatgatgtc	420
atcgtggtgg	gtgcgggcca	tccggctgcg	aagcggctgc	ggctgcggcc	aagctcggtt	480
cgcaggtatt	ctcatcacgc	cggacatgaa	caaaatagcc	caaatgagct	gcaatccggt	540
gtcggaggaa	tagctaaggg	ccagatagtc	agggagatag	acgccttagg	ggacgaatgg	600
gtatcgtcac	ggatgctacg	gccatccagt	ttcgtatctc	aatcggagca	aaggccctgc	660
catgtggagt	ccgcgcgctc	agagcgccgc	atgcgcttca	tggaagcgtg	gcgcgatata	720
gtggagcacg	agcctatctg	tacatgtggc	aggacagtgt	acgctgcctc	tctattcgtc	780
aggggccgtc	gcgggagtcg	tgacggctct	cggggtagag	tttcaggctc	gtacgtggtg	840
ctgactacag	gcactttcct	cggaggtgtc	atgcacttcg	ggagcgtatg	atcgaaggag	900
gacgaatagc	cgaaccggct	ttccacggca	tacggagcag	cttcgtgatc	tgggcttcag	960
aaccgacaga	atgaagacgg	gactccggca	cgaatcgacg	gccggagcat	cgatttcagt	1020
ctgaccacaa	gcagtcggga	gaagaggatc	accaccgttt	ctcctatatg	gatacgcccg	1080
aagggtgcta	cgccaaagga	gttgctacgc	actctacacc	aatcccggtg	tcatgagata	1140

gatactgccc	cagcatagag	accaaatcgt	caccttcgcc	tcaatggctt	atcggccctc tgcaccaact ctcctcgtct cagtgcacat	1200 1260 1320 1380
ttgccttgga ctatcgtccg gcttgaaacc	gggtatgcca	tcgaatacga	cttcttcgat	ccacacaatt	taagacatac	1440 1455

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 481 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...481
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372

	agtactraga	acaagtaaaa	aaatgaccgt	catagctatc	atgaatgaag	60
gagagggaaa	agegeeeugu	ttaattttt	natnantaaa	ggtaaaagca	aaatctttcg	120
aacggcaacc	tgtgttctct	LLUGLLLLLLL	gatgagtada	acconnectat	acaccaaaaa	180
atatgggtca	ttttcgaagc	tgaaaaaacg	gaatattcac	cgaaaaatat	gegeedadaa	240
+++	aacgaaaagt	gtttggaatg	attccaaata	agcacttctg	agagaicgaa	,-
ageceean	actacctaac	atgacageet	ttttcagatc	gaaaagctct	ttttttagtt	300
atteggglaa	agtacgtact	tootttt	catttatata	taatcetttt	cattttgtat	360
cgatgaacaa	tctatatatt	aattatttt	gatttatata	tatataaata	acaacttcct	420
ataaatgatt	ttcaataaat	atatagatcg	aaatgatttg	tatataaatt	acaacttcct	480
aaaggetttt	tcttgaggga	taacagaggc	accatcggat	tttctcttga	atcgacggtg	
auabbeece.		0 00				481
C						

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 741 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...7\overline{41}$

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373

ggcgatgagt	tcgacttctc	cgtattggca	ctttatgatg	aaaaacgcta	tcagttggga	60
			ttcaaactaa			120
			aggcaagatt			180
			caagagcctt			240
tttgtgatgg	ctatacgatc	ctccctcaga	aaggagttgt	gatcctccct	accgggagcc	300
gttcggaaag	acccttgccg	atgcgtttgg	cgatcctgta	ttgcgaaaaa	gtactgcttc.	360
			gccagcaagt			420
			cggagacatt			480
			ggtgtcaagc			540
			tcatcaatga			600
tcccatcaat	gtgtcgctcg	agaaccgagg	gctgatgata	tgcagcgcaa	aacgatgttc	660
ggtatagatc	tgaactacaa	cttttcaaag	acttcaccct	cggcggnacc	ttcatgcacc	720
tgagcgaaat	gccgcgacga	С				741

#### (2) INFORMATION FOR SEQ ID NO:1374

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 639 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...6\overline{39}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374

tcatcatctt	ccaaatcatc	gtcaacctgc	gcgacagcct	tcgcaatatt	ccaaagagag	60
			tcatgctcac	_		120
ccggccatta	ctcccgaagc	actctcccac	tacgagtggc	cattgggaca	gccatatcag	180
tactcttcgt	gacagaacat	acgggacgaa	taaagggcat	gggattcttc	attgtcgatg	240
catggtgcgt	atcagctata	cggagatgta	cgtgggcatc	gtggttttag	ggatgcaggt	300
tttttccttt	ttttgctcgt	ggatggtctt	gagaccgcac	tatcagatgg	aggaacagtt	360
agccatacaa	tcaaagaaat	catcattcaa	caaacaataa	cgatcaagaa	atgaaagtaa	420
aacatctatt	agctgcatcc	tgatgatgct	aggaacaggg	aatatttgcg	cccaaaagtc	480
cgcaaacagt	ttttcaatgc	aatcaaagaa	cgggttagcc	tcagtggtta	tgcgcaagcg	540
ggttttcctc	ttgtggcttc	cctacggcga	gttccgaaaa	nggagaacac	acacattcga	600
tgtaaagcgt	atcaaccttc	gtgccatgtc	gcatcacga			639

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1120 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1120
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375

- (2) INFORMATION FOR SEQ ID NO:1376
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1418 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1418
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376

					antanattea	60
++ andtactn	cogtaccoat	agacgaattg	aactcattta	teggetttgt	gatgagttag	
tigagigein	CBBCGCBT		actaccatca	gracasaget	tttcaccgtc	120
gacttgccgg	aagaggatcg	ggattttntg	egtaccatca	Bracagages	c c c c c c c c c c c c c c c c c c c	1.80
640000	1	atcaggaage	acacacctos	teeteeagag	tcgagtgcat	7.00
ggatccctat	CEBRCCACAA	accappaage	~6~6~6~6~	-96-58-6	tcgagtgcat	

```
cccgaaacga tagaactgtg gagcaggaaa tagatcgttt ggacaatgcc attcccaaga
                                                                       240
tgacgctttc atcttgccgg ggggtagccg ttctgcctct ttggcgcatg tttgcgtacg
                                                                       300
gtatgccggc gagccgaacg tcatatatac cgcttgagtg aagggcgctg gtagaggagc
                                                                       360
ctgtgatgcg ctatatcaat cgtctgagcg atatttcttt gctctggctc gaaaagaagt
                                                                       420
ttggcgtacg accggaggtg aattatttgg gataagacct gcgattgaga aaaggctgta
                                                                       480
gaatcaattc ggggcttaat aaagaaggag cgagaaaagg cttcggatat taggtttagc
                                                                       540
agaaaaatct ttttttatct ttgctgcttt catcgaccga ttatatcaaa taaaaacaaa
                                                                       600
tgattgcttt ccaagccctg caagccatct ctccgatgat ggccggtatc gcaacaaagt
                                                                       660
                                                                       720
agaagtactt agtogotatt tttcagagga tototaatto gotatogtgt aaaagtggag
gtggagtatt tcatcctctt tgcaatgaat tgccttcgct gaaagatgtg tgccctccat
                                                                       780
ctttgaggaa gagttgcgcc gtatatacca agactttagc gagaaggatg ccgacgtgta
                                                                       840
aaggaaatag aggoggtaac gaatcatgac gtcaaggotg tgagtattto ctcaaagago
                                                                       900
ggttcgaggc catggggata cgagatgcca agaatttatc catttcggtc tgacctcgca
                                                                       960
ggatgtaaac aatacggctt cccgatgatg atacgcgagg caatgaccga ggtttacttg
                                                                      1020
                                                                      1080
cccgctttaa ggagctggtg gagcagcttc atgcttatgc ccttcagtgg aaagatgtcc
gatgctggcc aaaacgcatg gacagccggc gtcgcccact cgcttagaaa ggaaatagaa
                                                                      1140
gtattcgtct atcgcttgcg caagcagatc gacttgtgct ggaagtacct cattcagcca
                                                                      1200
aattcggtgg tgctacgggc aatttaatgc gcatcatgtg gcttatcctg atcatgactg
                                                                      1260
gagcagatit cggcgtcggt ttgtaacttc tctcgggctt gaacgggaag aactcactac
                                                                      1320
                                                                      1380
acaatatcca actacgacaa acatggcagc cttattttga tgcctgctgt cgatcaattg
                                                                      1418
tgatactgat cgacctctgc cgtgaatttt ctggcaag
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 575 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...575
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377

tocaatogta ttoogottoa toaaaogggt tggottgggo gogaattaat tottttoatg	60
gcatgtgggg agatcttact ccccataata agcccggacg gtcggtagtt ttctctttcc	120
cgaaaatact atccccatga atcatactgg tacatggaag ggagcatagg tctggagaat	180
atcttccggc tcctgccatc gaatacttcc gacgcttcac ccaattacaa acgactccga	240
ataaagggga gtccgtgctc gcttccagat cactttctga cctctaaagg aaagggaaat	300
gccgaaactt ttcgttctga catttcctcc tcttcgaagc gatcttaata gaatcagagc	360
ttgatgaagc gttcggccgg tgtgctgcct tggtcatgag tttgatcaca taggcccgg	420
cggtcaaaac cttcacgccg acatgcgagt attctccata gagagcacca aacgacctga	480
aaaatcaaat tooggacaco gaagtcacot toatgottaa tattoagtac atcottoacg	540
gattggggta aaccccggaa tcagaagaaa aatag	575

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 576 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...576
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378

accatacaaa	tottcotcac	ctcgctaccc	gttccgcatg	ttgtgggcaa	atgatcagtt	60
gegacagaaa	gataagaggt	attttgcggt	cgaatgcacg	agtacatcat	ttaatccttt	120
	gatttagagge	tatcaatacc	graceteete	cgataccgat	tacgcggtcg	180
cagaacgaaa	taccagaga	accaanataa	tattcatcat	ttcgtcagaa	ggctcgcctt	240
aactggatat	tacggagtet	gccaagacgg	aggaagtag	catoccttca	tataggttca	300
gcccaatttc	tcctgcataa	Caaaatggca	ggggagccgg	gacgaattcc	tataggttca	360
tagatgaact	cgttggtaat	taccaagtcg	cgccccaa	gacgaattece	ttggcaaatt	420
ctgcaaaagt	gtcaaagtga	tgtgttacac	tctgagtttg	aaaaguugua	taatagtatt	480
attggttttt	ggaataatcc	taacttttt	tettetette	ttatccgaaa	cgtttgcgga	540
gatgtttcgt	agttcctctc	tgaaatccgg	gtgggctatg	gcaataagag	cttctgctcc	576
tggcgcaaac	tcttcctttg	agttgggctt	ataccg			376

- (2) INFORMATION FOR SEQ ID NO:1379
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1665 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1665
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379

gaagaagagg cttacttcat cggtgcggga tttgaaggat agatatggat aaggaagctt ggggtattgg aaaaggggtt tctccacgtt ttttcttatt ctttatttta ttccgggaaa atacgaaagg acgtgtaaag	gccgtattct accgtacgct ttatcccgca gggagttgct gggagtatgg acgatggctt	ccggtatcgc tttgaggaaa ccttgaccct ccggagggct gcgggagcga tgccggaacc	atgccttgcc tcatgcgccg taagaggggc tatccccatg gtcggaactc agacccgtat	cggaatccgg gatagattcc gattccggat ctttgttttc ctgttggatt ctttcgaagg	60 120 180 240 300 360 420
cgagttgctt aagccgtgga	ccaaaaagag	ataagagagc	aaggagtggt	cagggactat	480

```
atcagggaag gcttgagaac cactgtcgca gcgtggagat gtcggagacc cgtacctttt
                                                                       540
ggccgggaat atttgccatt tgtgtacgga ttttacggct ttgaccggga cggcttagaa
                                                                       600
agettgetea aggegettea tectaceeeg getetegegg atteceeegt aaggaagett
                                                                       660
                                                                       720
tggcgtgtat ccgggaggtc gaggtgatga acgcaaattt tacggaggat atttggggcc
                                                                       780
tgtgggtaag gatgcgcgag attgtatgtg aacatccgct cgatggaatt gtttcccggg
gcatccggct ttatgtggga ggaggtataa acggagattc ggtattcgaa gacaatggga
                                                                       840
agagacctcg gataaggcgg ctactctttt gaatgtgctt ggatacattc cgtcggagat
                                                                       900
aaggoggact ataaatgata atgoaagatg aggattogga ttattoggat aagaaaggog
                                                                       960
taagcgtatt gatggattta tcgagatgaa gggcatacgt aaactcgtta tgtcgcccgg
                                                                      1020
ttcgcgaaag ctcctcttct gttttctttc tcccggaatc ccgctttcga gaaatacgga
                                                                      1080
ttgcggatga gcgttccgcc ggttttttcg ctctcggatt ggctttgcct cgggtgaagc
                                                                      1140
cgtaggattg gtttgtactt ccggtacggc catgttaatt atgctcctgc cgttgccgag
                                                                      1200
getttttaca gggggattee tttggegegg taaeggeega eegteeggee gaatggateg
                                                                      1260
accaggacga gggaagacga ttcgacagga gggagctatg gccggtttcg ttaagtcgta
                                                                      1320
ttgagcttga gagcggaatt cgatacttcc gcctcggcat ggtatgccaa tcccgtttga
                                                                      1380
atgaggtgtt gaaccatgcc ctgatgcccc ggcgaggacc ctacacatca atatgtcgtt
                                                                      1440
ttgcgaaccg ctatacggga cttcctccgg tattccggaa aagagcgggc gataacgttc
                                                                      1500
gtgagggaac ggcaagaatg ccggaagagg tatgggatat gctcgtaaag cggtttttgg
                                                                      1560
aagctcccga gtgatgatcg tcccggtttt tatcctcccg acgaagacgt gtccgcccat
                                                                      1620
                                                                      1665
tgcaggatat atgcaaattt cccatacggt ttgtttgcga gagtc
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 734 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...734
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380

```
gggcttccat ttgggcatag tctgtatcac gcggagggct tccttgtcag tgcagggtca
                                                                        60
                                                                       120
ataccettaa caacagttge ttgtgtcaca gaaccatett ttegaccaeg aaacgaacga
                                                                       180
ttaccttacc ttggatgccc atttcggagc ctgctcggga tagaccaaat ttttactaag
                                                                       240
ccatttagag agagcatata accacccggg aactctgccg gactttctac cacttcgtgg
                                                                       300
atttttcctc ttcttcctca actttaacgg gggcaacggg cgcaggcggg ggcacggttt
                                                                       360
gctctcatcg acagagacca aagcgatttt ctccactttc tggtgttatc taccacctta
aattetteeg geagetgtae eteetgttge tgggttgete eggeteggge tgeteegget
                                                                       420
ccggctcgtt ttcttcgagc agacagtttc ctccatgtcg gcaatatcca ctttatcgcg
                                                                       480
tgtataggcc ctatcttatc gtaagtacga tattccaaag ctacatacac gatcgcgagg
                                                                       540
                                                                       600
ctacgacaag ccccaaaagg aagttcaaac cttttccctt ctccaagtgg ccttaggcga
                                                                       660
tttcttgatt tccatatctg atagtattgn ttttgattct tgctttgggg caaaaataca
                                                                       720
aagttttttc atnoccaatt ogttttggta gaaaaaatca ggogtatggg gcaaaattgo
                                                                       734
aggctgcaaa aatc
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 765 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...765
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381

rcttttatag	atgtacgatc	gtaaaaactt	ggaaataacc	actcgatcta	60
	acctcatagg	atrogragar	gateceatga	ggccccaaac	120
agaagaaaga	gccccatagg	tataccasca	aadaadtcac	gattataagc	180
caacggctaa	aageggeace	Latguedacg	aagaagccac	attataatta	240
tttccctttc	tcttagagcg	gtcgtcgaag	aggattgcct	accecce	7
atcagaacct	ccacctgaca	caatatccac	aaatccatgt	tcatgcctat	300
taacgcttat	agtggaatgc	ggctattatg	tttccccgat	gtcccagcgg	360
ggccaccaag	cgttgggcca	aaaactctgt	gctgtagttg	ttcggcttcc	420
cttctgccga	ttgtaccata	tataccgtat	gcaaggaaag	gacccgcttc	480
ccatatcatt	catcapotco	aaccecatec	cggcattgat	cggcagttga	540
	caccaggeeg	tataggtagg	aggaaccatt	cooctatate	600
gcgagtggaa	accateguaa	Lataggiace	aggaaccatt	anntactatt	660
ttggagccct	tcatcgtata	gttcagaccg	gagccaagta	gaateetett	
tgaattcggc	agcggcccga	cccgcaggcc	gacattcatt	tggtgtccca	720
tctctttcat	gctctgattg	ctgcctacga	agttg		765
E 6	agaagaaaga caacggctaa cttccctttc atcagaacct caacgcttat ggccaccaag cttctgccga ccatgtcatt gcgagtggaa ttggagccct	agaagaaaga gcctcatagg aacggctaa aagcggtacc ttccctttc tcttagagcg atcagaacct ccacctgaca agtggaatgc cgttctgcca ttgtaccata catgtcatt catcaggtcg accatgtcat tcatggaaacct tcatggaaacct tcatggaaacct tcatcgca accatgtaaattggagccct aggagtggaa accatcgtaaattggagccct agcggcccga	agaagaaaga gcctcatagg atcggcagac caacggctaa aagcggtacc tatgcccacg ttccctttc tcttagagcg gtcgtcgaag atcagaacct ccacctgaca caatatccac caacgcttat agtggaatgc ggctattatg ggccaccaag cgttgggcca aaaactctgt cttctgccga ttgtaccata tataccgtat catgtcatt catcaggtcg aaccgcatgc gcgagtggaa accatcgtaa tataggtacc ttggagccct tcatcgtata gttcagaccg agcggcccga cccgcaggcc	agaagaaaga gcctcatagg atcggcagac gatcccatga caacggctaa aagcggtacc tatgcccacg aagaagtcac ttcccttc tcttagagcg gtcgtcgaag aggattgcct accagaacct ccacctgaca caatatccac aaatccatgt aacgcttat agtggaatgc ggctattatg tttccccgat ggccaccaag cgttgggcca aaaactctgt gctgtagttg cttctgccga ttgtaccata tataccgtat gcaaggaaag ccatgtcatt catcaggtcg aaccgcatgc cggcattgat gcgagtggaa accatcgtaa tataggtacc aggaaccatt ttggagccct tcatcgtata gttcagaccg gagccaagta	cettttatag atgtacgate gtaaaaactt ggaaataace actegateta agaagaaaga gcetcatagg ateggeagae gateceatga ggeeceaaac aaacggetaa aageggtace tatgeecacg aagaagteae gattataage ateagaacet tettagageg gtegtegaag aggattgeet attgtegtte ateagaect ceacetgaca caatateeae aaateeatgt teatgeetat agtggaatge ggetattatg tteecegat gteecageg ggeeaceaag egttgggeea aaaactetgt getgtagttg tteggettee ettetgeega ttgtaceata tatacegtat geaaggaaag gaceegette egagtggaa accategtaa tataggtaee eggeattgat eggagtggaa accategtaa tataggtaee aggaaceatt eggagteet teategtata gteeagaeeg gaceaagta gaateetet egaattegge ageggeega eeegeaggee gacatteatt tggtgteea teetetteet getettetat getettatag etgeetaega agttg

- (2) INFORMATION FOR SEQ ID NO:1382
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 573 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...573
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382

01	cogtaaco	tetttagaag	atctttatgg	acttgatage	catattcgaa	catcaactgt	60
C	ceeceteae	caatgatagg	caaagattag	acaatgtgaa	gaçaaaacgg	aacgacgaga	120
2	aagaatacg	aatctcctat	ctgttgagaa	tagcggatgt	accgtgggtc	tgctttcggc	180

taatctcccc	ttggcaatgc	caagcatcca	ttgacaaaag	tgtatgcgac	actgtgactg	240
aaggtaagcc	ttcgaaagga	gaccatccgc	agaggctaag	tatattatcc	gcagtacggt	300
		caagcaccag				360
ctcttctcta	tggcgaagag	agtggccggt	attgagccgt	tttgcttact	atttcttcga	420
		cgagttcgag				480
cccgccggat	caacctgcaa	gcaactgcct	tctttttctc	ttaagcagat	gccgggcatg	540
atccgtagct	ataatatcga	taccgttcca	ttg			573

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 915 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...915
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383

```
tegataettt tgteagaaaa aattteggee gagateeege teegtttgae acateggetg
                                                                        60
cttgttcgta caaagattcg tattcggact cctgaagtca cggatgaggg aaacgaactc
                                                                       120
accaagacgg cgtcgggctg tagcactaga tcgggaagac ccttctgcga ttcggacagt
                                                                       180
acgtcccaca acgaacagaa gaagccgtgg ctatctcgtt aagacgagac agagtggtat
                                                                       240
                                                                       300
ctcctttcct cgcttgggat aattgattac acgcctgagt gcttcgtcat cattggattt
acgattagac gaaaataggc caggacgtcc ttgatctctt ttccgaatag aacgaaagcc
                                                                       360
                                                                       420
caccgtatat acgaaaaggg atattgtgtt tggaagtgct tcctcgaaaa ctcggctctg
                                                                       480
cgcattagtg cggtacagaa tgcgaaatcg gaataaggac aatgctcttg catgcgtcgc
                                                                       540
tegacgateg ateegetace gtataageet ecaaatacee egacagacaa eeegteaggg
                                                                       600
aatacgctca cctacttgtt tgttcgaaaa aacttgcttg gggattcgcc ctcattgtga
                                                                       660
gcaatcaagc tattggcagc attgacgatg ctctgtgact ccgatagttc tcctcaagtt
tgaaaagttt gctcccgggg aacgacttga aaagcccaga gtgtttttcc acttgggctc
                                                                       720
cacggaaact gtataactct gagcatcatc ccccacgacg aataccttgc ctttctccc
                                                                       780
                                                                       840
catcactgcc tggcaatcaa atactgtgca aagttggtat cctgatattc cgtgatcaat
                                                                       900
aaataatcga tgcggtcacg gtaggtctgc aagacatccg gaaatcacga aaaaggacat
                                                                       915
tgttttgaaa agcag
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 626 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...626
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384

taggatagga	ttttgagaaa	cattttaggg	atttatggga	aaaaaaatca	tagatgcctt	60
cacatcatat	acaagacett	gtgttatagt	tgtagttgag	gctcttttac	tggtaaatct	120
ataatatcca	atcatctatc	aaataaaatc	aattttcagg	ggtgctttcc	actgatatgg	180
ttcggaattt	ttttcgatta	gcactagaga	tagaaaaact	tatcaaacat	ccacgtatag	240
aatootoata	otoaattaaa	tattcaaaaa	aataatgttt	cgaatatgat	tgaaagatgc	300
togagattta	togaagcagg	agagagaaaa	ttattattga	gggatgcatc	tcacagaaga	360
ttttttgaga	aatataaaca	aacaagattg	tctataatag	gattagacaa	caaaagggat	420
ataaatgatc	ggctggattt	gaaatgaaga	ctacccgtga	ggaagtctct	aaaaaaacag	480
aagatgaaaa	aaacgaatta	atgaaataca	ttatggaatt	atcgagtgct	gtaaaagaac	540
attttaaggt	agtgaattca	agatattgaa	gatgcaagga	taagtgtgcn	atctggtaga	600
	ctcaaggagt					626

- (2) INFORMATION FOR SEQ ID NO:1385
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2430 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
    - (ix) FEATURE:
      - (A) NAME/KEY: misc_feature
      - (B) LOCATION  $1...2\overline{430}$
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385

					+	60
cactattctg	catgaacttc	acttgaacag	cttgtactga	tattataagt	gattagttta	
cttacaaaga	cacgacatag	agtgttcaga	atatatcgca	agatggtcga	cataagacct	120
cccectceac	tcacgagact	aaaacaagta	ctaacaaagt	tttgttctta	aactcttcaa	180
acaaactctc	tocapctaac	tatccttccg	gataactaaa	aaagaagcga	aaggagtagt	240
attagtacgt	cttaccoact	tecetatage	aaaggaaagc	attttttct	tacaaaatta	300
attatanant	tattccacca	tettetacat	atttatacoc	agaaagcgaa	caaaaaccgc	360
attituatat	Latticacca.	CCCCCacgc	accuracy		gaactacact	420
actactcaat	aaaaaatacg	cgatattgac	cccgcgagag	atgtagtcat	gaactacact	
caatgatact	tctcaggaaa	tccattttgc	tccaccagtt	attcaggcaa	aatggaatta	480
pecceatete	gattcggatt	cctattttta	agcattcacg	agattgtcgc	cggcaggcgg	540
gcatctctcc	atctaatcgg	aatctcattt	ctatatagct	gtctgttgac	attcaatatc	600
gcatectet	ttactataga	tarcaatara	asacotocac	cggttcccaa	acatacecec	660
atetgetttt	Ligitite	Lagcaacaga	uuucgcgcuc	CBBCCCCC		720
tgaacgagag	cagcatagcc	ttcttacttc	ttttctcctt	ttacattgag	ccttttgggg	
cecaaaeeta	ataatagaaa	ggtaattcca	atcgtctatt	aaattttaat	tcaaagggta	780
oogst oott	200000000	attttctcgt	ttacgacgcc	toaaagggtg	gcggagattt	840
CCgatagttt	acgegeegaa	accecee	t	-07000-0	tatametees	900
tttttgtttt	ggttcgggaa	gcaaaaaatt	tacgcgcgag	aagaaaaaa	tctcgctcca	900

```
catttgcagg aaacacgcac ccgcaatcga agattttcgg tgcgtatttc tgagacagca
                                                                       960
ggttattgac cgggacatcg agcaatggcc aaaccttatg atttctatat cgtttggaaa
                                                                      1020
ctgtcctaca tcacgtcttt accatacatc caaggcatac catcttagag ctgccaccgt
                                                                      1080
ctatcccgac accgctctcg ttccgttctt cattatgcgt ttttcatttt cgaccatatg
                                                                      1140
                                                                      1200
atttcctgtg aatatatttt ccacaggaaa ttgtttctat gtttgcaccg gaaaaacaaa
caaaaacaga aatcaaatat gagatcgtaa tcgtaggcgg agtcgccgga ggagctacag
                                                                      1260
cagcagccag actaggagaa tagacgaaaa agcagaaatc atcttgttcg agaaaggaca
                                                                      1320
gaaatatcgt atgccaactg cggcctgccg tattatatag gtggggtaat caagagagag
                                                                      1380
aaaatctttt cgtgcagaca cccgaaaaat tcggccgact gtgaacttgg atgttcgggt
                                                                      1440
acagagtgag gtgctgtcca tcgatcgctc gacaaacaga taagagtgcg cgaagccaat
                                                                      1500
ggtagagaat atagtgagcc tatgacaaat tgctgctttc ccccggagcc ttgccttttg
                                                                      1560
tccctccatg ccgggggtag atagcccggg agtattcacg ctacgcaacg tagaggaacg
                                                                      1620
gatgccatta aaagttattt ggacacccac aaggtgaaac gtgccacgtg gtgggaggtg
                                                                      1680
                                                                      1740
gatttatcgg cttggaaatg gccgagaatc tacatcccga ggcattgctg tcaatgtcat
                                                                      1800
cgagatggct ccacaggtaa tggcccggtg gatttctcga tggcaacgat cgttcatgcc
cacctgcaag aaaaggtatt ggtctctatc tgggcaaagc ggtgaaaagt attgaaaaac
                                                                      1860
gggagaagta ttgactgctt cgcttgactc gggcgaaaaa atcgaggccg actcatcctt
                                                                      1920
                                                                      1980
ctgtctatcg gagtgcgtcc gaatacgaag ctggcagctg tgcacagttg gctatcggac
cggcacgcgg aatccgagtg aatgaatact gcagacatcc gatccggaca tctatgccat
                                                                      2040
cggagacgcc atcgaatacc acaccctctt accggaaagc cgtggaccaa tttcctggca
                                                                      2100
gggccggcaa tcggcaaggg cgcatcgtag cggataatat gcatggacaa acattgggag
                                                                      2160
                                                                      2220
ttatgaagga gccataggaa cagctattgc caagattttc gatctacggt tgcagctaca
ggtttgccgg caaaggctct caagcgcgaa ggcctcccta tgagtcagtg acggtacagc
                                                                      2280
                                                                      2340
ccaacagcca cgccggctat tatccaatgc ctacccgctt acgcttaaaa tcaccttcca
                                                                      2400
cccagagage ggatgeteta eggtgeteag tgtgtaggea tagaaggegt ggacaagega
                                                                      2430
aagactccat cgctcaaatc atcaagcgca
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 467 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...467
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386

teggagagag aegtttttee ttegaaaaga taaetgeeat eeceeaaaae ttaaagggga	60
gttottooto atogtactog toogtaatot ogoogaogto tottoocaat atgtootoca	120
ttgtgatcag tccgcaagtg ccaccgactc atccacaacg atggagacat gcaccttatt	180
ggctctgaac tcctcggcaa atcatctatg cgcttgtttt cggggacaaa atatgcttta	240
cgaatagagg atgccagtcg aattcatcgc ctttatccat gtgtgggatt agattttgat	300
gtaaatcacc cctttgatat tgtcttctga cccctctgaa acggaagtct ggaataaccc	360
gacgaaacaa cgaagtcaag catcttacga aaggccagct cagatccaca tccacaatat	420
cgatacgcgg gaaccatgga ttcgcaggct ggcttattat aggaatt	467

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 687 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...687
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387

totatonage tec	ttccctg atcaactato	teceaaagtc	gcataattat	ttctcgaatt	60
totgicaage tee	gctccgg tcaaagacct	tttggccgac	tgtccaactg	tccatccgaa	120
togicigece ter	ttcgtca attctatatg	agtatgtgga	ggaagtacgc	aagcacatga	180
gtggtattcg tca	aacgttt tcccttatgt	ggaaaaactt	ttgggcggaa	agttggacaa	240
gctacgaaga gaa	gaatoga tatattoago	- ABACGCCACG	atcagataga	gctgagattt	300
acgttgcact aca	gaatega tatatteage	acceseate	gagggctacg	aactcaacag	360
ccgaacttaa gaa	cctgctg atcaaatact	catttatcaa	cacacaactt	tetceaagac	420
cgttctgcac gac	atattct cctcggaaga	cgcccgccag	cacactatas	atatcatcac	480
catcttttcg tgc	ctttgat tgtaaaatag	adaaggaaaa	cagactaga	agetetaeta	540
actcaaggta cga	tagtgga accgctacct	. algalicaca	caccastata	ottoootaga	600
agaaaatcac cgg	ctacaag atacaattca	tagatgeace	cactestate	googactcacc	660
tgtaatctcc ttt	tattgtc ccgatgtcg	ttttatgatt	Cacicguate	666	687
cgaaacgaat ccg	acaaggc atgtccc				

- (2) INFORMATION FOR SEQ ID NO:1388
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 552 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION  $1...5\overline{52}$
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388

caggacctgc caaaagaaaa	gtttgccggc	aaattatect	cggcaccatc	tctcggaaag	60
Caggactige caaaagaaaa	ctatagtaga	taasaaasca	tatatactga	tegaaagagg	120
aagaataggt agtagcaagc	CLALAGERGE	LEGARGEACE	cattetete	212022220	1.80
togoctattg ctaccgattt	ctgatattat	tccatttttc	ggttgttttg	acaggaaago	

aaatgtccct	tttgtgaccg	gtcgaaagta	aaagatccga	tgccacaatg	gaagcaccat	240
cagcttgaat	agctgtgcga	ggaaaagcga	ttcgaaggca	cgataggaga	gttcataccg	300
gtgagttcgc	taagctgcga	ataagaggct	gttacgtagc	gttgttaatg	gcatcagtta	360
ctgtcatacc	ttcgggtgta	atccatgcac	gcctgccact	acgagaggaa	aaggcatggc	420
aacgaggcgg	ataccacgat	tcgaacgagg	gtcaattcga	tacgtgtatt	cacctccttt	480
tgatcgaatc	gagaatagct	ttgcccgttg	cactgaatct	gtcctgtcga	gggtagtgcc	540
cttgatattg	gc					552

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 374 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...374
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389

ctcaaaggtg	aggggagaat	taccgagatc	aatgtagccg	aaactctcaa	gatgtacgtc	60
gtgccctttt	ggatgccgac	gtgaactatg	tcgttgccag	cagtttacgg	acttggtgaa	120
ggaaaaagcc	atcggccaaa	acgtgctacc	tccgtccgtc	cgggcgaact	gatggtgaag	180
atcgttcatg	acgaatggct	gctctgatgg	gcggacattc	tgtggatatt	aatctcaaag	240
gcagtcggca	gtaatcctga	tgtccggatt	gcaaggttcg	ggtaagacca	cctttccggc	300
aaactggcca	atatgctcaa	gtccaagcag	ggcaaacgac	ctcgctcgtt	gcctgcgacg	360
tgtatcgccc	tgcg					374

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1165 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1165

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390

```
ccaaattctg aatgtgtact cggaaggcgg gaacacacta cntccaatcg gaactgcaaa
                                                                        60
tccgtactca atagccgtgg ctatgggctc tttctggaga cctgaatgga atgcgcactt
                                                                       120
atgcgggaga taggatgtgg gctttgtcgg caaacgggaa atgccctatg atttagatcg
                                                                       180
tgatactaca caaatccttc actggaggag atgactcgct tggctataga gaagctgaat
                                                                       240
cgttcgagga aggctttttc cttatggtcg agggtagtaa agtggattgg gctgacatgc
                                                                       300
caacgatect gtggggattg ctaccgaata tettgettte gatgtgettg tgccgtggca
                                                                       360
ttcgactttg cccgtcgtga cggacaaacg gcgtcatcat cgtgccggat catggcaata
                                                                       420
gcggtgtaag cataggcaaa caagtgtgaa agactatgat aagcgttctg caaaagacct
                                                                       480
tttcgatcaa tctgtcgctt ccgcctgaca gcagacggac ttgcagggcg tttggctgaa
                                                                       540
ctcccgccga caaggtccag ggtttggtaa gcaatatctg cggattcgat tggacgccaa
                                                                       600
agagttggaa gctctttata attgtccgga ttataatata gtcctatccc caaagagcag
                                                                       660
cgcaggcaga cggaagaatc cctctaagcg gttcgctcag taccttcatc gcatcgcttt
                                                                       720
atacgaagca cacttgatcg gttttacgac gcacggacat actgccgaag aagtattgnt
                                                                       780
ggcgcctatc acccccaaag atacacgccc gatgggaatg gtcataaact atgactgaat
                                                                       840
gactatetet geegtetett egaattagga ageeaattge eeteettace gacaagatat
                                                                       900
ttgctcccca tacggaagta ttccaaggca tagctacagt atcaaagacg gaaagaagga
                                                                       960
aggagaactg cctgttcttg agtgaaaaaa ggtagccatc gcttactggc gagtcctttc
                                                                       1020
tecaatacgg tatetteaat aagaaagega tigatetgte tteegtagta gtetatgtga
                                                                       1080
taagactaag actttctatt tgcctcgtga actgcgttct tattcgggaa taagccgctt
                                                                       1140
                                                                       1165
 gatgtgtgaa gaaaacccat caaag
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 624 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...624
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391

```
gtatagcctt gacggacgaa tacgacacga ccgaatgagt cggcgatgag acgatcggca
                                                                        60
gattggtcgc atcaggcagg ttcgcagcct cccgtatctg gcggcattgc ggccttgaat
                                                                       120
atccagtccg aatacggctg tctcgggagg gaggggaagt ctgccggttt gtaacgcttg
                                                                       180
tgtccgtcgg catcgggaag aggaggatca gcttgcgccc ccactgctcg aagtcggctt
                                                                       240
tcacctctcc aaatctttca gagcatggtt ggtaggctcc tgaccggctc cgagatggcc
                                                                       300
atcgcgaagt agccgcgtcc tgtggtagag aggagcgagc ggtttctgca tgggagagat
                                                                       360
cgtggtagag ctgttcggca ttgatggagc cgtcacctga atgtcggtcg aatcgtgtag
                                                                       420
cagttcgagc ggttggcgag cgtcttaccg gcttctaccg tgaacttcct catccggcac
                                                                       480
                                                                       540
aatacgctgc actggccata cgcgtaccgg taacgaggaa ataatgacct gcattcattc
cttggggcgg tcgaagagcg tcttcaggtc agtcggttca ttttcatcta atagagcgtg
                                                                       600
                                                                       624
cggatgatgc ccgaggtgta gctc
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 921 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...921
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392

ctttgagatg	agatagtatc	aggattcaaa	gccattccat	tccatgagaa	gagcttacta	60
cgttgctgcc	gccatgagct	gtcagccagt	ccaattgtcg	gaagacagac	agagccaacc	120
ctgaccatcg	ccatcggcat	cgatagtgtc	cattccgctg	gtgcctctcc	atgagtagaa	180
gactcgaacg	tttccggaag	tctgcgcgct	tgccattggc	cttgatctca	acctcatcaa	240
ggtcgtgtag	aacatatccg	tgctttggaa	gtgacggaaa	gcaacatatt	tcgtcctgcg	300
ggaaggtcta	ccgtcttctg	gcgccaagta	ccctgtatac	gacacgaata	gctttcggcg	360
agcgaacacc	ttttgccgta	atcgtctctt	ccacaaagca	ttcgtgaagt	tggatgcatc	420
		aaccgcatag				480
catacccaga	agtcaactta	cctccgttag	gcaaatccaa	tgccggtgtt	atcagatagt	540
gtcaggggta	agaactccta	taccaccaag	accgaatgac	tctgaataac	acaaccattg	600
ctattgtagc	cagcgattcc	gggagcattt	ccaggctcca	gccatgcccg	tcaccgtctg	660
catcgatcgt	cttccatgag	gcaggatacc	attttcgaat	gattcggaaa	gtgtagttgt	720
tccgggattc	ggattggatt	cggatttgga	tttggattcg	gggtaccatt	aggtgcatcc	780
cactaagcgt	tactttctgg	ccgactgcac	taccggtcag	gttctgtaca	ggacaaattc	840
attggatcct	tctaccgtaa	cgtctttaca	taccttcgga	gaacgccggc	tgtgtactta	900
acttccacgc	aatactcatg	a				921

- (2) INFORMATION FOR SEQ ID NO:1393
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 804 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...804
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393

	cttagatagt	gaggattggc	aggacactta	tttcgagggt	ggaagaaact	60
gggaacaaaa		agacagtta	trotoartra	ccttcgatat	tgtgatggct	120
caaaaagctt	agaacacgca	aggacagica	ctgcgaccca	taccanatac	datatoaocc	180
aacccaccct	ttgcgggaga	ggtcaagaga	geograface	Lgccaagtac	tacaccacca	240
gtagtatgtc	tctcgaaagg	tgaaaatagc	ccctaaggga	gcaaccatcg	tggagggcga	
gccgactttt	ctgaagctct	cgctaataca	ggagaaacca	tctatcagat	gagtatggta	300
catatogaaa	gaccaagctc	aagcaagctg	ggaatatgag	ccggacatcc	tctttgtaga	360
cacacegata	gattttctca	apccppgcpg	tctatggcta	tcgtattacc	tcaagggcgt	420
gcgcaacccc	gattetteta	actttacaca	aatacattoc	cgatcgctgt	cgcatccttg	480
tttaacaaca	gcagcgacaa	accurace	acctentaca	agtactaaga	coaprotace	540
cagtggtagg	ttgcatggca	atgtatttaa	geeteataca	ggtactaaga	cgagcgtacc	600
tttgtgcaaa	agtgggacga	ggagctatgc	ccacgagtag	aggattacac	atcttctttg	
ctaccatgca	agagccaagc	aaggacaata	gtggcgaaag	atttatcgca	gcaccactaa	660
Casaasaaac	gagaatgttc	ctttgctgac	acccacgggc	atcttatcgt	taagcacgat	720
	accatoacto	accoasosto	gcatagetna	agcctttgca	gagttcgcta	780
			8	5 0		804
agaagagaga	ctctctttt	CECE				

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 629 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...629
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394

accastasts	ocotcatcca	cacgcaagac	gatgggtgga	agagcaaagc	atccgtcaca	60
gccgacgaca	astattacca	cacagcatca	atetccateg	tggctgaaag	ggtgcattgg	120
cggatgageg	attectecte	ctactttcgc	ccaccaagt	COAPPOCAAD	gtcagcgtca	180
ggtggttcat	tecestet	tactteege	cttcagtcta	tettteeact	ttgcttgata	240
atgataatct	tacgacgatt	tgcgtgaagg	ctccggccca	tectestant	ccgtaacgaa	300
cggttgcggt	agggagactg	catccgaaga	gucgggcgag	coccttatta	cattastccc	360
gtgtctttct	tctttggcgg	gggccttgtc	ttgtgtgtct	cccctgttg	cgttgatccc	420
tgttgggcta	ggaatagtag	ttcttcaccc	gtatcttcca	tacgggcttt	ccgaggagcc	480
cgtgtagtgt	catagttgct	ttacattgcg	gtgtcaatcc	aattgaatga	ggctttatga	
gccttcgaga	tcttcaagca	tcgtcttgaa	tagctctgac	actgcaaaat	gtataggcga	540
atgagcacgc	ccgaatagcc	tangaaaggg	aaggatgtat	tanggagagt	gggaaaacaa	600
	ttgggctcca					629

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 567 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...567
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395

gctccttacg	ctttaatttg	gtttgcaaaa	atagtaaata	tccttagtat	cggaaaaata	60
castcoctco	tetetegate	tttcctcgcg	ggatgagaga	aggtagagag	aagagcgact	120
Caaccacaaa	taatctctgt	cgggtgccgc	ggcctataat	cgagatcttg	tatccccggt	180
ccttatagtt	ctacttgaag	etccegatat	taccgtccgg	ataaaaccca	cgcacgatga	240
tcaaggaccc	gatoggotot	gtccggcctc	acgaacgatg	tcgctgacat	cggccccgag	300
cttaccaatt	ggcggttgat	cgaaaggatg	atgaatcctt	tctgatacct	gcatccttga	360
atttcccga	orttacagag	gttacctcta	cacataagaa	acaccatagg	atcgcatttg	420
ttcagcacta	agggtetttg	atgatectcc	caatacattt	ccggtcgatt	cgnccggtga	480
ttaccgaagt	cttccttcat	tettcttea	gcgtgacngt	cagttccttg	gtcgcttcct	540
	gtcagcttca				-	567
acka-cka-ck	M					

- (2) INFORMATION FOR SEQ ID NO:1396
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 915 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...915
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396

ctttatgccc ttactccttc cgatgcccgt accatacagt aaaccacatc gtggatccca agaaacgcgt gcgttatatc ttcgtgcggg	tatgctacaa gcaggcagaa actgccgtac accatcgtgc tttgaggaca atccgacagg ttatctgcat gctacactca acagaacaat	cagcattgtg tttttattct cgattttgtc tggcagatga atcctccatt ctcttatcgg tcgatggtct agggggcaat gtgagcatac	tttgcgaaac caggctgaga gaacggcttg gaagatctgt aaggttggga tattcgcatt cggactttat ctatagtggg aacgatgccg aagtagtccg	gcggtatcag tggtatttc tcgatgtgtc tacaccttta cagagactta ccttccgaca gcttatgtat agttcgatat ctggacggtg	aaaccttggc gctattttcc tgcatgggat tatacaatgt tacctcggca ggctgggaaa ggataaacgg cagtgcggcg cttcttattt	60 120 180 240 300 360 420 480 540
agaaacgcgt gcgttatatc	ttatctgcat gctacactca	tcgatggtct agggggcaat	ctatagtggg aacgatgccg	gcttatgtat agttcgatat	ggataaacgg cagtgcggcg	540
ggagggacag cctcgtactt ccacagggga	gatatgttcc ccattcggga aatatcgtag	atatgagcgg tcattaataa ccgtcgagat	attgcatgcg cgagcaagtt ggacaacaga gggaaagtgc	atgtctatct gcatcccgaa gacggttcgg	gtacgccacg tccgactata ctgcacgtaa	660 720 780 840

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	•		
		•	

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1029
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:943

catacttctc	tcgactatca	tctaatttct	gatatacata	tggcttattc	tttaaaaatc	60
tcgtctttga	agggggtggt	gtaaaggcat	tgcctatacg	gggccctcga	agtgctgcag	120
gaagaaaaga	ttttccccaa	aatcaaagag	tagccggcac	atcggccggt	gccatcatgg	180
ctgtgctcat	cggactggtt	atacaccgag	tgagatcaaa	gagataatgt	ggtgcctcaa	240
tttcagaatt	tratogarga	ttcgtggggt	atcattcaag	atacgaaacg	gctgtcgaga	300
nattogatta	at acasagg	gatttcttcc	gcaattggct	tgggacctga	tcaaggccaa	360
agiliggilg	gracadagge		beautigge	+000	222222	420
gaccggcaac	agcgaatcga	cctttgcgga	ttggctgcaa	tgaaaggaga	aaacaaattt	
ctcgacattt	ctctcatcgg	cccaatcttt	ctacaggctt	ctcagagatc	ttttcggcag	480
aacatacacc	cgcatctgta	tagccgatgc	tgctcgtatc	tctatgtcca	ttccgctgtt	540
ttcgctgcta	agcgcaactt	ccgaaacgat	gtatatgtgg	acggcggttg	ctgaacaact	600
atcccgtcaa	ggtgtttgat	cgtaccaagt	atgtaacaag	aactttacac	gaacgggcta	660
ctatgaacct	atcaataaga	agctgggaaa	CECCCCAEEA	agattgccga	ttacgtatac	720
ccacgaaccc	cattagette	cgactcgaca	осааарараа	gatagccttc	ttcagggaca	780
aacaaagaaa	Callegette	Cgucccgucu	gcaaagagaa	5-1-0-1-	occupations.	840
acgcgaacct	cctcatcgag	atatcgacag	cttctttgac	tataccgtgt	cgcattcggc	
actctgctct	ctgctcaaga	cgatgtacac	ctgcacagtg	atactggcaa	cgcaccattt	900
acatcgatac	gctgggagta	aagactacgg	atttgccatc	agcgatgccc	aaaaaaaagc	960
tttgctggaa	tccggccgct	atacactcag	tcatatttgg	agtggtacaa	taacagcgaa	1020
	- 55 5	Ŭ		<u> </u>		1029
gaaaaagtc						

- (2) INFORMATION FOR SEQ ID NO:944
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 497 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...497
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:944

ccgccggcaa	tgctttcttc	ccgtctttga	tttctcccgg	tacgggtata	gcgatgtcac	60
tcagtcgcaa	ggagtacagc	cttacttctc	tatcgccaac	cgccgatgat	gagcgtgatg	120
acagetettg	tcctctctt	cgtactcgcc	tgggtttggc	cggcatggaa	agccgt <u>g</u> gca	180

		ttcaggagat	tatcaccaag	ttgatcgcca	aggttattat	240
tgaagggaat	gatgcagatt	CCCaggagac	tateaceaag	tesacetes	aggenanted	300
cccatgctgc	ccatctatat	cttcgggatc	tttctgaata	tgacccatca	gggcaagtgg	360
tgaaggtgtt	gtccgtcttc	cttagtatca	tcggtatcat	tttggccttc	atatcatcct	
actantatta	castactcto	tegcaggatt	caagccaaga	agaatccttt	cagaatgctg	420
gergatette	t	ttcaccactc	traatarara	gtcttcggca	gccactattc	480
		Licategett	ccggcacgca	600000000	8	497
ccgtcacgct	aagagtg					121

- (2) INFORMATION FOR SEQ ID NO:945
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 953 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...953
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:945

```
ctgaccaatt atattcgccc tacggacttt cgctcgatga ctatttcata accgcgagga
                                                                        60
ttcgccacgc gatgaatccg gagactatga tttcgaatgc tctacgcttt ggatctgccc
                                                                       120
cttttcaata aggatctgaa gcagatgtcg ccggtgaaga agtgagcctg cccacctatg
                                                                       180
acttcgcaac cgggataggg tctacaaagg aaataccata cagctgaaag acggagatat
                                                                       240
cctgacctcg aaggcattca tgcgctgaat ccggagctga tacccggtgt gcccaatcaa
                                                                       300
gtacgtataa gatctatgtg agcgctctca ctgcaatagg attgatgctc acaatcggat
                                                                       360
ccccagtacg gacaaccgac tgatcaggcg atggtgcgcg actatcgcta tcgcaattac
                                                                       420
tccggtctgg ggacattgcg tgttggcaga gtgtccgacg aggagaggaa aaatgggtat
                                                                       480
tcccgttcca gagaatgcac acgtcatgtt caatagtgcc atgctctacg agttggctgt
                                                                       540
ttgcgtgctt acgcggagcc gatcttacag gcaatccctc gtaacgaacg gaatatgctg
                                                                       600
aagcccgtag actgctacgc tttttgagca gtttccgatg ataccggcac gtttgcttcc
                                                                       660
gaacaactct ctgatgcgtg agttcccgga ggaagcacat tccactactg atgccgaatc
                                                                       720
                                                                       780
agtccgtaat agcagaacaa accgagactt gggtaacatt tgaagacgcc ggctgagtca
tatccggcat attttcagca aaggaaacga cgtaatcggg ctatataacc gactcaattc
                                                                       840
                                                                       900
tcaagaatac gaactnagag cgaaagcctt tttggttcgt aatttgtttg gaccccctga
                                                                       953
tcgagtgttc cgaatcggac tcgtcgggaa gagctttttt tgctactttt tgc
```

- (2) INFORMATION FOR SEQ ID NO:946
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2471 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...2471
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:946

```
60
ggccatcgag agcgttttct cattggcagg agcacgagtg gaattcgacc ctcgtacaac
ggctggcaac ctaatatcca gtcgcacatt ctcgaagtat gagcaaagtc ttcgaagagt
                                                                       120
                                                                       180
attacggcca aaagcccgaa gtacagggat gcatgccggt ctggaatgcg gtatcatcca
                                                                       240
aggogtaatg coggattgga catgatotog gtaggtocog aactocaato gocacactot
ccggagaaag gattcatatc gaatccgtag ctcgcacatg ggaagtactg gtaaagtact
                                                                       300
ggagcgagtg taaggagtag aagtcgagtt cggaggtatc tgcatcgttt ttagagatag
                                                                       360
gtcttacgaa ttaaagaggt gaaacagaac aacggaatca taatcaaaac aataacgaaa
                                                                       420
                                                                       480
cagagatgaa agcatttgta tccccggtca gggagcacag ttcgtaggaa tgggaaaaga
                                                                       540
cctgtacgaa agaaccccga ggccaaagca tattttgaaa aagccaatga gatattaggt
                                                                       600
ttcgcattac ggacatcctc ttcaacggca cggcagagga gctgaaacaa ccaaagtgac
                                                                       660
ccagccggcg atcttcctcc actcggtgat tctggccaga cgatgggcga agacttccgt
                                                                       720
cccgatatgg tggcaggcca ttcgctggag agttttcggc attggttgca gcaggtgcca
                                                                       780
tgaccttcga agatgtcttc gtctcgtatc gaaacgtgcc atggccatgc agaaagcatg
                                                                       840
cgaatacgcc cctcgactat ggcggctgta ctgggtctgc ctgatgaaaa ggtgaagaaa
                                                                       900
totgtgccca agtgaccgat gaagttgtcg taccggccaa ctcaactgcc cgggacagat
cgttatatcc ggttcggtag aaggagtgga cgagcttgcg aactgctcaa ggaagccgga
                                                                       960
gccaagcgtg ctcttaagct gctgtcggtg gagcattcca ttcccctctg atggaaccgg
                                                                      1020 <
                                                                      1080 /
ctcgtgaagg ctggcaaaag ccatcgagga gactacgatc agtcagccga tctgccctc
                                                                      1140 '
tatcagaacg taacggcttc tgccgtcacc gatccggcag agattaaaag aacctgatag
cacagotgac ggcacoggtt cgctggacac agagtggctg aatatgacag ccgatggtgc
                                                                      1200
                                                                      1260.
cgaccacttt atggagttag gccccgaaat gtattgcagg gtttggtgaa gaaaattgct
                                                                      1320
cctgaagcga caacgaagga cgtcagtaat caggtcttaa gaccctctaa gagaaacggt
                                                                      1380
gtacgagate geceaaacag egaeteegge acacegettt ttttattget egaggettat
acgactacct ttttctccgg aggettcttg tcatacgtct tgagaagata gacggttcgg
                                                                      1440
gtctattcgg aagaggaagg cggaggatta ttcctcctgc gggactttcg cttggcactg
                                                                      1500
tacttgctct ttttcttggg ccggaagccg aacttttagt gatttgcagc ctctgaccgg
                                                                      1560
gcttgacgag gaggacttca agccgtttgc cctcttaatg gctgctaccg tagtgcctaa
                                                                      1620
                                                                      1680
cgtttggcga tggacaagag cgtctcacct tgcttgacat tatggagatg gcggttcgtc
                                                                      1740
cogatectee egagtgttgt eegeettget eagggaatee gatacegaag eetceaagte
gggggaataa agcgaatcgc gaacttgtcc aatttcttga tggaagcgac gggaaggcgt
                                                                      1800
agtcggcaca gctggtatta ccggggatga tccccctttt gtattgaggg ttgagcagtt
                                                                      1860
                                                                      1920
gcattegteg ttgeteacae eggacaatag aegaatgega tegaaagata etgtegggae
agcataatcg tatccgtagc caaaggaacg ccggtctctc ggcacagatc tcatgttcga
                                                                      1980
tatggtagtg catggcatag tacgcaccgt gaagagcggg atgtagttcc gcgtttcgcg
                                                                      2040
                                                                      2100
aggaaggtag ggatagattc ccagaagtcg gtcttgccac cggacattcg gatggctttg
                                                                      2160
ttcacatgcc gagtccgcag ttataagccg cgatgcagag gagccagtcg cgatagggtc
                                                                      2220
gtacatgtcc ttgaagtagc ggcaggcagc ctctgtactt ttctgagatc cagccgttcg
                                                                      2280
tcgacgaggc tgtttatagt gagtccgtat atctgcccgt agccagcatg aactgccaga
taccggctgc tccggccggc gatctgccgt agggttgaga gccgactcca cgatggtcag
                                                                      2340
                                                                      2400
gtacttcagc tcatcgggag gttatgacgg tcgagtgtct cttcgatctg agggaaatac
                                                                      2460
agtcggcgag cgagagcata tagcggacaa ggcgacgacg ttcctcggtg agagcttgat
                                                                      2471
gcactgcttg a
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 333 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...333
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:947

actoccooa	occatgatog	cccttcgaaa	gtgaagggcg	gttgcgaagc	ggtaagaagc	60
acceccega	setacacete	tactecetes	ccgtgagctg	ggcgatacgg	aaaccctcat	120
tgatgaacaa	CCCgcacccc		***********	andadatac	tarragrage	180
ccagcatccg	gccagcatga	cccactcccc	Cacacacccg	aagagegege	tgccagcgac	240
atatccgaag	gactggacgc	ctgtccgtgg	gtctggagaa	cgtggaggac	atcatcgccg	
acctcagcac	ggtctggaca	gctgatctaa	acacccaagc	tgataaggct	gacaaagaca	300
*********	daaadtcaca	acgacttcgg	etc			333
Latgaatte	gaaagccgcg	206200000	0			

- (2) INFORMATION FOR SEQ ID NO:948
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1444 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1444
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:948

agatgtcttc ca	acgattat	ctgacggact	atgtgatgac	gatgctggtc	gtctctccgg	60
ctcttaccgc tg	CACCERAR	cataaggagt	ttcagccgtg	aagcgtatgg	ggtggaatgc	120
tctcgatgat gc	tacctcac	gactgatgat	agaatgaagg	aatacgaaaa	gaaanccaag	180
agtaagtaca aa	atacacca	gascaacac	tcaactatct	ctatctectt	acgatcgaca	240
gtcgcaccca ag	atacgeeg	accatactac	ccacatatat	ttcctcgata	ttctggccga	300
gtcgcaccca ag	cicicgig	tttacatata	cogcacgcac	ccacatactc	cacogtotae	360
tcccttccgc at	atttccat	LLLggalalg	ccgcgagccg	ccacgtatte	tecacacac	420
ggcgtaaggc ac	tggccgat	gatttcctcc	gtctatccgt	gagcatatta	cccgcacacc	480
ggatcagggt gc	gcactttg	cctgccttca	ggcggatatt	attggtgcga	cegtegetat	
ggtatgcaga gg	aagcgatc	gaggccttcg	ctcgtatcgg	tacgtctcag	gacageteta	540
tatcgaaggc tt	gcagatgt	ggctcctcaa	tcagaaaaga	actcagcttg	gccgagtctg	600
ccggcttctt cc	gatgcgat	atatgctctc	ttgttagtgc	aggaaaagat	cgaatggtag	660
aagccactgt gt	ctetccee	gctccttacc	tgccttgtca	ggtacatttg	ccggtgcagg	720
cgaaagtcgg at	cetaceet	ggaagatett	CCCCAACCCA	aactaagtgc	agagcttgct	780
cgttcggaaa ag	resttact	tagacttcct	tettoorgoa	atacgatgcg	ccgcggcgga	840
tctcgtagct ac	Seactcett	acttatcaat	ananaannat	ctttctccga	gcaggtgata	900
totograget ac	gggtaatg	geregeege	agagaagtat	altageage	gotagacggc	960
gatggcaagc ta	acgetegt	acctctccga	ggggcgaccg	gurggaaguu	882220088	

```
tcgtgacgca actgaccatt cgctcgatcg cgatatggac ttcattgtcc tgacggacaa
                                                                      1020
gcgaacggcg cggtggaacc tatcggccaa ctttcgggtt atgattatgc agccggaagt
                                                                      1080
tctactacag agaaataaag gatagcagta cgcgtttcta tttcgatgtc tggtaagagg
                                                                      1140
                                                                      1200
atcctacaag ctccaatact ccaccgttgt ggttcgtcgg gagcttatgc ctcaggtatc
                                                                      1260
gctaccgtga gcagtgccta tgcacggagt ttaccggtca taccgatggc ggcagacagc
tgcaaacagt tccgtcgcaa atactcaata aactaaagaa gcaaatgaac caacaaccaa
                                                                      1320
tcaaatcgcc gtattcggac tcggtggagt aggtggctac tacggagcca tgttgctctc
                                                                      1380
cgcgcagctg cgacggatgg cctcctcgaa gtttcttgga tgcgcgcgga gcacatttgg
                                                                      1440
                                                                      1444
aagc
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1068 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1068
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:949

```
60
gttctgggac ggaatggccg atatggatgg acatggagtg tttacgaagt gcttgacgat
                                                                      - 120
cgcaatcgcg ccggcaactt tgtgctgaac atgggtttca tcaggatgca tcaggccttt
                                                                       180
tggcgtttta cgacaaggct ctttacgacg cttcgctatt ccggcgggca tgactgtcgc
tgccgagctg aagatcgacg aggagtgtac agcggtcaag taaagctgac agagcgttcc
                                                                       240
ggcaggtccg tatcgatggc gactatctga tgggtacgga taagtatcgg ctcgtatgca
                                                                       300
ggtggacggt ctgaatttca gtgccttcat gccgaaggat agttcggttc catgcaggca
                                                                       360
gtgcttcatg ccgaagggcg tggattcgat ctttcaataa acgtactgtc tccaccatac
                                                                       420
acacateggt caaacacate ettggaaaga aegagatttg gacagtatea etttegatge
                                                                       480
ggcattgaac aaggagtgct cttcgcttca ttcaatagca ccaactcctt cctgaacgga
                                                                       540
gtatgcaatt ggatgccctc cttggcaaaa acaaactgga cggctctgga tggtgcggat
                                                                       600
ggattcggcg gatttcaatg cattgggctt tgcagaccca cttttgcggc agcttttgtc
                                                                       660
cttgagggtc atgtgaaaag cgatttgctc agacacatcg gttcgaagcc tcggtacgcg
                                                                       720
attgttacat gcagccgaac gctataaagt aataccggag cgaatagata tattagccga
                                                                       780
taccatcccg atagcatccg tctggatctc gtgtcgggcg acttgaaaat ggcctcagag
                                                                       840
tgggagaagg catagatgcc gttacggtcg tgtcccaatc tccgggaaga agatagagat
                                                                       900
attecgeaac gactetatte agegtetgeg atetettega tittteaaga getgeeteat
                                                                       960
gcgaccttta ccttgcaagc cgatcgctac aatccgctcc acgacttgat gggaagtaaa
                                                                      1020
                                                                      1068
cggtatgaat acaactccat ccgtggcaag ctggacagtt tcgcccga
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 594 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...594
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:950

actctagagg	atccccgatt	ccatttcctt	caacaaccag	aacatatgtc	ccggagcctg	60
accetagagg	tccatactga	agacactcgt	ccctgctata	${\tt attccttggt}$	cattgcagcg	120
agaatatata	ctacactatt	ataaaactta	tecgatatet	gccggcaata	ttcaaactta	180
acttettete	Cigiggigii	acaaagcctu	gaaccatgca	cgaagagctt	tggcagctcc	240
ccgaaacagc	cagticgaac	gaccggcgcc	gaaccacgca	tgaagagatc	aggtcgccga	300
ggtcaagtac	atgtattggt	ttegtteata	tacgcaaacc	tgaaaggatc	tattctacct	360
taaagggata	agtctctttg	cgaaccacta	ttgtcagcgg	caggatatag	tattctacct	420
tatcattctt	gttaagacct	gtaaagctat	aatatagtga	cctgttgatt	ccatcgtcat	480
atcagcagcc	ttaaagctac	cgaaccattg	atacgatagt	aacattgtac	cggcgagata	
gtagcattgg	gcatgagacg	acatctgctt	cgatcttata	atcagggcct	gcctgttcgc	540
cagtatcggg	tagtgcttga	tatagagata	gcccttatcc	gctacctctg	agta	594

- (2) INFORMATION FOR SEQ ID NO:951
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 526 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...526
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:951

cadacada	ctctatctcc	tttcggaaga	ttgcagtaag	atcctcgcga	atttaccgta	60
Cadagacaga	ctttactttc	taacaacata	ctatccctgc	cttaaatgac	gataacggac	120
tactatacat	caatacaaca	gacggacgat	gacgttccaa	acgggtacgg	ggagtggatc	180
arcttccgaa	ctggacgcgt	ctatgtatac	cccaatccgc	taaggccgga	atatcccgat	240
agecteegat	teccepacte	caagccggct	gtagtgtcaa	aatcaccgat	accacggcag	300
actoctatac	cagactgaga	gcgtaaccac	cgaagtcaaa	tggatgctcg	aggtgccgat	360
pocaatagge	tagcttcggg	cgtatatgcc	gtgcagtgta	cgatccggta	tcgaaaaagt	420
ccaaactaat	tcgcttcgca	ggattcgctt	gacacacggc	cttttctctc	gtaaacaaca	480
ttttaatcca	actaataggt	aatgaacaaa	aagatttttg	gtgcat		526

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1274 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1274
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:952

```
ttgaagatta tccggttatt gtaatgagca catctcaaca ccacgagctt aaatcgggtc
                                                                       60
aatatgeeca tecaaaaega aagaaetete geettggeta tecaeateee aagaaettee
                                                                       120
                                                                       180
ttatagccct gtcgttaagt cctacgctag ataaaccgtt ttcttgatta tcttgcctga
                                                                       240
ttctcttact ttgaattaga caaccatata acgcctgtca agaggagaat tttgccattc
                                                                       300
aagggagatt ggattacttt attagtaata atggatatgg cactcgtaga aaggttattt
cgtatatatc acaaaactta tcttctatat ctgatatatc tgaacgctca tttgtttgac
                                                                       360
                                                                       420
atagagtgag attacatgct tttcaatata aatttccaac tgttcatctt cgccatgtac
aggatgetat ceteetegga tactaeggga geteegttge catategggt ttteagagge
                                                                       480
tatacctcat gcctttaggc tcctcgactt aggcaatccc catttagctt gcataatctt
                                                                       540
                                                                       600
tagtgcgaca aactgtcgga tgcgacgttc gaccttttgt tcaatccgca gactacaccg
                                                                       660
gaaagtacta cggagtggcg tttgtaattg cctcccgcac ggctcattta acagcctctg
gactategtt caaccaatte aggettatee ttgtgettgt etttetacet egteatteag
                                                                       720
tcgccacttg gcaatagtgg acttatgcct ttactgacat gctacactcc cattgggttt
                                                                       780
ccccttggat aagtggttga tagtaggtta cttcaaagaa cacgaaccta atcatagcta
                                                                     840
aggagatatt tattgtgctg ccttatgggt gctctttcca aaatgatttc aggtttattg
                                                                       900
tcgtaaaaac agtatgccac tatagctgag acggattcat gatgaagtta ttgattgatc
                                                                       960
gatgtcttga gtgtacaagt tgccggtgtt tttcagcata tcattgatgc attctatgat
                                                                      1020
                                                                      1080
gtatcttttt caacatgatt ctgtcacacg agggcataag tttgttcttc atatttgctt
gattccggtt acaagatgga tgccgtcatc aaagaggctt tcaaagattt aggcgagaat
                                                                      1140
atcccttatc tgcaaagagt tttccgtata gttcttagcc ggaacctgcc aaaccttcgg
                                                                      1200
                                                                      1260
gtttctgnca tccacgttag caccttaaga caaaacgtaa taaactcttt acgatcattg
                                                                      1274
catacgaaat caag
```

- (2) INFORMATION FOR SEQ ID NO:953
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1057 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1057
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:953

```
cgtcctactc aaagctactt atctgcttgc cgccggcaac ctctaccgct gacctataaa
                                                                        60
atatatcccg atggtgtggt gaaatgtgaa aggtgcaatc tcttcgacag atatggagac
                                                                       120
                                                                       180
cgacgaatac gaatggtccg aagctgccga accgctacat tctcccccgg cagagaagct
                                                                       240
ctgcgcaagg aagctttatc ctcgaagtgc ctcgtatagg tgtacgcttc cgccttcctg
cggagtgaat gaggtacgat acttcggaag agggccggat gagaactata tcgacgcaac
                                                                       300
tacggggcga ctgtcggtct gtacaccact gctgccgata agagtactac aactatgtgc
                                                                       360
gtccgcaaga gaacgggcat cgtaccgata cggttggctg atgctgcacg gacgaggctt
                                                                       420
gggcttgggc atagtagccg agaaacgatc ggcttcaatg ctcttcgaca agctgtcgag
                                                                       480
gacttcgact agaagaagcc aagcacagac cctaccagtg gaacaactat tcacagacca
                                                                       540
gatacaaaac cgagatgaga gcaaagctcg caacgtcctc cgtcggcaca tcatgtcaat
                                                                       600
                                                                       660
gatgtgcctg tgcgcgactt cgtagaggtg tgcgtggtat gaaacaacaa ggagtaggag
                                                                       720
gatacgatag ctggtcggct cttcccaacc ttggcaccgc ctaccgtcca atcgggaata
cagttggggc tttaccttct tccggtacga tcagtcggcc aaatggccac tgccacccga
                                                                       780
tacgactact aagcacaggg cgatagatgt ggcaaacacc atgaggtgcc aacacactca
                                                                       840
                                                                       900
tatatcttat acggataaaa tacagcataa cgcatgaagc aatgaatgaa atagtagcac
atttccacac cgagggaagc gtggcagaga tgcaccctta ggtgccggtc ttatcaatga
                                                                       960
                                                                      1020 😸
cacttacaag gtggcaacag cgaagccgat gcacctgact acgttttgca' acgaatcaat
                                                                      1057
cacaccatat caaagatgtg gaaatgctac aggccaa
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 995 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...995
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:954

60
120
180
240
300
360
420
480
540
600
∙660
720

ggettetgee	ttcatacggc	attctgcaaa	catagccctg	aggatattcg	catcaagagt	780
taaataaata	caagtagtcg	ctttttcttg	ttgagagtgt	cgattgtaaa	ttcagagagc	840
ctctgtaaat	ccggtcataa	ppccpactec	acttgcagca	tttcttctct	ctctcctcac	900
ttacatagaa	CCERCCACA	cggaggcagt	gntttagtat	ttggacactg	cctctgtctt	960
tttcatggag	attaccctcc	aaagatcaat	cccgt		-	995
tttcgagcgg	attaccccc	aaagattaat	CCCEC			

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1245 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1245
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:955

```
acgccggcta cactgatagc ctgctcgtcg agtattttgt aataagttct gtttgggcat
                                                                        60
tgagccggca ttggcaatac ccagctcgcc ggctatagag cgagttcagc ttcagccttt
                                                                       120
tcgttcaaat cgacgatcgt gtacttcgca taataaatga tgatgagctt tttagaaata
                                                                       180
                                                                       240
tgataagtgt tgatagggga tacggcatct cggaatgaga ctgtcaggat actcgatacc
                                                                       300
gcaggcgaaa ggatagagaa taggtgtcta tttcgttttc cgtcgtgcaa atgtagaaat
                                                                       360
aaatcgaatg atggtcttac tccctccgcc ttattcgccg aggcggctgc gcctgcggat
                                                                       420
gctacggccc acgggggcga tgcggagagt cgtcgcaaag agcgggacgc cgccccctt
                                                                       480
cgtctccata aacgacacga cagagtattt attttactgt ctgccgaatc gaactatttg
ggtacetttg egeggtttge agacegeece egeaagtegt ggeegeece teggteageg
                                                                       540
                                                                       600
cgtgcgggag gagccgacgc acctcacggg aggaaggccg agagcctccc cgggaaacgc
                                                                       660
cgggacgtgg ccgtggccgt ctgcaatatc ccctcgaaaa acgtctagac gttttgcccg
aaacgtctag accttttgct cgaaactcta gacgttttat tcggaacgtc tagacgtttt
                                                                       720
cctccgaacg tccagcgttt tttttcggag gacttgaggg atgtatcggg tatgagtggt
                                                                       780
catcaataac aagaaactaa taataagcaa gttatgtccc taaagtatgt gataaaaagt
                                                                       840
ctgtcgccaa gatcggcccc aaagccggac agaccatcta tttgcccagc cggcggcaca
                                                                       900
                                                                       960
agactotgta accttocaca goototgcaa ggaatagoog aggagtoggo totgacotoo
                                                                      1020
gccgacgtca aaggcatcct gaccgcctcg tcaatatcct cagcgaggag ctgcccaacg
                                                                      1080
gcaagacggt cgcatcggcg agctgggcag cttccgcctc tcgttcggtt ccaaacaatg
                                                                      1140
gacgacccca agaatttctc tgtagatcag atccagaagc acaggctgtc ttcatcccct
                                                                      1200
cggcagagct caagagcatc cccgcacgcg gcaagcccgc ccggggtctt cagccctggc
                                                                      1245
cttcgactac gacgtgtgga gccgagccta agaagaaacc cggac
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 618 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...618
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:956

caataaata	toottoocga	tataaggttc	atcggccgga	gctgctgttc	60
Caaacaaaca		catootaaoc	totogtocac	tacagggcag	120
tggcggcccg	Ctttgatgtt	gatggtaage	toopso	000000	180
agcggcgtgc	cgactcgcaa	aggagaggag	acaacccaga	gaagccaccg	
ctgttgagag	gtgccacgta	tcgctgcagt	tcggctacaa	gcaaggcgca	240
casagactac	tattttctct	toggotocga	gtatttttgc	ttcgactctt	300
Cgagggccgc		+ancanatat	ttattacaga	tocactoggo	360
cgtaatatac	cgttcggcac	Lgacgagege		attattataa	420
tccttgtgcg	tgttgcggac	ttgatatagt	ageegaacae	aligitataa	,
pactgggtat	tccgttcgct	ctatctcctg	ctgctgtagc	tigatiagat	480
ctatatacca	gtgcacgcag	ttcgtcgagc	gtggcatcga	cgccatgtgg	540
Cigialgeca	gegenegeng	acot caaaca	traceteage	aatatottet	600
cgcgaccgag	agcggccgga	gcaccgggca	ccaccccage	44444	618
cttgcaca					010
	tggcggcccg agcggcgtgc ctgttgagag cgagggctgc cgtaatatac tccttgtgcg gactgggtat	tggcggcccg ctttgatgtc agcggcgtgc cgactcgcaa ctgttgagag gtgccacgta cgagggctgc tattttctct cgtaatatac cgttcggcac tccttgtgcg tgttgcggac gactggtat tccgttcgct ctgtatgcca gtgcacgcag cgcgaccgag agcggccgga	tggcggcccg ctttgatgtc gatggtaagc agcggcgtgc cgactcgcaa aggagaggag	tggcggcccg ctttgatgtc gatggtaagc tctcgtccac agcggcgtgc cgactcgcaa aggagaggag	caaataaata tcgttggcga tataaggttc atcggccgga gctgctgttc tggcggcccg ctttgatgtc gatggtaagc tctcgtcac tacagggcag agcggcgtgc cgactcgcaa aggagaggag

- (2) INFORMATION FOR SEQ ID NO:957
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 566 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...566
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:957

			acconstant	tactacacac	ctecceatee	60
gaagtgccgg	gtacggagcc	gcgcgactgt	ggcaactgcc	cgccgcacac		120
ccaaatatga	ggccgagaaa	tacctgcgtg	aggtactcat	gtagcgacgg	aggagaaccc	
tatece	dact dacaac	taccapatet	gcatggggct	tacagtccgc	tctatttctc	180
gaactattet	gaccgacaac	-5655-6-	centeccata	uucaggacaa	togcatttca	240
acgtctgcat	ctctaccctc	atgtcttctg	Caacgacaca	ggcaggacaa		300
pccacaacgt	acatctaaag	ctcatgattg	ctacattcaa	ttttcaaaac	aagtcgaatc	
Setatataa	acattcasat	catagaggaa	agagactaaa	aatttcaaac	gcgatcgccc	360
Catatgicag	agacccuacc		ant ant ttt	caacttcatt	coaccaaatt	420
tgacaggctg	ccccggggc	cgatgcatta	aatggtttg	Cggccccatc	cgagcaaatt	480
totoctcatt	ggtattattg	gtgctattgt	gtgccgatgg	cagccggatg	gattattgga	17.1
	tatcaactca	tatogacoca	atotoaatca	gacggcacag	cgtggcgcaa	540
gccggaggcg	Catteggereg			8 00 0		566
aggtgcatac	acggggagca	aggega				

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 445 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...445
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:958

ggcaaagtcg	cacgtggcag	taatccaaat	gggcatatgc	ttataattga	tttgtgtata	60
togttgagcg	tcagcaaatg	ctcgtccgac	catccggcgg	accgccatga	ccagcataat	120
taagcaggat	aatacccgac	tgaagggttc	cagcatcttt	ttctttgcac	ccggaatgct	180
atacaaccca	ttctcgtgac	atgcggatat	acgtcctgaa	aggcgcgtac	cggcatgatg	240
acadacata	acectteace	gtatcgatca	aacgggaagt	ctcggttgcg	tgctgtcccc	300
attatctacc	gcaaaacagg	cacgaatacg	ccaggcacca	ctcctcgatc	ctcctcatat	360
canatagtet	totccactec	gatgcgagct	tcgccggagt	acgtacgggg	aatogooota	420
	ataatgcgcc		0-00-0	0 0000	_	445
Lagulatati	a cauce ce	~~~6-		•		

- (2) INFORMATION FOR SEQ ID NO:959
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 525 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION  $1...5\overline{25}$
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:959

ctcggtcgcg ctcctg	tggc caacctgtgt	ggcatccgcg	gtgctgtatg	tcggaatggc	60
tgatgaacgg gctgtt	copa ttcopaacoc	tetteetett	ttctgcgttt	tttcgctatc	120
gctcaagctt atgggt	otco tcasacosta	tctotcotoa	aacegctgat	attctgcggt	180
gtgatgacct tttgga	gage ettgeagetg	cattcatcta	casactttca	ggtctcgaag	240
gttttttcgt tggggc	gate treeseastes	acastacaca	ctatttctca	aacgaatata	300
ggtaaggccg gactga	ggta tgtatggtta	agaatggata	thecatage	atagtagtac	360
ootaaggccg gactga	tcat agttctgctc	gtccttgccg	teacatageg	gragiggiac	ع بي ح

gcagcgaatg tatgggtttc ttccgccgtt tgtgg actgccgaag aaagagagga aaataatcat gacga ggctacgaca gggtgaaagc gagaatctct ccggc	gtorg addatgaget geteggedde
(2) INFORMATION FOR SEQ ID NO:960	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:         <ul> <li>(A) LENGTH: 486 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: circular</li> </ul> </li> </ul>	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONA	S GINGIVALIS
<pre>(ix) FEATURE:      (A) NAME/KEY: misc_feature      (B) LOCATION 1486</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID	NO:960
gctaagctca tcatctcctc gtttgccccc atgatgcatacaag ggcaatgaga gcagctaaaa tcacctgaccagcc ttgacaattt gcttcgcccc aata acaccaaaca tcagcctatc ccaagaaaca ccaagcgcagga agagttccca aacgtgcaac ccagataatcagca ttgcgatgac aataggtatc ccca cttcttgcaa aatattacag cgttgttcat ccta attctgctgc aaaggtacag gggatacagg gtcgtagcac	agagtg attactgaga tggaagetac agcgag atatatacac tccgcccca 180 cgataa agggaaaaca actgatncgg aaagta tctaccacat tgtaattgcc 300 actttg tcaggatttc atcatacttc taatct gtatcttctt aagtaaataa 420
(2) INFORMATION FOR SEQ ID NO:961	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:         <ul> <li>(A) LENGTH: 1598 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: circular</li> </ul> </li> </ul>	· •
(ii) MOLECULE TYPE: DNA (genomic	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMON	AS GINGIVALIS
<pre>(ix) FEATURE:     (A) NAME/KEY: misc_feature     (B) LOCATION 11598</pre>	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961

```
tecceggeeg atgeegetet gaaataegat aaggaataea aetgattgaa aaggeaaaga
                                                                        60
aggagetteg acaagactgt ggageattte ttacaatagt atggeageae egeetetata
                                                                       120
gctcgttaag ctatggggcg gatgcttctt tttggagcct gaggtcattg atccggggat
                                                                       180
gctcaatcgg gatagtgccc cgatttcttc aacgccaagg tgaaagtggg cgatctcctc
                                                                       240
                                                                       300
tgggcggcaa cgtagagatt cattgcaggg cttcggattg ggtccgtcac gggctcatct
cgatccggct tatgacaatg tagtactcca tgtggtagag acgatgacct cccgatacgg
                                                                       360
caccgaatca gcggtgaacc tgtccccgtt tggttatgca tgtagacgaa cggcttaggg
                                                                       420
                                                                       480
caaacgccga ctttatgctc cgacgtccct tttgccgggt tgtaaggaca ggctccatga
                                                                       540
acttgatage tegaagteea egactggetg gacaegeteg tegtagaaeg attggagega
aggetgeega agtggategg etetatetgt etacgteeat ggattggatg caaeggeeta
                                                                       600
tatcctgtta gctcgtcatt tcggattcgg gctgaacacg atgccctcga gcggcttgct
                                                                       660
cgcagcctgc cctttgccgc catcgcaagc atcggagcaa tctcctgcaa gtggaagccc
                                                                       720
tectgetegg geaggeggtt tgttggeega cettgaggat gaatatgeeg agaagttgge
                                                                       780
                                                                       840
ttcgaatacg ctttttgag acataagttc gacctgcagc ctcttgatcc ctcctctttc
                                                                       900
gtctgcatcg cgcccgtcct gcctctttcg tacatcgtcg atgggacagt tggccgccat
                                                                       960
tctgcatcgc tgcgagttcc tgttttcttc tttgtggaga ctgtgtccgc taaagaactg
                                                                      1020
gcacagaagc tcagcgtgga gcatcgtctt actgggcttc gcattatcgc tttgggaagc
                                                                      1080
ccacccctgt ccttcccgta gtacgcttgc cgctatttcg tcggatgccc tgctgatcat
                                                                      1140
gtagcagccc cacttcgcta tgcttggttg agggggcaga gcatggagac taccgcgagc
                                                                      1200
ggacaataga cttcctgcgt ggcatcaaac ccgaaacaac aagccggttc gtgctttctc
                                                                      1260
ccagatctgc cgacctgcgg atgctccgaa agccaagccc tcattcagct ctatcgcgaa
tactgcgagc gacgaaatgc ttcttttgtc gctggggcta tcgcttgctg agctgctgca
                                                                      1320
aaggtaaggg tgcatcggtt tcgggaagaa gtccgaggcc aaacacttcg tctttactac
                                                                      1380
cggtccgtca atagggaata tgtaaggcgg cttactgtct ccaagaggcc tcccacttga
                                                                      1440
                                                                      1500
ttttatcgct ttatcatagc gaattgcatc cattgcaaat acgtttttat agatgctgtc
tattagagca tagatgaaaa cttgattgtt tttgtaattt tgaaacgttt tcagagcatg
                                                                      1560
                                                                      1598
taactaacac gatttatcac aacacaagaa ttatgtca
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 492 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...492
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:962

cocpaatoge	agggtaagat	gcaggagtcc	atcaaccacg	ctgagggagg	gagcaggcca	60
agattctcag	agccaaagct	gaggcagagg	ctaagatatg	gtggccaagg	cagaggccga	120
agctatccgc	cagatcagcg	aagcagtgcc	ggtagtggtg	ccaatccgac	ccaatacctc	180
attgccatgc	agtatacgaa	acgctcaagg	acatcaacaa	gggcgatcag	accaagaccg	240
tttactcccg	ttcgaggcta	ccggtatgct	cggtgccttg	ggcggtatga	aggattggtg	300
aaaggatgag	actctctgcc	attcttatcg	ctttgattgt	gatctgcctg	ctgtgcttag	360
cgggcagcat	tattattcca	tggcgggaga	gcactggaga	cggacagcat	tcgtccgaac	420
gaactctcgg	catcgatccg	agtgcgcttt	tctttcggaa	caatgaatac	caatgcacgt	480
tcggtcaaaa						492

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1779 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1779
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:963

```
60
gtaagtcagc caagcaggct ataatgatcc cgaatggtac cgccgtggct gccaaagcca
                                                                       120
ccttcccaag tgacgaatat cttggccgga ttggccaata gtatgccggg tcatagaata
                                                                       180
ggacatgtcc caaacgcgct ccgacgatag tacctacaaa agacatagac ggccagggac
                                                                       240
togaaccatt tggaatcago ttotogtgtt cocacatttt tttototato caagggooca
                                                                       300
gaatgtcagc cccaatgcaa aagagcaaac cgtaccagac aatagggtgc ccgagagggt
                                                                       360
aaatagaacc ggatcgaaat cccatgtgat gaatgcaggt agttcataat gttccgatta
                                                                       420
acceptitagt tgagtaatct ttttcaacaa agtttcctat ccactgctcc ctgtctccgg
ggagaaggtc tatgacgggg attcctgtaa ggtgtaagct ccgggttgtt ggcgcatggc
                                                                       480
tgctcgagct cacagaccag tacttgtccg gtgagagcgg ggttgtttat ctccatgtca
                                                                       540
                                                                       600
atgacattcg ctggttttgt gtggagccgc ttacaccctt acgcaccagc ggacgccatg
                                                                       660
ccccatatcg atgagggcat ccacttcatc tacctgttca cgtgggtttc gtcatgaacg
                                                                       720
aaatactcgt ctgctttgat ggcagcgata cctcctccaa gttgtgtccc ggaagcagtt
ctacgtaaac catgcacgat gtacacccgt tccgagagga atggtcatag aaagtgcggc
                                                                       780
cttgcaccgt ctatggcttt tacggctacg gtgtgcccca tgctcatgcc cggccgaagt
                                                                       840
                                                                       900
togtgtaggt gatocotttg ggtacgatag cotgcatcag tggcgcacta cagagtogct
gcccggatcc cagcctgaag cgatgacggc tccgccccac tttttccggc ggcgtctccc
                                                                       960
                                                                      1020
aacgatcgac gcaaggccaa ataccgtcgt ggatgtcgaa actgtcagca gtgcatattc
cctitttcat atctccaagg ctgttcgctc tacttcacga cttggtgagc aaaccaagcc
                                                                      1080
acatcgaccg attcgagttg ctcgatgtcg gatactacac ggaaaggtgg agctcgaagg
                                                                      1140
gaacctcggc cggattgcgg cggacaatgc cggctattca aaatctggag cttctctaag
                                                                      1200
cgcttgcaag gcataccgac cgatatgccg tagcctacga tggctgcccg aatctttttg
                                                                      1260
tegtetgtea tttgeaaate tgggggatag etgttttgee eetgetetta tttgagtagt
                                                                      1320
ttgctttctc tctgagactt ttgaccacag catccagcaa cccgtttacg aagttccgct
                                                                      1380
cttgggtgta ctgaacagct tggagaggtc gatgtattca tgatcgttac caagaccgga
                                                                      1440
                                                                      1500
atattcggga agtggagcag ctcggcgata ccagttgcat gatcagcata tccatgtccg
                                                                      1560
ctatgcgatc cacttcccat tgatcagatt ttcacggatg atatggcgat attcctgtcc
                                                                      1620
gttgatgagg cattgcgcag tagggtggtg ccgaatacgg catcgtcttt ctccttgatg
caggaagcag gatagccgat ggatcggtgt cttgctcgat ccgtcgattg tcttgaggac
                                                                      1680
gaactccttc acgatttcga taggtgcatt ttccttagga tcgtttggta gttgccatcg
                                                                      1740
                                                                      1779
gcaactgctt gtcgtaccga catgtccacc tcctctatg
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1037 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1037
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:964

cocoaaaatt	ttttcgttgt	ggcgcgagaa	gtaaaaattt	ttggaaccaa	acgaaaaatt	60
tetegegegt	gttttcgcca	aaacacgcac	cgcaatccac	cgtttttggc	CCGLAACCEC	120
cccacactag	gaagetettt	tcatcggtcg	tgtagctcct	tgtgagaaaa	taaagatatg	180
ccgacagcag	aaataaatto	poatttatta	ccggttacgg	cgcggaatac	tctcttctct	240
CCCgaaaggg	2000000000	tgacctttt	tatccttgca	ggcaatccta	atgagaagat	300
ttatttttt	gccggaagcc	nancaactee	cttgcgcact	gtctactggg	gttgccggat	360
actaccacac	gttaccaacg	aaacggcccc	actacastac	Caadadtat	gaatccgtgt	420
tcgaccggcg	gagcacctgc	tetegeegae	actacgatgc	etagagecae	tactogatgt	480
tacggggcac	ttatccttcg	gcgaggatat	caagatagaa	atggatgeeg	caccegacge	540
actggtgcgt	atggcataga	ggtgctccgt	cccgagccga	tagcaaacta	taattagatt	600 ₹
++ acccacas	tgtggctttt	gccatcgatg	acaaactctt	cgtatcgacc	tgatageega	,
tratacccac	gagtccgaag	ccttttcgcc	catttggatt	gtgtcggaga	gagecatetg	660
gtacgcctta	pogaagatat	tcatgcgaag	gcggagacat	cctgttatat	gacgatatic	720 -
ttttcatagg	cacctccttc	agaaggatta	tccttccttc	aagacggccc	gaaccaacgc	780
acaactataa	acttcttccg	cgaattttc	ccacacaaga	ccatcatacc	gatgagctga	840
tesaccacae	caccoatccc	atgcgctcgg	tgctccacct	cgctgcgctt	tccaacccgt	900 :
ccaagcacga	caccaccatag	tctaccacca	agattectge	actctgagag	cttcggcctg	960
aggeegeage	tetoggtage	aggeogect	attragagatt	acaccceage	aagetatatg	1020
		gggacaaccc	geeegagaee			1037
atgaatacca	tatattc				2	- 1

- (2) INFORMATION FOR SEQ ID NO:965
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1677 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
    - (ix) FEATURE:
      - (A) NAME/KEY: misc_feature
      - (B) LOCATION 1...1677
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:965

catagtatga aatttatcat aattagttgc tacagcagac gacgcacaat ggaagataca tttactttaa gagetgetee ataggeattt ttttactgaa tattgaaagt gegeetttte

```
180
gttgtctgca agttgatact tatagattta tattcaccct gtgaagtcac atctgtatga
                                                                    240
tttatttcct cgaaagcatg gttgtaccta acgaactatg gttacggtga ttgctatact
ccacctattc agcgtgtagg acttcggtac tttcagatag atatttctaa tcttacacca
                                                                    300
                                                                    360
ggacgatatt cattggcata ttcaaatgca ccagagccga aacacgggcg tagtggttag
caacgcgtcc cagatctgtt ggagtacatt gtaaatgaca tgtggatcgg taccgtttac
                                                                    420
aacaaaagta cccatgatgt aatctcgggc acaagtatga gacaagttaa cggattggct
                                                                    480
tcatcccata cggtgacaca ttggcggtag agttgtagaa gaaccactcc ctaccgactg
                                                                    540
                                                                    600
cgtatctact ctatgagcat tctgggatgt tacccgataa cgggtaacac atccactttg
tctctatcaa gcaatccacc agcaggaagg attgaagaaa atcccagtcg atcacctgct
                                                                    660
                                                                    720
ctgcattatt atttcggcgt attgaaggaa tgtcgtatat ccatctaccg atacaatctg
                                                                    780
aaccccatca cggaaatctt aatatcggcc gaaagaggag taagcgtttc tactcgatcg
                                                                    840
acaccgtagc caaaacaaaa cgggcgccca aagacgaagc agtaccatgc tggtagaagt
cgctgtaatg ttgacttcgt ccatatatag ggctttagcc aatcgtaagc cgatatattg
                                                                    900
                                                                    960
ctacgagatt gacgggtccg catcgtataa tcgtccagcc caacgaattg tcggcacgtt
ctatcttagg caccgaagtt ccgcacctct accgcaggga ggatcgcagc ccaaaacata
                                                                    1020
1080
                                                                    1140
agttgaatac ctctctaatc ttatactcca caaccatttc gtgattattg tacagtcgta
                                                                   1200
tttcacacca tggagggtta caaaacctct ttcttgctgg gcgaaacgat agtcattgtg
                                                                   1260
tttcctgatg tcgtgatatt tgcataggga ggttaatcgg tggagtgaaa actaaggacc
cgtctatcgg atgatttta tattggtcca ttctatatcc gatttgggag gcatagtcat
                                                                   1320
                                                                    1380
acctgcggga atactatttc taccacatac cgcgtattgg gattggcgta cctatattat
tatatgagct gaggatggaa tagtaggaag tcattatctt cggtcgaaag gcgtatcctt
                                                                    1440
ctctattaca gtaggcatgt gagaggcatc tgtaccgact cacgagacaa atacaaatga
                                                                    1500
gtactagaaa gattgaaccc gtgttgggat ctatccatga ggttctatca caagatgtct
                                                                    1560
                                                                    1620
gatatagttt ttaagaatca agcccctatc ggacaaatca tttggagcgt tgttgcagcc
gtaaactgat cacactttag ccgcaccgtt acagtaatcg taatagagct ccgacag
                                                                    1677
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 860 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...860
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:966

```
60
ggatcccctc ttcgatctca acgaatacac cgaaattggt gaagttgcga cacgagcatg
                                                                       120
gtgacgagag cctacaggga aacgagtttc gatatcagcc aaggatccgg cttgagttgc
                                                                       180
ttcagaccga gcgacatttt gcgttctcgc ggtcgagcgt caggatcacg gcttccactt
                                                                       240
cgtcgcctac atgcagaagt cctgagcaga acgcaagtgc tgtgtccatg acatttcgct
tacgtgataa gaccctcaac gccctgtgca atctcaacga aagcaccgta atctccatca
                                                                       300
                                                                       360
ccacaacttt accettcace ttategeeta cettaagete gettegagag cateccaagg
                                                                       420
atgaggcatc agctgtttga gtccgagagc gaacgcttgc gatcttcatc aaagtcgagg
                                                                       480
ataacgacat tgatcttctg accagctgta cgatttcttc cggatgagcc acacgacccc
                                                                       540
atgaaaggtc gtgatatgga taagaccatc cactccaccg aggtcgataa atactccgta
                                                                       600
gaagtaatat tottgacgat accttcgagt acctgccctt tttcgagctg ccgatgattt
                                                                       660
ctttcttctg ttgttcgagc tctgcttcga tgagcacttg tgggaaacaa ctacattctt
```

tcgcgaatgg cgacatcata	ggcgccgtcg ccacccttgg	atctgtgatc tacgacactt	ccgggaggaa	agcctcgata	tgcatcgtag ccgaatacat cgttttttcg	720 780 840 860
agagcctcgt	tcacgcgctc					500

- (2) INFORMATION FOR SEQ ID NO:967
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 583 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...583
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:967

ggatacgtcc	ggagaaggtg	gcagcagtgg	taagcagggc	agctccgatt	attcacctcg	60 120
ccttagagaa	ttgtctccag	cctgtgggtg	teggatetae	LECCERTALA	accedaces	180 240
cgtccaccag	gtaacttgga	aacggatctt ctgggcagac	caagccatag	ggtcgaaagc	caagtatttg	300
toaataccoa	caggtttttg	tccatcgaaa	cacctacata	ccgacccgac	tgtcgggtct gtatgccgcc	360 420
cagaagtgga	tcagcgtgta	caagcagcct	ctgggctgcc	gtccgattgt	acgaccaaag	480 540
actttacctc gccgagctac	ccgacaaaag	caaggcagcc	gcgaccaatg	agc	atggagaggg	583

- (2) INFORMATION FOR SEQ ID NO:968
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1401 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1401

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:968

```
gcacggctgc acgaagggct tccctatccg attcttttt gatggccggt tccatttgat
                                                                        60
cctgttgcca agtctgccgt agtcggtatc gctgaaccca aatggtgtac acagacttcc
                                                                       120
gacgtgattc gcttttgtgc tgtgggttat cgttgcggaa gagactcagt tctttctctg
                                                                       180
togatagatg caggattgca gacgggcatt catcototog gocagotoca cogottotgo
                                                                       240
                                                                       300
cgatggcggt aacaagcctc ttcactacgg atgagaggat ggaaatgtat gtccaatcat
tcccgtattt ggctttgtag tgctctttgt tggctcggat gattcctctt tttcacagtg
                                                                       360
cgtggcgatg agcaggtcgc attctccgaa tatttctcca gcgtttcctt attgtccaca
                                                                       420
agcatattgc cggtagatga acgaggaata gcttcagacc gggtaccaga tgcttgtcca
                                                                       480
cccgtttgat tcatcgatgt tgtcattcgt gccaccgaag aagaagccgt agttggccct
                                                                       540
gccgtgtctg caccgatctg ccttttctcc agcagtcgct cccacatttg gtaggaggat
                                                                       600
togtattggg catatocata aacgaagtga ctccgncgct actgctgccc ggctttcaga
                                                                       660
ggcgatggta gctttgtgcg tcagtccggc tcgcggaaat gaacttggtc gtctatacat
                                                                       720
                                                                       780
ccggggaata gcctcgaccg ctacactcta tgacttcatc ggcggagaga ttgtcatccg
cgggagctct ccttcgataa tacgggagat aaatgcgcca tcaatcatca ccgaccgggg
                                                                       840
                                                                       900
aaggtttttc cctcgttggt gataagtgcg ttgcgaagaa gattttcatc tctttcgtac
                                                                       960
tattttcttt tgggaaatcc tttgaataag tccagtagcg tagcttgatc acgcccgtaa
aagcttcacc gaaaatagaa tgttcatttt cgacgttccc aaaacacgat tgacgaaagt
                                                                      1020
gatgggtatt ctttcaggcg aaatccgaga caataggccg tgtatttcat ctcgatttga
                                                                      1080
                                                                      1140
aagcgtagcc cttgaaatgt accgaatcaa gatcaatggt ttcaagactt cgcggcggta
                                                                      1200
gcaaacaaat ccggcagtcg tgtcgcatat attcataagg tcacgagacg cacatatacg
                                                                      1260
gatgcgtagt agctcatcca tacgcacttt taggccagtc cttgacgcct ccgcccgata
                                                                      1320
catagogoga googtogota catoggotto tootooggog caggoattgt atagatogat
caattgtcta ccgggtggct gaaatcgcag tccatctcga atatatagtc atccctcgcg
                                                                      1380
                                                                      1401
cgatgctcca tttgaatccg g
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 768 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...768
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:969

```
60
ggacgatccc tcctcctgt gnaattgaga aaccgtacac ggctaccgag gtgatattat
                                                                       120
ttgtactcat tgttctaaat aagtggtatt cataatttta ctccacaaaa atacaaaaga
                                                                       180
acgagcggtg tatcaaaggg ataaaaaaag gtgtgcaaaa atcgcctaat tgcgatttcg
                                                                       240
acacaccctc tttccaaatc gatttaatta ttgtctttcg ctaaccgtcg aatcagctca
                                                                       300
gtttgggatg attagaccgg aacgaagttt cggctcgaac caagtagtct tgggggcatg
                                                                       360
atattgcccg aatcagcaat gtccatcagc tgtttcatcg atacggataa agagcgagag
                                                                       420
caacacgcat ttcgccactg tctacacgct tttcagttct cccagtccgc gaataccacc
                                                                       480
cacgaagteg atacgettgt egageggaga tetttgatge etaagatete atecagaate
                                                                       540
agattcgaag gatcgtaaca tccagtacac cgataggatc gttgtcatca taggtgccgc
                                                                       600
ttttgctgtc agcgaatacc atttgccacc gagatagaga gagaagtttg cagcttggag
                                                                       660
gggcgatatt cttccgtccc tttgcattct acttcgagtg tcgagacagt ttctgcaaga
```

attcttcatc	actcaagcca	ttcagacttt	cactacccgg	ttatagtcga	tgattgtgag	720
ctgatcggca	gggaacatac	agccatgaag	tagttggact	cttcatcg		768

- (2) INFORMATION FOR SEQ ID NO:970
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 431 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...431
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:970

gcatcgttgt	ccacggaggc	gggccattga	caggaacaaa	taccctgttt	tcagaatcag	60
agagttcgtg	tacggttgtt	cattggtggc	caaagcgcat	atacctcgta	cttcgttccc	120
catececage	tctgtgctgc	gaagtagctg	ccatatcttc	cagggcttgg	tgctgagggt	180
gattetcage	cactttctga	tgaggatttt	gttcggtgcc	aaatacttgc	cccaacagtc	240
cacatgttga	tatattcgcc	gttcggatct	tgtaccacat	catgatgtgt	gatgcgagat	300
agctttcatc	ttttgattac	ttgagcttga	gacagagagg	agtctccgta	tatgcgatat	360
gtgactgcac	agcggatcca	tatccgtccg	tctgtagttg	ccaccggtct	gcttgagctt	420
catcccgaac						431

- (2) INFORMATION FOR SEQ ID NO:971
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 561 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...561
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:971

ggttaccaat ctcaccggaa ctgcttccaa tgacgaagtt tctttggacg ggacggtgtg gaagagaaag ctgaagagcc ggcaagtgat aaagcagtag ctacaacgtc tacaagaatg

gaaccttgat	cggtaataca	gctgaaatca	ttatgtggag	accggtgtag	ccaatggtac	180
stacetegae	gaagtgaagt	aaagtatoot	gacggtgtat	ctccgaaggt	ggctgtaacc	240
atatattat	gaagtgaagt	ttanacasta	tanatunaca	gactccttac	acatocoapt	300
gtgacgtgac	caacagetea	Ligagiaalg	Lagatggata	ggetetetae	acatgcgagt	360
agaaggcaag	aagattattg	cggaagccca	tggtatgatc	acgtctacga	tattaatega	420
cgtaccgtgg	ccgtagcccc	gaatcgattg	gatacatggc	gcaaaccggt	ttctatgcag	
tgcgcttcga	tgtggggaat	aacaccatgt	atcgaaaata	caagtaagat	aaagcagata	480
ctttcccctg	ctaaagacaa	agaggctgcg	tcgagattat	ttttcgatgc	agcctcttct	540
	atgcccgtat					561
ttlyclacic	acgeeegeae	_				

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1315 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1315
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:972

```
gagtetatte agacaaagea atteettgag ttttteette tteetteget eagtetatgg
                                                                        60
gcaaagctac ttgttggcga agagtgatcc gccacaaaaa ccgtatcagg gcaaaaacag
                                                                       120
aagcgcgagc tgctgattcc attcgaactt ttatcaagcc aagcccggcg ttgcccttgc
                                                                       180
                                                                       240
tattgggaaa tacgtatacg agatgaagcg gagacgatga caacggaaaa atcaatccgc
cgaaaagtgt agcaggcatc atctcacagc cgatcggttt acgtgccgga attttgtgtt
                                                                       300
tgcagtttgg aaaaacgtgg tgcgtaaact ttttcgcttt ggccgagaag taaaaaaatc
                                                                       360
                                                                       420
tcgaaccaaa acgaaaaaat tccggcacca cctcttcaga aaagacgcgc cgcaatcaga
ggattttcgg ctcgtatcgg tggatagtgg ttgatggata ttgactcgat agtagagctg
                                                                       48Ò
                                                                       540
tectecaacg cageectaag aaaaactega taaaaaaage actattetea ttgeeggaet
                                                                       600
cgaagagatc gtcaaggacg aaccgaatga aaaccaatga gatctcatgc cctcttcgac
gaaataaccg atcgttccat ccgccagcag agtcataccg agtaggcact cgatcctgaa
                                                                       66,0
ttgacaacaa cgggagcgga ccagcgccgg agacatgatc gaagagatag acagctccat
                                                                       720
                                                                       780
cgcgacgccc atccggccga gaggcaggga gtgcagcact tgatcccttc cgttcctttt
                                                                       840
cactgaagca tagctccatt acagccgggg tcatggatgc cctcgaactg cttgctctct
                                                                       900
tccaagtaag gccatcgtcg gaggagagag cgaagaaacg cttcggctct cctgccgtcc
ctgattgcgt atgctcatca gtaccctgcc acgggcatca atgaaagctt tgcctcatcg
                                                                       960
ccacggcggt atgcacagtc gaaagctgcc atgtatcagc cctcatcgtc gctatagagg
                                                                      1020
                                                                      1080
acatagttgt caggacgtac tectgeeetg attegeggat ggeageeaca aacgtgateg
accggatgge agcacaagce ettgteeega agcacaaaag gaggeeacca gegaetgegt
                                                                      1140
                                                                      1200
cccggatcgg cacaatcctt gccgaagatg aaatggttat atcccgagga ggcgaccaag
                                                                      1260
tcagtccttc gtcccgactt tccgaatata agtgcgctga ggacgatcgg gggtagactg
                                                                      1315
ccacaggeet acteacegae aaagateate aggagettte etgettgggt ttgea
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 419 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...419
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:973

aggcaataga	catagccgat	agtatgttga	ggaaagcaaa	ggaagagaag	aggaaaagga	60
ааадаадааа	gataccetae	ctatatccat	acagaaacca	gtgggcagaa	gatagagttc	120
ctactgccgt	gtaagcatag	taccgatagt	gtaaacaaga	aacaggccta	tacaaaaagg	180
caaccaact	tatacoactt	ttaaggaaga	tgacagtatg	ctcaacagtc	ttatctattg	240
caaccgaget	attangeree	ttttcaccga	cgaggtaccc	tataccaaga	gcgacaatgc	300
gatagagatt	gttgagacaa	agatoacaga	agaacgaagt	attraactrt	gaagaagtat	360
ggcttgacaa	Citicgacga	agattacagg	gcgttgaaga	casacaacta	ctacacaca	419
ccactccatg	catcactccg	aagateeeee	guguugaaga	Caaagaacta	Cigcacgca	712

- (2) INFORMATION FOR SEQ ID NO:974
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1905 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1905
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:974

aacttcaccc	gaggggcaag	ctgaaagcat	catacttaat	tcgctcacct	acttccgaaa	60
				cttgataatg		120
				tcaaggatat		180
				ggagcaaagg		240
				ctcagctccg		300
				ttattaatcg		360
				gaggcaatga		420
cttgacactg	gcaaggtgtg	ttttgtacca	caaattgcca	tttgtaccac	aaagaccctt	480
				cgatggacaa		540
				caacaagaat		600
gttggagatg	tgcataggct	ctattgccag	aatagattat	cttcatatgc	atatgaacct	660
gataagtcat	aaatctttcc	taaacctgat	gattttttgc	tetcattaat	ttttctccta	720

```
780
aagaataata gacaaaacac atctagaatg tgaaagatat tctgacaaat agtcttttcg
                                                                       840
catactaacc cctttaagct tccacccgaa tatttaccga aacgatttca ttgtggatat
atctcttact acacctcttt cggctgtgta taactttaag tctccataat gtgatggttg
                                                                       900
ggcatgcata cttcgggcaa ccattcatta gatcatcaaa accaagctat tttcctgcaa
                                                                       960
ttgagactca tatgacaact caatttaaaa cctacacctt cgtagctatg attcttttcc
                                                                      1020
cattcatctg ttgtcgaatg taggtctctg cccaagggta ttcattccac aaataatcgt
                                                                      1080
gcttccattt aggcattcag gcatccatcg cccatagaag ttctgttttt agcccatttc
                                                                      1140
                                                                      1200
ttgtaagcac tcaactcttc tttcttaatg aaagcacatt ggtatacaag aagagatctt
tgatggtacc atctgctgct tctgtttatg cccatcatag ctcgttagca gcacccagtc
                                                                      1260
                                                                      1320
tgcattatcc ttgttttcaa gagcaaccgc ggagctggta attgataccc tctatccatc
catgeteatt ateaacatta ttaactteet etaatagatt gattteaaaa gaataaaate
                                                                      1380
ttttccttgt ctacccaata gtgatggatc tattgtggaa tttcgtctgt caaccatgga
                                                                      1440
                                                                      1500
taagggttcg atgccatatc ctcttgtttg gtatagcata accataatat ctacctttca
aaatcgaaca ataatcagaa gtattgcatc tgttttatac aaggccatcc aaagatattt
                                                                      1560
tttaccaaac gctccgtttt gttatcatgt cttgatgtac tgtatacccc ttcgtccatt
                                                                      1620
ttccaagttc atcatcccag ccatattcat tcaatataat gcctgcatta cacctctaat
                                                                      1680
atgctgcaat tgaacgggtt gatattcccc tccttaatct cgaagaatac acgactcgaa
                                                                      1740
ctagaagaat tagacccgag gacaatctat taaaatcaga aaaaccgcac aatgtataat
                                                                      1800
gcaatctttt agaccatcag aagagccaaa ataggtttct ttaccctcca attgtgacgt
                                                                      1860
                                                                      1905
cataacgaat aagggctctc tgctatgaag ggaacttcta tttcc
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1448 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1448
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:975

```
ggctgttgga tatgcctaca cgcagtcgca ttatatcgaa gataacgaag ctggtttgct
                                                                        60
accgaatact atcgatccgg ggaaaagctt ttctccgaat tatgaagttg caaaccaaag
                                                                       120
                                                                       180
atgtgagtgc tttttgctgt ggcaagggaa gcgcatcaaa ttctataccc ctaaatggta
                                                                       240
gaccgagage gggaaageta tgaatgacaa aaaactgetg gttgegtaeg acatateete
                                                                       300
caacagcgaa gacgtaaggt tgcacggata ttggagcagt gtggtatacg catcataagt
                                                                       360
cggtattcat ctgcagcctg cgagagctga caatggacaa gttgtagagg ctgttacctc
                                                                       420
acagacaget aagagagaca aggtgttttt teteetetet gteageattg ttacaceget
                                                                       480
gcttggatga gcggacatcc gccctcccta agagccggag aaaaaggaaa agtattgtgg
                                                                       540
tttagttttt gaaaaaaatc gaacctcaca tcgctctttg acgtattgat tatcagtcgt
                                                                       600
tgcaagaaca actctttct cctgtttttc gaaaatagga gaaaaggaaa ttgggacttt
tattttcgaa aaatagaggc ttttcgctat ttgtaaggtt tgattatcaa acggtgtctt
                                                                       660
                                                                       720
tctctatttt tcgaaaatct aaaaaagaag gctccctctt tcttattttc gaaaacggaa
                                                                       780
aatcaagaaa totoatgtat atcaatgaga tataatcaac toaactgcaa aaatagtgtt
                                                                       840
gtagtgcatt tctcaacttg tattttcgaa aaaaatagaa tcgttctctg ccatgcgtta
                                                                       900
cgtttgggat tattcgtaac ttgcagtcgc tcaagtactc acatacatac acagtccgta
                                                                       960
aggotattaa gactoactga coatgaggta agtaccoatt ctatoggact cactatacat
                                                                      1020
acacagtccg taaggctatt agactgtttc gccatgactt aataagtttt acaatttttg
```

actcactatc	atacacagtc	cgtaaggcta	ttaagacatt	actgatagca	ctgcaataca	1080
gcgaatacca	agctcactat	acatacacag	tccgtaaggc	tattaagctg	tcgattttct	1140
		tgttggctca				1200
cagcccttct	taattcccct	ctctaaaacc	tcactataca	tacacagtcc	gtaaggctat	1260
taagacctat	catcttgcta	tcatctgata	aagccctacc	caaaaactca	ctatacatac	1320
acatccgtaa	ggctattaag	actctaagca	ttatagctat	accatcatta	atcttggctc	1380
actatacata	cacagtccgt	aaggctatta	atacttgtga	gatagggctt	ttctactcct	1440
tcttcctc						1448

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 398 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...398
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:976

gctcctgccg	taatgagctt	tctggagcag	cacaacctca	aaggcaagac	atcatcccct	60
ttgtcacaca	cggcggtggt	ggcatgggca	agtgtttgac	gaaatgaagc	gactggcacc	120
tcaagcgaca	atcctcgacg	gcatcgtatc	gacggcaaga	aagccaaaga	atcggccgaa	180
gaagtccaca	acagccgaaa	gcgatgggac	aaatcaaata	acgacaacca	tccctactcc	240
agaccctgag	gaatgataga	ggcaagcttt	ccccacaaa	tcaaacacaa	gctcctaccc	300
tccccggttc	ttttccccca	caaaaagagg	cgccatccga	cgctctttt	tatacccaat	360
aaccaccaaa	tacgcaccaa	aaaacttttc	aaaacgaa			398

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 611 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...611

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:977

aggaaatccc ggccacctat ttcaacgagt	tcctgccggt ccctgacagc tccgccaagg cttctgctcc tgatctgatc	tcgttatcag atcgcttttc gtcaggatcg ggagatcctc attgtctcta aaaacgggct actcccgatg atgcacctgt	tgaggtgcgg ccgttaagac taggactatc ggagcggtac ctcaggcgct gaggttttgg ctacagcata gggagagacc	tgtcggggat aatacgtttt ccaatcaaaa cctcttgagg tcgtgttgca ccgcctcttt	aagaccattg atgccgtgga cctgatggag ctgatcgact ggaacaggtg gccaaaatgt aaatgcttcc	60 120 180 240 300 360 420 480 540
ttcaacgagt	tttcgggtgg tggaaggcaa ggctcatgac	actcccgatg	gggagagacc	ttcccgatgc	gccaaaatgt aaatgcttcc cgtatctcca	,

## (2) INFORMATION FOR SEQ ID NO:978

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 575 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...575
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:978

gtcagtgctc	tecceagtgt	attccttttg	gtcaggattt	gatcggttac	tcgattggat	60
tttagegett	ttcctcatat	ctaagatcaa	aattaaactg	atggggtgct	tcataagttc	120
titgactget	catcasactc	otctocoaaa	tccttagctt	cgggggtcaa	ctgtgtccat	180
attituateg	gatgaaatte	aaaccacaaa	agaatgtgcc	taggacatac	tgacaagcct	240
gtaggtgtgt	gatttaccac	taccattatc	gcctattaaa	aggttgactc	ctggagaaaa	300
taagacagac	getereceat	atctctaaac	tettegatgt	gaatctacta	atcataacct	360
aatagctcca	agicaccaac	acticance	taactcgaga	cctttgaaaa	ataaggaggt	420
acatatatta	caactagaca	aatatatata	nectastast	caatcatagt	tttgagtata	480
ggaggcaggg	caaccgcatc	aaatgtaagt	accigactat	aaattagcac	tttgagtata	540
tncttatctt	gagtataatc	tccgaaatgc	aattattiga	aaaccagcac	ctggattttt	575
cgaatttttg	atgcgttgcc	ctgtgcaagg	tctta			

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1223 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1223
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:979

```
60
gacttccgag tacagattca ggcactgtat tagcaggttg cccggtgtcc aggtattggt
tgtcttaggg cgaaaacgcc gattgcgtgg cattaagtac cgggctctta gcagtcggca
                                                                       120
                                                                       180
taacctatac cgaccgatcg aaacctcctc cgaagcactg cttactgtat taatgaataa
                                                                       240
ctctctanag ccggcttcgg taggctttct ttgcacctga ggtactgata ataatggact
                                                                       300
atactgtatt taatgtcagt tcgatctaag cgcaaatagg ggagttgggt ctggtcgaac
tgacgttata gttaaggcaa taaggtttgc gacatcctcg tttgtttagg aacagcaata
                                                                       360
tgtgcattat gcttaccttt gctcatcaag gaccgcaacc gcatggctgt aggcttcgga
                                                                       420
                                                                       480
tgcatttcca ataatacaca tcgacaaaca aatgaacttt gtagaagaac tgcgttggcg
gggtatgatc acgatattat gcccggtaca gaggaacact tgaacaaggg tatgacctcg
                                                                       540
                                                                       600
catacgtagg cattgacccc acggctgatt cgttgcacat cggccacccg tgggtgtgat
                                                                       660
gatgctgcgc catttccagc gtgccggcca tcggccctcg ctcttatagg tggtgctacg
                                                                       720
ggaatgatag gggatccttc gatgaatcgg ccgaacgagt tctcttggac gaagccactc
ttcggcataa tcaggctgca tcaagcagca actggccaag ttcctcgatt tcgatagcga
                                                                       780
tgcaccaatg ccgcaaagct cgtgaacaat tacgattgga tgaaggacta ttcttcctcg
                                                                       840
                                                                       900
gtttcattcg ggacatcggc aagcatatta ccgtcaatta tagatggcaa aggattctgt
                                                                       960
gaagaaacgc cttagtgccg agagcagcac cgtctgtcct ttacggaatt ttcctaccag
                                                                      1020
cttctgcaag gctacgacta ctctatctat atcggaatga gggctgccgc ttgcagatgg
                                                                      1080
gcggttcggt cagtggggca acattaccac cggaacggag cttatcagac gcaaggacga
ggagaggcct ttgcccttac ttgtccgctt attaccaaag ccgacggggc aagtttggaa
                                                                      1140
aaacggagag cggcaacatc tggctcgatc ctgccaaact tctccttatg ccttctacca
                                                                      1200
gttctggctc aatgtgagcg atg
                                                                      1223
```

- (2) INFORMATION FOR SEQ ID NO:980
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 550 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
    - (ix) FEATURE:
      - (A) NAME/KEY: misc_feature
      - (B) LOCATION 1...550
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:980

ggctaagaag	gaagaggata	caaagggaga	gaagggtgac	atgtttacgc	ggctgctgta	60
tattcggata	tggcgatagc	cttttcgttc	tcattcgcac	aatggtgtag	acggtgtcgt	120
ccttggacag	ctctatgagc	aactccacgg	gatgcaccga	agataagaga	taagaactcc	180
ggcagaacgt	tcgaacctgc	tatactgcga	acggggcctg	ccggaggagg	tgtctcgacg	240

aagctttgtc	cgtaccgttc	catttcgaac	ctgtcgcgat	gtttttgccg	gtgagagtgt	300
ttgcgactgt	gctgtcatca	tgaggccggt	gagcccccat	acacgatcat	cagactcttt	360
		actttttat				420
gtcgggaggt	cattcgccaa	agtccttggt	gccgtagagg	gtattgatcc	acatggcaaa	480
		gaccttgttg				540
tgtttgcagc						550

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1017 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1017
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:981

```
cattettetg titacttgca gagecataca etgeteatga tetteeetgg atgagaetgt
                                                                        60
tgcatggagt ttcattgact ctttgctgca gagctgatct tagtgccttt gggaaagatc
                                                                       120
                                                                       180
aaacctccgg tatatggaca tcgagcaaca gaaatttccc caagtttcca ttagagaagt
                                                                       240
actcctttcc tcgtcaatag gcgagaaata agaaacgatt gtcggctgtt tcttgcttcc
tgcacatgca ggacgcgatt gtcggctgat tcttgcttcc tgcacgatgc aggagcgatt
                                                                       300
gtcggctgat tcttgcttcc tgcacgatgc aggacgcgat tgtagctgat tcttgcttcc
                                                                       360
tgcacgatgc aggacgcgat tgtcaactga ttttgcttcc tgcacgatgc aggacgcgat
                                                                       420
tgtcggctga ttcttgcttc cgcacgatgc aggacgcgat tgtcagctga ttcttgcttc
                                                                       480
                                                                       540
ctgcacgatg aggacgcgat tgtcagctga ttcttgcttc ctgcacgatg caggacgcgt
                                                                       600
tgtcaattga ttcttgcttc ctgcacgatg cagggcgcaa ttgtcagtga ttcttgcttc
                                                                       660
ctgcacgatg caggacgcga ttgtcggctg attcttgttc ctgcaccgat gcaggacgcg
                                                                       720
attgtcagct gattctgctc ccatcatgcg ctaactatca gctatttgca actatttat
                                                                       780
aggactttca ttaaatcttt tgccgcagag ctgattctta agtgtttttc aggaaagatc
aaactcatgc ataagggcac caaacaaata gaaattactt gaggtttgca gaggatcgca
                                                                       840
tgaagctctc ctttcttcgt caaatcaatg cttgtgtctg tctgatcgat atgaggaggt
                                                                       900
gggaggttat tgtgcaacag tctctgagat aaaagaatga acccatacga gaggatacta
                                                                       960
                                                                      1017
tggtcttcgg agtcgtacag tctataacca aatccactcc ataaagcaaa gaangag
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 901 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...901
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:982

```
ccccggagcc atgattgccg atgcggtaca ctcgttgtct gatctgctgc cgatttcgtg
                                                                        60
gttttcattt ttatctccat ttcgggaaaa ccatccgaaa gaaccacgat tacggacatg
                                                                       120
gtaagttcga gaccctcgcc actgcgacat tgctgttacg ctgatcatca tcggagctat
                                                                       180
gctctgctcc gatggttgac caaggtatat cgctatctcc gctttgggga cgaattggct
                                                                       240
cgtccggatt gatagccttg cttatggcct ttgtctccat tgtggccaaa gagtgctgtt
                                                                       300
ccgcataacg cgatgtgtcg gaaaagagga aaatagtcgt tcatcatagc caatgcctgg
                                                                       360
caccaccgta gtgacgctta tacctctgtg gcactttcat cgggattggc tgtgcttttc
                                                                       420
ttttggggcg cggttggatg acctcgaacc gctatcggct gctgtagtaa gtgtctttat
                                                                       480
catcaaggta gttttcaaat ggccgttccg gctttccgcg atctgctcga acagagcttc
                                                                       540
cggatgatat tgaagaagag atagaaaaaa tcatttgttc ggaatcgagg taaaaggtgt
                                                                       600
tcgtcggatc cgcactcgca atatcggtaa ttactatctg tcgaagccga tattttgatg
                                                                       660
gatggaggcc tctctgtggc actatccatg ctgctacgca gagggttgag aagctgctgc
                                                                       720
                                                                       780
gtggacgata cggccaccca cacatatagt catccacgtc gagccgtttticatgatatat
gttgccataa ccttttcaaa ttctgtaaag ctttatgacg actgaaatca aatggaagaa
                                                                       840
atgcgttttt atgcccgaca cggtgtgctt gagcaagagc cgcaagtggg ggaaccggtt
                                                                       900
                                                                       901
```

- (2) INFORMATION FOR SEQ ID NO:983
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1437 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1437
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:983

agtatttgtg	ttctgcatac	gcacaagata	gtttccgcac	cgtttcggta	gaataacagt	60
				aagcggaagg		120
				aagcgaaagc		180
				atggggtgga		240
				tcgaaccaac		300
				caacaaacga		360
				ttatctatgg		420
aaaatcatac	agattcgtat	cgcttccggc	agtcgtaaga	tcagataaag	aaattctgcc	480
				acggccatgc		540
				tgttcggcgt		600

trottragag	gagaaataag	caaacgcaag	ctaccgcact	tttccctcgc	ttggatgaac	660
ntagtateag	ataggacact	ctgccatctc	tctactgaaa	agatgggcta	tactataact	720
stoottataa	acceptitate	gagaactatt	gctctgctga	ctataatcat	gactaaccga	780
accectacaa	aatatcotct	attcaptcpt	ctgaaacaat	cgttttccac	ataactgtcg	840
agacgacaca	trasasttro	ctoataaaaa	cttgtttatt	ctttgtccga	tccgaaagaa	900
tettentata	agattattet	tctocaaaga	caaaaagtta	gcagcaaatt	ctcatcaact	960
tetteatata	attactcacc	ctcgcaaaga	aaacaaacag	accoaattoa	ccetagaaac	1020
tttgccaagg	actacccaca	cccggcacaa	taactatcaa	cattcaacga	agtotatacc	1080
aaaagttttc	acattecgat	ggaaactcat	tggctatcag	coctacctat	tcaccaaata	1140
tgttagtaag	ctatcagtat	Ctattccaaa	tctgttaatc	ctetacctat	tttcttttca	1200
gttacaagcc	ttatcaacag	tttcaaccga	cctcctctc	ttacacactc		1260
aaaaggaata	tataataaaa	agaaatcggt	tgcccacctg	ttgaaaggtg	aagcaaccga	
tcgtgtcaca	gataagaaaa	gtagctatga	attttatttg	atcagtagcc	ggattatcgg	1320
ttggggatca	gaaattgatc	ttttgtaccg	acgaaaatcc	ttctgggctg	caaggaccgt	1380
atacgtaagt	agaagcttta	cccggtccct	tgtccgtgtc	ttctgaatag	ctgttga	1437

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 447 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...447
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:984

gcaattatgc ctaatctgct	tggctttcat	ctgccttttt	tttctcgatg	ctgtggtaac	60
aaaaatacat ttcgtgtcga	agggtcgatt	gccggttaga	agacaccgca	caagtgtatc	120
tgaccaagat cattgggagc	gatcttttgt	actcgattct	gtaaatcctg	accgaaaagg	180
tcgtttcagt tttgtacaca	agcggactcc	acaccgtctt	tctaccagat	taaactcagg	240
aagcacatat taattttgcc	gcaaggatcg	gatcggaaat	caacatacag	gtggtccgta	300
acagetttte egattaegtt	attgaagaca	accaagggcc	tgaaattaac	aatattcgca	360
aggattggcg ctattgaaag	agcaagcgga	tatcgtttgg	atcattttgt	accgttcata	420
ccaagagaac aaactggatg		2 00			447

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 870 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...870
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:985

tggatgatat	tgcagccggt	cgcaagtaca	tgaaagtgta	caagcagata	aaatgtacaa	60
			caagaagtga			120
			tccccgtttt			180
catggctcga	tatctgtagt	ccgcttgtcg	gcaataggcg	atgtggcaat	gacaataccg	240
gtttttatgc	ggtagccaag	gcatacccac	agcatagttt	cacactgctg	actcgccttt	300
			caatttggaa			360
cacgaagagt	cttccttggt	cggtcttctt	actatatcgg	acgactcaag	gatgaagcag	420
			tacgttccaa			480
gctttttcgg	gtcaaaggtt	tcagtctgaa	gaaaccgcga	ctacagcttc	ggcagcttag	540
gccaagccac	ccaaaaagcc	aacccgattg	ccttccgtaa	tagaacgaac	gctcaggttt	600
ttcacaaagc	cgggcttgaa	atacatcctc	cctacccatc	cttctgaacg	actccggaca	660
tatctctacc	gaactgccga	tagtgggata	ggctccggac	accacctcat	cgggatagca	720
ccgtttgccg	gtcataagcc	aagacatatc	cgccggaaaa	aatgcacgag	gtagtgcgta	780
ccctgccgag	agagacgatg	tgcagatttt	tcttttcggg	ggtaagggga	aagaaaaaac	840
atactggagc	agtgggcaga	cgaatcgcca				870

- (2) INFORMATION FOR SEQ ID NO:986
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 459 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...459
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:986

cgttcaggcg	aaacgaaccg	acaagaaagg	acttgtgcct	gtcatcgggg	catctcagtg	60
ggcagaaccc	attcaggctt	ctccaccaag	tgcaagaccc	gctcgctctt	tgggacagcc	120
gaaaacaacg	gctcatcggc	aagagtgaat	ggcggtgtcc	gtcaatcaga	aactcggtga	180
atgcaccgca	ctcatcacgc	acgctttcac	gaactctgtg	aaaggaaaga	aatttttacc	240
gccacgacgt	gagggatgcc	tatcaggggc	aaatccacca	ccaagccctg	ctctggagag	300
			gcgcataggt			360
			ctcgtgagta			420
taagagacat	tcccctttca	cgttggataa	agcctttat			459

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 888 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...888
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:987

```
cttttggtcc atacttatag atactcctta ggttgcatta ttttttaccg tacaagcctt
                                                                        60
cgaaagtatt catggtcaga gcggcatata atgattaaac atataaaaat aaatccatca
                                                                       120
                                                                       180
gcaagattgg ccttgctgat ggataatgta ggaagagaca taccaagccg acgaaatcgg
                                                                       240
ctgcttgtct cacttgccga ttttagccac gaggctcgcg gtggtcacga tcaccaccac
gacgtcgaag ttacgacctc cttcgcgtcc tccttcacgc cgctcacgcc gctcctcggc
                                                                       300
                                                                       360
tgaggctcca cgtagccttc cggtttttcc agtagcacct tgcgctgagt ttgaacttgc
                                                                       420
cggtcttcgg atctatatcg agcagcttaa cgtgatggat tcgccttctt tcaggttggt
gtcctcgatg gtctcgaatc gttccaatcc acttccgaga tatgcagaag tccttccttg
                                                                       480
                                                                       540
ccggggagga ttcgacgaag cagccgtatg gcatcacact tgtgatcttg cccggatagt
                                                                       600
ttctccgact tccggcatag ccacgatgcc cttgatcatg ccgattgcgc atcgatgcag
ggtttgttcg taccactgat ctcgatgaca cccatgcatc tacctcttcg atgttcactg
                                                                       660
                                                                       720
tggcaccact cttctcctgt atgcctggat gatctttccg cccgggccta tgactgctcc
gataaactcc ttgccatatg catcttctcg atacgcggng catgaggcta tgaggtcatc
                                                                       780
                                                                       840
tettetegg getgagette catgatettg eegaggatgt gtaggegtne tigttggett
                                                                       888
gctccagagc attctccaaa atctcataag ctgagaccat ccccttga
```

- (2) INFORMATION FOR SEQ ID NO:988
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 465 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...465
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:988

cacaaatagc	agaccataga	acaggagcaa	ccaatatgcc	atcctttgcg	ccctcctatg	120
ccatagagtg	gaaattttt	catattctca	ggggagaata	tcaatcagtt	tatgaatgct	180
			cgcaggcgag			240
ggatgcgtat	cgggagtacg	aagaagccat	tgtcctgaag	atgttcggcc	aacgaatgca	300
					ttctatgcct	360
			gcgaatcctc		ctctccatca	420
caaactcagg	tagccgacgg	atatcagatc	agtccatcct	atcgt		465

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 510 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...510
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:989

gattgttttt	gatttatata	tagatcgttt	tccatttata	tatagatcga	agtcatttgt	60
			cggaagctaa			120
attcgtggcc	gaaccgtgcg	ggtgccttgc	ctttaggaga	agtattaaga	gggtttattc	180
ctacttattc	gtcatagggt	ttatactgtt	tgtccgaata	tcgaaatgac	atggtaggtt	- 240
atggggcgaa	aggatcggcc	ggaaagatcg	ggggtataaa	ggtgttcggt	gcactgttct	300
gttatagtct	attatccatg	tagttctatt	caagcaatcg	gcttctcggc	agcgacatcc	360
aacttccgac	agagagcttc	atcgggcgac	aatgtaagaa	aatatggttc	atccgacatt	420
cagcgtgacg	gaggcgtggt	gaaggcatag	agtcttaggt	tgaagtattg	ntgatctcta	480
aatccatatg	cactcttttg	agtacctttt				510

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 128 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature

#### (B) LOCATION 1...128

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:990

gccttaaaaa gccaaattc ccaaggtcca atagagcct cgtttta	gcagagagtt t atagtttcgg	agttttcgtt atagaaatgg	agttcgaatt acataatcct	gattcttcga aatttgatag	60 120 128
---------------------------------------------------------	----------------------------	--------------------------	--------------------------	--------------------------	------------------

# (2) INFORMATION FOR SEQ ID NO:991

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 268 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...268
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:991

aaataaaaca cactaataac caatgtgttg tgccattcct ttatatcgac tcacgttaag 60 aaaagaccaa tggtcatatc gcaaaaatgc cgtacaatgt ctctaataag ccccctgggc 120 gatgttgtac ttcttctcga tggcatattg ctccggggct gccgaggtat tcttccacaa tgtgaagacg ctcggatcgg tcaaatgtt cgacatgatt actgcttttt ttgacctctc 240 cgattcgtac acgtcagttc gtaaaaat 268

- (2) INFORMATION FOR SEQ ID NO:992
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 498 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...498
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:992

actaccggtg	gattccgttg	aaactactag	tagattcttc	caaaaccaca	gtagttttgc	60
		ctctgaaacc				120
		gatggtatca				180
		aggatttaca				240
		atacaaaaag				300
		acctgaaatt				360
tgctgcagca	caagtgccac	aatcaataca	tgatcagcat	cgattttata	gatgctacct	420
		cttcatcgat				480
attaacgtaa						498

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 388 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...388
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:993

cagactttgg gcgttgag	ct gtatttggaa	gccggcatcc	gtggtgttgg	atcggttcta	60
tccttgcaga ccgtgacc	cc gtgacgaagg	agaaccgcat	ccgcgtctcg	agctcctgcg	120
tctggctatt ccgcgtcg	ta catatacaac	aaccacatgg	atgttatcgc	tgctgcggta	180
aagaatgtat acgaccto	gc gaaagcatta	cacgtggcta	tgtgattaca	tatgagaatc	240
caatctgcgt cacttcac	tg ttgagctgga	aaaagccaag	taagcggtaa	gaaactgtat	300
aaagaaaacg gtaaagga	gg ttgcttccat	gtcgagagac	cagggaagca	actttcttt	360
ttttgtggat aaaaaggt	tt tttgtttc				388

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature

#### (B) LOCATION 1...620

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:994

gacccacagc	atttgcgtca	cggtaagggg	cgactccgta	cccacaaatc	gccgatcaga	60
				gataaaacgg		120
				ctgaaagaat		180
				ccatcgagag		240
				cacgggcacc		300
cttcctgcag	caggcgtaca	agcctttcct	tgtccatcgg	acggcgcggg	acatgatacg	360
cagttcgcct	atccgagggc	gcagttcctc	gtggttaggg	ctgcgaaatc	cgacccggtg	420
atcatattcc	gctccgtaca	gtttcgtccc	acagccctat	ttggcgaccg	atctcccggg	480
cggtacccgg	gtatcgcccg	ttacgatttt	cacctgaatg	ccggccttca	tacagtcgcg	540
atcgcttcgg	gaacgtcgga	gcgaatggat	cggctatgcc	gactatccat	gaagcggagg	600
tcatgcacgt	ggagacgcca					620

# (2) INFORMATION FOR SEQ ID NO:995

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1151 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1151
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:995

tctcaatttg	aatcttgaat	ctctgacaat	atgaattcgt	acttgtttta	taattgaatg	60
tagcaatcat	gagctttaga	tgtacgttag	tggctgaatg	cgattgccct	gttacaaacg	120
				atagtaataa		180
				aggctttgtg		240
				gtagcatgca		300
				gtgtcgagtg		360
				tcaggggaag		420
				ttgtatggct		480
				gtgtcgggcc		540
				actcattaca		600
				ctcagcgtat		660
				cttgtctgca		720
				gccatcagtg		780
				ccattctctc		840
				gtataacctt		900
				aacccattcg		960
				gcgtccggcg		1020
				actccggccg		1080
				tgggtggaac		1140
atctgaagac			-			1151

.

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 624 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...6\overline{24}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996

tctctttgac agagtata	atg tcctcgtcga	gagacggttt	cgtcaataaa	gccggtaaat	60
cggccctcct ctctgcga	aga gggcagaaat	cctgcaagaa	tggcgaagcc	cttctctctc	120
cttcttgtac tacactti	ttg ttcttcgatg	aacaatgtca	atgatcgcgc	tccgactgcc	180
ccctcccaa tctccgat	tcg aagcccttca	tgtggcggac	agtgggtgca	aaagtaaaac	240
cttttccgaa tcggcaaa	aat caatcgaatc	ttttttcagg	gctgacgctc	aagaaaagct	300
cgtcgcctga tcctccc					360
tcaatcgggc agcaatcg					420
tctttcaaaa tcttttc	tca acopttopac	ааааааааас	agcccccgaa	gaaaaggact	480
ccctcccaag aagacaa	aaa aagaagcata	tatataatat	agttcgcgcg	cetaagagaa	540
cccaaaagga gcgcaaaa	ana aagaageataa	0220202222	aaaattotog	caaaagactt	600
		gaagagaaaa	uuuuccccog		624
ttcagtccca aaaggcgg	guu gguu				02.

- (2) INFORMATION FOR SEQ ID NO:997
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 665 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...665
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:997

tagi	ccgctt	ctttgcgatt	agctgtttca	atcttgttat	ctccgcacac	tccagaaagt	60
aats	tgtact	ttagcatcct	cttcataaaa	gcaatgacca	acggaagaac	gcttcggata	120
atti	ttaatg	ccggtgttaa	gaaacaaaca	gatctcaata	atcactgact	gtactgtacg	180

atgacaaagg	tgcgattatt	cttacaaccc	ttttcctatg	cctcgcttgg	tgtacccatg	240
		aagctcctgc				300
		taatggaacg				360
		actgctacaa				420
		ctatacatat				480
		cgtgccaacg				540
		aaaaatcatc				600
		ttgtccgaac				660
agcga	0 0 0	• •				665

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1230 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1230
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:998

```
ttcggcgact cctttctcag tatatcccat taggtcaggg caaaagccga tacagctccg
                                                                        60
                                                                       120
gtgtcacgac cggtagagtc gatccgcgga ctacggataa agcataatag gcacgaaaga
                                                                       180
tgagagcata agcatcaaga aggaaaatcg ctcggtcata tcgaatctta gttagagggg
                                                                       240
ggatttgaaa aaaaggaggg gaagctgtca ttcggcaagc ttcaggacga gagcagagcg
                                                                       300
agccgcagat agaggttcaa atactgttca tgggtaaacc gatctttact cccaccggaa
                                                                       360
gagtaaagtg ctccacccat tcgtccacac gaccgaaacc ttctacttcc gtgcatcggt
                                                                       420
actcatcgct accgaatact taccggccgg aaagggatgg gataatccga ataagaacgt
                                                                       480
tcggggtgaa aattgaaaac gagaagaaat cgcctcgacc gtaacagatc acctgctctt
                                                                       540
ctctcttgag cagtattcgc gcaaagggag tttgtgaaag ctctccaccg atcgtatcag
                                                                       600
gctatcatat cctgatcaaa caagtgcaga cctgcatagc gcaagaaaga ctatcggcca
                                                                       660
gactccactg cctgcgggca tacttgtacg accagccttc ccttcgcgag ggaagtctat
ccactcggga tgtccgaatt cattgccatg aaattgagat aaccaccatt catcgtcgtg
                                                                       720
                                                                       780
gcagtgaaga gacggtcatc ttcagcagtg caatgcctct gtccacgcta tgtacacaac
                                                                       840
tctgttgttc atataccaat acatatcggc atcgatcagg cgaaatatga ttgcttgtcc
                                                                       900
ccgaccaaag cctgatcgtg actctcggca tagctgatcg tctttcctcc tgacggcgat
                                                                       960
tggtcagttg ataccagatg tcgccgggat tcagtcttcg tcacgatgct ctttgatgag
                                                                      1020
cttgatccag aaatcgggga attcatggct aaacggtagt caaagccata tcccccatct
                                                                      1080
gccaagggag agctaatccg ggcatgccgc ttacctcttc ggctatcgtg attgcatcgg
                                                                      1140
gcaaagttcg tgaatgagtt tgttggccaa gatcagatag gcaatagatc gccgtcctga
                                                                      1200
tggccgttgt aatagctgtc gtaattgtcg aacctacgcc gagtccatga ctatagtata
                                                                      1230
gcatggacgt cacaccatcg aaacgaagcc
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1784 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1784
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:999

```
ggactgtcgg tttgcatctg cccgaacggt ctggaaaggc atgaccgatg gccacaagct
                                                                    60
ccctgatggt tgtacggtgt caagettegt gccacgegta gaggatatag agteetteec
                                                                   120
ctttcgactc gactacctgt ttcttaaccc cgtgttcgac agtctgtgca aggtgggcta
                                                                   180
                                                                   240
tgcaggacga ttttccccga ttctttgggc gatcgtctgc agcgactcca tctgcccgtg
                                                                   300
gtggcctggg cggcattacg cccgatcgtc tgccacagct tcgtagagca ggcttgcctc
ggcagctgca ctcggctatg tgtggttggt cgaaggccgg gaatgatgcg ttggcaggaa
                                                                   360
                                                                   420
ttgtgtacgc cggctgttat ctgtgtcgga gggtggatcc gtcggccgga gccggcatta
cggcagatgt gcggacggcc gaaacatggg cgtgcgggct tataccgtgg ctacggctat
                                                                   480
                                                                   540
tacctttcag ggagtggcag ctatcggggg gagcgatggg tggattcggc ggacatcatc
                                                                   600
ggcagatcga atctttgtcg gccgagatgg agcctgccgt cgccaagacg gcctgatccg
                                                                   660
cgactcggac accetetete tegtagtgga ttgtttgaaa aggtttteee etegattegg
                                                                   720
atogtatggg atocogtact cagagotogg cogacagoto ogogggacaa goggatogtt
tcaatcttga agataaacgg ctttgtcccg gatagacttc atcacgccga atcttcccga
                                                                   780
agctgccacc ttttgggctg cgaaccggac gatgagaccc tgttagactt ctacgaagga
                                                                   840
                                                                   900
960
cgtttacgac ggtcgatgcg aagctctccg atcttacgcg gcggtacggg gaagcatggc
acgggttgtg cccacagcac gcttttgcag ctgctttggc cttggagcaa gaacctttta
                                                                  1020
cggctgccgg atggcacagt tatatgtcag tcgactacgt gagcgtgctt cggggttgtc
                                                                  1080
gctatgcaca aagacctgcc ggtcgatccg gtcgtcaggc tgatgaggaa atagatttgc
                                                                  1140
1200
tataggtgtg cgctgggtac agcttggatg aaggaggctt cggacgaaga gatgcttcac
                                                                  1260
                                                                  1320
acggcttgtg ccgtaaggct gtctgccgtc accacggagc actttttgtc gtcaatgacc
                                                                  1380
gtgcgaaata gcccgtcagg tggatgctga cggcgtacac ttgggcaaag agatatggcg
                                                                  1440
atagtogaag ogogtogoat cotoggttog aataagatoa tggaogoaca tgcaatacga
                                                                  1500
tggaggatgt gcgccgagca tatgccgaag agccgactac gtgggtatag gcccgtatcg
ctatacggag acgaagcagg tttagctccc gtcctcggac tcgaaggcta caaagccatc
                                                                  1560
gccgcctgat gcaagccgaa ggcatccgac tgccggcctt tgccatcggt gggataggga
                                                                  1620
tgcagacatt cccctcattc gcgactgtgg cataggaggt attgcctgag cggcagcctt
                                                                  1680
                                                                  1740
atcaggaaaa taaaaaagaa ctaatcggat gatctccttc cgtatcgaac gatcatcttt
                                                                  1784
tgataaacag gaaaaaatct aatgaaacgt tacaaattgc cggc
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1239 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1239
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000

```
naggatecce gaaattttet egtttteeeg geteeaaaat ttggageaea eegttttgee
                                                                        60
aagaatgtgc tgacgctctg tcgcacggca aatatcgcaa actgaatccc aaactgcccg
                                                                       120
agctggaaaa ggctatcgaa atggaggttt ggctctgaat ccgcccgtcg cgaacgagct
                                                                       180
gacgcctcag gtcataccct cgacgaggaa cgcgacagag cctatcaggc gctgatgtcg
                                                                       240
cgcgtcgttc gtatgctttc gacgaggaca gccagctgcg caacgcggca gccaaatcga
                                                                       300
agacgtggcc gctcgctacg gcaacgtgat ccgaatgaac tatacaagga gacggccgcg
                                                                       360
atagagaatt teeteacega teteaaggge gaaacatteg eeceetegta aegaaacteg
                                                                       420
gcgtgacggc actcgttgac aactggaaaa gaacaataag gccttcgccg acttcttcct
                                                                       480
ccgccgtctg gcaccgacca acgaggcaaa tatgacgtga aggcactccg tgccgagacg
                                                                       540
                                                                       600
accgcacatt ggtagccgtg gtgcgccgca tggactccat cgacgacagg agccgagccc
ggagatccgt gcgctcatcg agctctacaa ccgactctgg ccaatcgccg cgccctcttg
                                                                       660
                                                                       720
gctcgtcgcg ccagctacgg agaagcgccg tggagaagcg tcgtgccgag atcgccgaga
                                                                       780
tgctccgccc cctgccgccc ggatcgtgga ggagaagaag acggccgtct ttgccggtcg
caccteggea egggeaagaa eegecactat eteateacat tegtageega gaaggegaeg
                                                                       840
                                                                       900
aggaggatcg ctggtaccgc atcaacgggg agcaactcgt cttgtgcccg aagacgaact
ccccaagccg aagaaaaaga agaaacccgc agcagcacgg acactccatc cgagccgccc
                                                                       960
                                                                      1020
gtcctgccgg atccatcgca ggaggcagca gtagcggcgg tggcgagcaa ggctctaccg
                                                                      1080
geggeggace tgatecece gtgeegteet geeggeegea geageacagg caacegagat
aaaagacaaa ggggctgtga ccaaattcat ttttggcaca gcccctttat attcgaaaaa
                                                                      1140
ttaggtgtta gccctgatta gcctttttct ctgnttcaaa ctatgtctaa agaaaagtct
                                                                      1200
                                                                      1239
atgctaggac ttanccaaca accgcttttc ttacttgcg
```

- (2) INFORMATION FOR SEQ ID NO:1001
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 504 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...504
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001

totaataacg totgtgtcgc attgataagt totttaatot catcacaacc cgttotttga	60
agtcgctttc attaaatagt ttagattttg aaaatacaca tttacattgc tttgctgtgc	120
tgaggattta acagcgtcaa gatactttgc aattttatat catcttcatc ggatgagcaa	180
gtttttagca tatctgtact acatcgctaa attcacgcaa gtaattctct gcagattctt	240
cttgcttacc ttcatatcac tctcaaactg ttcggagtcg tttctattgg tattagtagc	300

tcaaattgtt tgatgtattt agcctttcca ttaaaacgac tagaatagca tctagggtga aggttttcc tgtagaacgt tttccataca tatattgaga cccgttgata acttttgtcc attcggaaat attggaaaaa gtttattcct tcttccgaag tcagtgatac tttagtctta tccattagac gagtttcagt gtt	360 420 480 504
(2) INFORMATION FOR SEQ ID NO:1002	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 525 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: circular</li> </ul>	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS	
(ix) FEATURE:  (A) NAME/KEY: misc_feature  (B) LOCATION 1525	,
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002	•
ggcgaatgtc tctttggttg gacgacaagc agatagggat agccgatagc cgaattccaa gggcgacaca acgctgcgtt tctctgcatc gctctcgcgg ttccaggac acatcatttg ctgctcaaga gcttgcttct cgaaggcata ccactgctac ggatgtgcgc gtagtcctca agccgaagac cgctcggatt cgtcggctct ctatcccaac tatacgggca aggagcggct gagcccaagc acatgatgag cggcacattt ctatcgggag ggagtctctc tccacgggca agtatgtact tacttcttat cgggtaagca gggataataa gccgctgtga cctataacca gctgcgcgat gccaaaggaa atatcctgct catctgaacg aaaaagaggc ccttggttgg atgccgcatg aagatatgct gtggtgattc gcaaggaagg aaaatgcgaag cgtttggtgg ctttcgatcc atggggaaag gtgaaaaaac cttggtgcc caatt	60 120, 180 240 300 360 420 480 525
(2) INFORMATION FOR SEQ ID NO:1003	1
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 1390 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: circular	
(ii) MOLECULE TYPE: DNA (genomic)	ì
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	;
(vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS	
<pre>(ix) FEATURE:    (A) NAME/KEY: misc_feature    (B) LOCATION 11390</pre>	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003*

```
60
ggccgagtgt tcgaacagat ttcggactat gatttgcaat atctcgcgca agggagttct
atttcacgac tttggtataa atcttcgatg gcctgttcgc ttttgcttga ccttctttga
                                                                       120
ttggcagttg tttcaagtat cgttcaaatc ccgtggatca aggccttttt ctttgatggt
                                                                       180
tgccatgatt tgggtagttc ctctctattc tccaattggg tcaagtagtt gtaggctgct
                                                                       240
tggtgttgga ttcagcaagt cgtttctcaa aacaggcaat aaaatctcgt atttttgatc
                                                                       300
ctccggcttg aatgaagtcg gattttgggc ataggcctct aatcttgttt taggttgatt
                                                                       360
cgtgtggtta ttcccacatc gtgtttcgac catcatttac ggcatattcg aaagcggatc
                                                                       420
ggatctgctc atcgacttca gacgatgaaa actgtggata ttcaagccga ttttaatagc
                                                                       480
tgcttttaat catactcgcc taatgttgta atcatacttg taatgtttgt ggattagttc
                                                                       540
aaatctatag aaaattaagt gtgtggcatg caaaataata tggaaaaagg gtacaaagaa
                                                                       600
gagggcatgc cgaatcatag cccggacatg ccctcttaac agtaaaggaa atgtagagtg
                                                                       660
gcagcagagg tattatgtta tagaacgata ccctgccggt tttgtgcttt atccgcattt
                                                                       720
ggaageteeg caactgtgea tageaggeag cetteettga taaaccaatg teteetgace
                                                                       780
                                                                       840
gcaatcggac atacctgtcc cgacagggtg gtgccattgg ggaggtaacg tttagggcgc
                                                                       900
gctccacgcc gttcttccat gtattgatgg attcatcgtt cacgacatgc cctgtacgag
atgtaccacc tgctcgatag gcataccgta ggcaagacgc ccgagatgag cttggcatag
                                                                       960
ttccagtatt cgggattgaa ttgctatcca agccttcgat ggttaccttg aaacctttct
                                                                      1020
tgttgcagac tggaagtcgt agtgtcgttc gccgttttcg tccctgttct tgattatctg
                                                                      1080
ccgtgggtaa cgctcttcgg taccatgata ccttcgtcgt catcggcata ccggtgaaga
                                                                      1140
tttcgtaagg acgtccatcc ttgaggccta cgaaaggatc cacttttcac gattgttttg
                                                                      1200
                                                                      1260
gaagcgaacg acctctgcct ccagccgcgc ggacgggaga taagcatgct ctgtactgtg
                                                                      1320
gttiggagag ctgcggctcc tctttcttgg ctttcttctt cggcttgtca gtgataagga
                                                                      1380
cgcactgcgc gaaccgtcgc gatagacagt acagcctttg cagccgctct tcatgcttcc
                                                                      1390
acatacaggg
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 938 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...938
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004

aggatccccg aaattaggg	ttgtaacttc	tatatcgtga	cagttcctac	cccatagatc	60
acaatcacac cccggactta	cggccacttt	tggcagccgc	gaaacaattg	gaaaggtaat	120
cggccaagga gatgtggtg	g tgtacgaagt	acggtgtatc	ccggtgtaac	agaagacgaa	180
tgtattccga ttatcggaa	gtttcgggtc	tcaaatacaa	tgtggacttc	tttgccggat	240
acagtocgaa cgaatcaat	cgggagataa	agttcacaca	gtagagaata	taaaaaagtg	300
acatccggtt ctactccgg	a aatagccgac	tatgtggata	gaagtataat	accgtgttgg	360
tcaatggcac acacaaagc	a tcttccataa	aattgcagag	gcttcaaaaa	tcatagaaaa	420
cgcccaacga gatgtaaac	a tgcatttatg	aacgaaatcg	cgaagatttt	caatgcaatg	480
gacattgata gcacgaagt	a ttggaggctg	cagctacaaa	atggaacttc	ctacctttta	540
gccgggcttg gtcggtggg					600
caggtatatg gagtttatc					660
gctcctatat agcctcgca	a accatcagca	aatgaataaa	gcaggcatca	tggtgaaaga	720

tocacoaatt ct	gatttagg atttacatto	aaagagaatt	gtccggatat	ccgtaatacc	780
aaaggataga Ca	cgtacage accetgeaag	, aatacacgaa	aaatattata	gtaacgatcc	840
ttgggcaaat cc	ttctatcg ctgagcaag	. atatggaata	aaattcacaa	tgaattccct	900
aaaggaaaat to	gatgccat tattattgc	gggatcct			938

- (2) INFORMATION FOR SEQ ID NO:1005
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 656 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...656
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005

atttgtggcc	aacccgcttt	gtatcccaaa	caatcctcgt	tcttcggagt	gatcaagtgt	60
tcttttgtcg	gtgaggcaga	gaaaatcgca	gagctggagt	cgtgatgcgg	cgcgactatg	120
gagacaaatt	gaatatattc	cgctctttga	aacgctgctt	gagtgccttc	cgtccgaggt	180
gcagaagata	aaagcctatc	cgacctcttg	gacaagctgg	atttgtcacg	agaggaactt	240
gtttcgtcgg	agacagctac	tgcgatgtgg	agatgatcca	actggccggc	ttggtgtggc	300
cgtggcgaat	gctcgggaag	ccgtcaaagc	ctgtgccgac	tatttacgac	gagcaacgag	360
gagaacggtg	tcgcccactt	ggtggacaag	taatccgaca	cgaatatgaa	gccgttcctt	420
tctccgtaga	agatgtcaat	atattgtgcc	gggtacgctc	atggagagcc	ttggtattcg	480
ctgcaccaag	tcgcgcgtgg	ctatgtcgag	gcaacgatgc	cggtggatat	tcgcactcgc	540
agcctatggg	tattttgcat	ggaggagcca	gcttggcttt	tgcagagacc	tggccggatt	600
cngtttccgt	ggcantctgc	aatnccgggg	agagataang	gtggggattg	canggt	656

- (2) INFORMATION FOR SEQ ID NO:1006
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 619 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...619

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006

aggtttgtac	ageetetega	agcggcgatt	ctaatccgga	ttgttaaaac	actaatacca	60
aggictgiac	cataaaaata	tacaagacaa	atgaggtgaa	aacatctcca	ttttgggtag	120
acgacticat	catgaaagtg	cacaagacaa	acastactet	trangataa	actostasas	180
ctccggcgcc	ggaaaaacca	CCCCCgcgag	gegatgetet	tcgagggtgg	agegaeaaat	240
cgtagaggaa	gcatagtgca	ggcaatacgg	tctgcgacta	tttccccgta	gagaaggagc	
atggaactct	gtattctcta	cggttttctc	tgtagagtgg	caggataaaa	agctaatttc	300
atcgactgcc	cgggagcgga	cgactttatc	ggcggtaccg	tctggctctg	aacgtcacgg	360
actgtgccct	cgtagtagtg	aatgcgcagt	atgcgtggaa	gtagggctta	tcaatcaatt	420
ccactatata	papcagttgc	aaagcctgcc	atcttcatca	tcaaccagtt	ggatcaggac	480
esaccasct.	caactctact	gtatcacago	ttcgggagcg	atatggctcc	aagatagtgc	540
aaggeegaet	cgactecgec	gcaccacage	attcaster.	ataatcaaat	getgaagatg	600
		CARRAGCARR	gillaatgee	gtggtcgagt	00.00.00.00	619
aaaatgtatc	gctggaacc					019

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2208 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...2208
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007

```
aacatccaaa agagcaggtt gccaagctgg cagagaccgc cttcccactc tttgccgatc
                                                                        60
                                                                       120
ttcccctgac tcaataccaa accttcgagg taccccttcg agcagtcgga cgaccgacat
gacgccagac ggagaaggtc tctccggacg tatgatcata ccgtgcagct tggagatggc
                                                                       180
                                                                       240
cagtcgcaga ttggttgttt gttctcttgc atgtacatat ccacatcctt cagccggcgc
                                                                       300
ataatagcga ccgatgctcc atgaccggat aggaacagcc atgagaattg tctccttcgc
                                                                       360
tggtaaagcc catttgatcg aagaaaagca gtccgacaac ttgggtgaag aatgaagtat
                                                                       420
togogtocca atttgcgtot togotogott cgaagatogg ttgtatgatg cgtatcatat
                                                                       480
aaggtotgtt togattggao toaaagotaa ogattgtoot ototooatgo ataatoocat
                                                                       540
cagaccgaaa atgggcaaat gattctgatt ttgttctatc gatacaaacc atcggttgaa
                                                                       600
atttacgcac cggagtctct ccgattgcgg ctcgtaaaat tggaaaaatc gaacgagttt
                                                                       660
tttctcgttt tggcgcgaga attttttact tcccgaacaa aatgaaaaaa ttctcgaacc
                                                                       720
acatcttttg gccccatgga tgatgttttc cggttcgtaa agagatggca gaaaaaattg
                                                                       780
ccgagcgaac tgttgataat tggattttgt ttctaccttt gcaatcgcaa aagaacaatg
                                                                       840
ggcattacca gagtggccaa atggggctga ctgtaactca gctggcttac gcctcggtgg
ttcgaatcca tcactgccca ctcttcactt ttgtaaaaac aacgttaagg tcgcggaagt
                                                                       900
                                                                       960
agctcagtcg atagagcatc agccttccaa gtgagggtcg cgggtttgag ccccgtcttc
cgctcttatt gaaatcaagg cccggatggt ggaatggtag acacgaagga cttaaaatcc
                                                                      1020
tttggccata tcggctgtgc gggttcaagt cccgctccgg gtacatggtt tcgttttctt
                                                                      1080
ttctaccgaa gttccatttc gggatagact gcggaagtag ctcagttgta gagcataacc
                                                                      1140
ttgccaaggt tagggtcgcg ggttcgagtc ccgtctccgc tcaacttcga aagcgataag
                                                                      1200
                                                                      1260
ggggcatcta aaattacagg tottgaatto cocaaagtog attogtotto ttotttotto
                                                                      1320
acatecece cacaacagag attitietat tigeetitigg actgatgett tigecattet
                                                                      1380
cgttttgcag agaatcctgc acctgaacaa tgcttggcga aatcgtcggt atgacacaca
```

```
ttgctttcga cggcttctct atctgatcca aaaacttctt ttcaagcctt tttcttgtag
                                                                      1440
                                                                      1500
catcatggca catacgactg atgttttta ggatggttgt tttcgaatct ctttaggtat
tacttttgtt ccattggatt tggctcatta agccgggaaa aggagagaaa gggacaaacg
                                                                      1560
attttctcct caaataccgt taatagatca tgaaggaagc tattncccga aagaacagta
                                                                      1620
                                                                      1680
tataaagctc aacggtatat acagattgtc attcattctg ctatgcgcct gctatgctct
caggcagcta tggcacaagg cgtcagggta tcgggtatgt gctcgaccgt ggggaaaagc
                                                                      1740
                                                                      1800
cgatcccgtt cgccggagtc aaaggcgtgg tacggggaca ggcgcatcga cgaatctgaa
                                                                      1860
aggatactac gagttcggat gaaggccacg acggacagca tcacgatcga gttcagctcc
                                                                      1920
atgggtacca aggggtaagt cgcagctttc cgtctctgac caaggacact cgctgaatgt
togtttggca gaggoogaga tggagottto gagogtgacg tacaggocac aaaacgcaga
                                                                      1980
ctcaacacga tggagcgcgt caatacccgg accttcgtgt caatgcaggg cctacgggag
                                                                      2040
gggtggaatc gctcatcata cctacgcagg agtaacgcag aacaatgaac taagctcgca
                                                                      2100
atactcgttc gcggaggaag ctacgatgag aatatggtct atgtaaacgg agtggagttt
                                                                      2160
                                                                      2208
atcgcccgct gctggttcgc tctgcacagc aggaaggtct gagctcgt
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1013 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1013
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008

```
gttcaggaaa agaatatcac cttccctacc gatgccaagt tgcataaaag atcgtgcgca
                                                                        60
agattttgga catcgtccat aagttgaatc ttcctcttgc caaagctata cctttgtttt
                                                                       120
                                                                       180
gaagcggatt tatcgcgacc aacgcttcgc catcatccca agaatcgcaa gaaggcgctg
                                                                       240
aaggcagaca ataaatgcga acaatagccg gacgattggt tcgagagctc aagcgtaatc
                                                                       300
ttggaataat tctctctacg ccgaattgat tgagaggttt gaagccattc tttccaaaga
                                                                       360
cgtaacagcc cccaaaagat ttattccatt catgagccgg aggtcaatgc atcagcaaag
                                                                       420
gcaaagagca caagaagtac gaattcggca ataggtatcc gtcatacgct cggctacggg
tattatcctt gaagcccgat ctttcgaaat gagtatgacg ggcacacgat agaagcttcg
                                                                       480
                                                                       540
ccggaacaag tgaacgactc acacacagaa agatcaaaat accggccggg gacagaggta
                                                                       600
tcgaggccgg aaagaagtta acggaacccg gattttaata ccggataccc caagcaatca
                                                                       660
gacagcagac atcagaggtg caagaaacac aaattatctg caagcgagca ggcatagaac
                                                                       720
ccaccatcgg acacttgaaa tcagatatcg tttaggctgc aacttttaca aaggattggc
                                                                       780
cggggatgct ataaaatact gttggctgca gctgcttata acttcaaaag agccatgaaa
                                                                       840
gctcttggga ctttatcaaa ataataagcc agatgccatt tgccaatggt ttccgcttaa
                                                                       900
agaggttttt taagggacga ctatgtaaga tacaccgtca gaccgagaga ccggattgct
                                                                       960
ctgaaagaag gcagtcgtaa tctccgaaaa aaatagagct gtgcagaagg gaaatcctcc
                                                                      1013
ctatgcacag ctctattttt cagcatatcc aaactactag tagtttcaga aaa
```

#### (2) INFORMATION FOR SEQ ID NO:1009

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 846 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...846
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009

60 gctgattttc caagatgata ccgcactgtg tttgtggaat gtccccagac aattacaggc 120 ttacgacgaa ctgttatcgt atttccgttt ttcagtgtat gatggagtag tccacttcac 180 gttgcctgtc atatttcatg ttttccatta ccggtgaata tcgatatgat ttttatcgaa ggccatgaac tccgaacatg tcggctgtga tgacagcccg tgcagagatt gaaaaacgat 240 300 cgtagcgtac gacgccttcc tgcacggtgc aggagaccag cgtaggccta 'cggtctcatt acaacatgct aattatcagt gcattatggc caattaaagt aaacgagaac gaccttagaa 360 420 attttccctg ttttgcgtct tcaaaattcg ttcccccctt gtttgggaag ttcagactca atagcagatc gacgacctcg atccccttgt cgtatttgaa gcatcatttc ttataataga 480 540 aagaagacac tgaagatggt gatgatgtca tttttcagta cacatcgcct tttctttatt ttgtagagca tggtttcgaa tttgggaccg gcttttgaaa tcagatactc taagaaacgt 600 ttcaaagaac tatgttattc gaatcgatta cccctgtcaa tggtggctga tagcaggtat 660 cctgctcttt gtttttgaga tttttacccg ggtttcttct tggcttgttt cggtatggga 720 4 gettttgetg ceatttaceg geggeettgg ggttgtetat tgtgtggeag acegttttt 780 840 ttatgtggct tegetgetet egetetteet geteagacet tttatgeaga agaggegeag 846 aaggct

- (2) INFORMATION FOR SEQ ID NO:1010
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 558 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...558
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010

tggaggactt taacttcgat gctcccaaaa caaaggcttt caaggctatt ctgccgcatt 60 gaaggtgggc gaaaagaaag tactctacgt ccttcccggg tgaataagaa tgtgtacttg 120 tctgctcgca acctgccgaa tacgaattga ttcttgccaa tctgatcaat acttacacag 180

tgttggcttc	caagaactcg	tgctgacaga	gcgttctgtt	gccgttgtta	atgaactatt	240
taaagataag	gaggatttgg	tatatgggaa	tcatcattaa	gccgattatt	tcggaaagat	300
gacggctgtt	acggaaaaga	tgtcggagcg	ttatggcttc	cgctttctcc	taacgcgaat	360
aaaatagaga	ttaagaaggc	tgtagaggct	attataatgt	gaaagtcgaa	gacgtgaaca	420
cgatgagata	tgacggtaag	ctaaaaccgt	ataccaagag	tggactgatt	cgcggtaaaa	480
agcttctttc	aaaaggcgat	tgtgacgctt	aagaaaggag	aaacgatcga	cttcttcaga	540
tatctaagaa	aaatggga					558

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 669 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...669
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011

```
cgaggaaatg aaagctcggc cggcagcgtg ggcaagatcc gcgaatgtgc gccttactgc
                                                                        60
tcaaatactg caagactacg ggtatcccgt catcgtcacg gacacatcac caaagaaggt
                                                                       120
agcatagccg gaccgaaggt gctggagata tagtggatac ggtgcttctc ttcgacgggg
                                                                       180
ataagcatca tototacgga tactoogagg acagaagaac ogotatggca gtacttooga
                                                                       240
gctgggatat acgagatgcg gcaggacggt ctgcgtggcg tggagaatcc gagcaacatc
                                                                       300
tcatcacacg caatagggaa gacctcagtg gcatagccat agcgtagcga tggagggcat
                                                                       360
tcgcccgata ctcatcgaag cgcaggcttt ggcagctcgg ccatttatgc caatccgcag
                                                                       420
cgttcggcca cgggcttcga tttcggcgga tgaacatgct cttagccgta ctggagaaac
                                                                       480
gtgccggctt aagctcatac agaaggatgt gtttctgaac attgccggag gtatcaaaaa
                                                                       540
gccgatccgg ctacggatct ggccgttatc tcggcagtgc tggcgtcggt ctggacatcg
                                                                       600
ttatcccgcc ggccgtatgc atgacgggcg aagtcggctc tccgganana tacgtcccgt
                                                                       660
gagccgcat
                                                                       669
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 593 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...593
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012

tgcgtgatca gtttcata	itt gcggggaaag	agtgtggagc	cggccggacc	tgtatgcgca	60
aagggagttc tatttcac	ga ctttggtata	aatcttcgtg	gcctgttccg	cttttgcttg	120
accttctttg attggcag	tt gtttcaatat	cgttcaatat	cccgtggatc	aaggcctttt	180
totttgatgg ttgccaga	itt tgggtatgtt	cctctctatt	ctccaattgg	gtcaagtagt	240
rotagetget tegtett	gg attcagcaag	tcgtttctca	aaacaggcaa	taaatctcgt	300
atttcttgat cctccgg	tt gaatgaagtc	ggattttggg	catggcctct	aatgcttgtt	360
ttaggttgat tcgtgtgg	tt attcccacat	cggtttcgac	caatcattta	cggcatattc	420
gaaagcggat cggatcts	ct ctcgacttca	gaacgatgaa	aactgtggat	attcaagccg	480
attttaatag tgctttta	aat gcatactcgc	ctaatgttgt	aatcatactt	gtaatgtttt	540
ggattagttg caaatcta	ata gaaaattaag	tgtgtggcat	gcaaaatata	tgg	593

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 713 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...713
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013

aactttcttg	tcacttggca	tcgagggcgt	tcgccgatga	gctgcgcagc	60
сосававсов	atccgctaca	gccggctcga	attcagccac	ggatttggca	120
	tagetategg	gantanettt	ccacatccct	ttecetecee	180
Caatageett	Lageigeegg	gggtagettt	ccacacccc	2-6-6-6-	040
tacggcgtga	attcctgcaa	agcggcaggg	ttgttttcgc	ggaaaaattc	240
gattettete	atcetteaca	taagtagcgt	agatgtcatc	ccacattcct	300
Buccesses				+++0000000	360
cgaaggcttc	atgacattcc	agccgtaggt	atteggatag	LLLCggcaal	200
gcattctgtc	cctctttgag	ctctcttgga	tataagtagg	attgaggatc	420
gcaccccgcc	ccccccgag			++=+=====+	480
cttcgacgcc	gtggcttgtt	tcagctcttg	cacgcgcgtc	ttgtggcgat	,
++assatsta	cttccggatc	tttgcccgtc	acttggcgga	cagagagcgg	540
ccgaagcacg	CCCCBBacc			***	600
tgaattcata	gacgtggtcg	aggctcaagg	ctccccacta	ttgctttggc	
cacaacatca	cattctgcaa	gctgcttgaa	cataccttgc	tggaaatctc	660
Cacagoacca	carrengena	800800		1 - 4	713
tgcataccgt	agatgcccca	tgtgtgaggt	aacatctgca	ECE	/13
	cgcaaaacga caatagcctt tacggcgtga gattcttctc cgaaggcttc gcattctgtc cttcgacgcc ttgaagtatg tgaattcata cacggcatca	cgcaaaacga atccgctaca caatagcctt tagctgtcgg tacggcgtga attcctgcaa gattcttctc atccttcaca cgaaggcttc atgacattcc gcattctgtc cctctttgag cttcgacgcc gtggcttgtt ttgaagtatg cttccgatc taattcata gacgtggtcg cacggcatca cattctgcaa	cgcaaaacga atccgctaca gccggctcga caatagcctt tagctgtcgg gggtagcttt tacggcgtga attcctgcaa agcggcaggg gattcttctc atccttcaca taagtagcgt cgaaggcttc atgacattcc actcttgag cttctgacgc gtggcttgtt tcagctcttg ttgaagtatg cttccggatc ttgaattcata gacgtggtcg aggctcaagg cacggcatca cattctgcaa gctgcttgaa	cgcaaaacga atccgctaca gccggctcga attcagccac caatagcctt tagctgtcgg gggtagcttt ccacatccct tacggcgtga attcctgcaa agcggcaggg ttgtttcgc gattcttctc atccttcaca taagtagcgt agatgtcatc cgaaggcttc atgacattcc agccgtaggt attcggatag gcattctgtc cctctttgag ctctcttgga tataagtagg cttcgacgcc gtggcttgtt tcagctcttg cacgcgcgtc ttgaagtatg cttccggatc tttgccgtc agcgtggtcg aggctcaagg ctccccacta cacggcatca cattctgcaa gctgcttgaa cataccttgc	aactttcttg tcacttggca tcgagggcgt tcgccgatga gctgcgcagc cgcaaaacga atccgctaca gccggctcga attcagccac ggatttggca caatagcctt tagctgtcgg gggtagcttt ccacatccct ttgcgtgcgg tacggcgtga attcctgcaa agcggcaggg ttgttttcgc ggaaaaattc gattcttctc atccttcaca taagtagcgt agatgcatc ccacattcct cgaaggcttc atgacattcc agccgtaggt attcggatag tttcggcaat gcattctgtc cctctttgag ctctcttgga tataagtagg attgaggatc cttcgacgcc gtggcttgtt tcagctcttg cacgcgcgtc ttgtggcgat ttgaagtatg cttccggatc tttgccggt aggctcaatgg cacggaggtgaattcata gacgtggtcg aggctcaagg ctccccacta ttgctttggc cacggcatca cattctgcaa gctgcttgaa cataccttgc tggaaatcc tgcataccgt agatgccca tggtggggt aacactctgc tggaaatcc ttgcataccgt agatgccca tggtggggt aacactctgc tggaaatcc

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 508 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...508
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014

ggctcttcgc	gagctggccg	acttcctgat	cgacatccat	tctcagcaca	aaatctcctg	60
ctcggcgaca	gtttgtttca	gctcaatgtg	ctggatgcta	tagcggaaaa	cccgacttat	120
atgcccacta	cagcaaagct	taccggggta	tgccgaaaga	aaacaaaagt	tggaagacct	180
tcgtaaggca	gccgctcgac	agcgtcggag	tatgactatt	ggcagtttcg	ttttgagcag	240
ttggaaaggc	cggtctcgaa	tcgggagaag	aagctcgttt	gcaagaagaa	caggtatgct	300
gacgcatgcc	ttggacatta	aaagagagct	ggggcattcc	tatgccttct	ctccgacgat	360
gagagaggac	tactgtcggg	tctgaacaaa	gtgaagatgc	tttggccacc	atagagagct	420
attatcccga	ctcggcttct	ttcggcagcg	agtacgcgat	gttcgaatag	agttggctga	480
tattgcatcg	atttgggcgg	cgttcgga				508

- (2) INFORMATION FOR SEQ ID NO:1015
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 655 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...655
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015

ccttgatctc	aacatcatcg	aggttgatcc	agaagaagtc	cgtacagcca	agtgacggaa	60
ggcaacatac	ttagtacccg	caggcaactg	taccgtcttt	gataccaggt	gccctgaaca	120
cgagtgccac	gaatggcttc	cggtgcctaa	caactgtctt	ggccgtcagc	acttcttcca	180
acaaagcgtt	ggcgaattgg	aagcgtcgtt	acccgtagaa	gatgcataca	cggcatagtg	240
ctctgtgcat	aattggcatc	ttgtgcacat	acccagaaag	taagcgttcc	tccgtaggaa	300
gagaaagctc	cggtgtaacc	agatagttat	cagggttctg	aggccttcaa	agttgatata	360
agaagccgaa	gagacacaga	ttgcactgtt	gtacctgcaa	aagaggagcc	tccgggagga	420
ggggtcgtcg	tccaattgtt	gcgtcaccgt	ctgcatcgat	cgtcttccat	gaggcaggaa	480
taccattttc	aatgattcgg	aaagtgttgt	tgttcccgga	ttcggattcg	gggtaccata	540
ggtgcatccc	acttgagcgt	tactttctgg	ccgactgcac	taccggtcgg	ttctgtcagg	600
agcaaattca	ttggatcctt	ctaccgtaac	gtctttaata	ccttcggaga	tacgc	655

- (2) INFORMATION FOR SEQ ID NO:1016
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 521 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...521
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016

tttgcttttc cgtgtgaacg	tttctttttc	gaccggaaaa	agttccacct	ttcaatcacc	60
gtcaaacctc tccgtaccga	ttcttcgaaa	gaaatggatg	ggaagaattt	ttcctcaaac	120
cgggattggg ataagggccg	atcggctgct	ggcatctcta	tagtaagcga	acacttgacc	180
atacgaatac atacctgacc	tctaagagca	tcacgtgggt	gaaagattct	tctctgcctg	240
ccgagttgct ttcccatgcg	taaccgtgtg	gatggtcatt	ggctgtacct	ctgctgagaa	300
atgagtaact ccgcttatgt	ttccgttata	ggaccataca	gctcttctcc	gttggttgca	360
tcggcatttt cacgtgtgta	tacagtcgcg	ccgcatatcg	ttgcgggttg	ttggcaaaga	420
aggcgtccca actgctccat	aattaggatc	gccatagtaa	ggccctacca	actcggggtt	480
tgcatagctc catagatgct	tccccacgtc	cagncgtatg	t		521

- (2) INFORMATION FOR SEQ ID NO:1017
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 711 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...711
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017

faccactc frackcar casasaraa acabaatar feccareas agained	ttgacggcaa	acatgccgta	gctctcgcga	tagttcttcg	tgatccagaa	gcatactgct	60
- CPC	tagccactcc	gtatggcgat	Ceeegetaaa	acggagtgtc	tcccgttggg	gcacttcctg	120
caccttgccg aacagctcgg atgtagagct tgatagatcc gcgtttcctt ctccaatccg 1	caccttacca	aacagetegg	atgtagagct	tgatagatcc	gegtttcctt	ctccaatccg	180

agtattcgca ccgcttcaag	aggcgaagcg	tacccacggc	atcggcttct	gccgtgtact	240
ccggacgtcg aacgacacct	teaceteect	ttgagcggcc	agattgtata	tttcgagggg	300
cgagtggtct gaatgatgcg	taccaaagag	gagctgtccg	tcagtccccg	tagtgcagat	360
teatcaecce ctcgcgcttc	atgtcccgca	ccattcgtcg	agatagaggt	gttcgattcg	420
trrretatte aargaagarg	acggcgcagg	ataccgtgca	cttcgtaccc	cttttctatc	480
agaaactogg gaggaaagag	ccgtcctgcc	ctgtaattcc	tgtgattaat	gccacttttt	540
tttcataatc ggaaagaccg	gattcctaat	cttgaccggc	tcaagcaata	atatgattee	600
ctgcaaaagt actcattcct	cccacgataa	tgcaggagct	ttgtttttcc	tccgaaatga	660
cagtagaggg ctgcctttgc	tgagacccta	angggatccc	catcgagact	С	711

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1896 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1896
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018

```
60
togagttgto gaagcattog atatgtttog goggaogato caagtgcaat cottttggat
                                                                       120
cccgtggacg atatgtaggg cgcgttgctc gggattgact tctcggcacg tttgagtttg
togagottgt attgagotac gttottoogg ataattooag cagtttoogt ttgtotooac
                                                                       180
gtcgggggat cgtagtgtga tgctctctcc cgtttgccaa ccggtgtcga acggcaaaac
                                                                       240
                                                                       300
gatttgtgag cgttgctttc gaatctttgt ctcagctctg ttatcgccgc tgcagaagtt
                                                                       360
cttctttcga ttcctctatc tgctttctgt actccaaggt gtaacacgat tgatccctcc
                                                                       420
gtgctctatg tgcatgtagt tgatataggc cggtgctcgt cttcgtcgta agagaaaaca
                                                                       480
tctacgttgt ctatattacg cgtacgaccg tgtgcttggc ttcgtatcgc tcaagaagct
                                                                       540
ctattctctc ttgcatatct gtgcctcttc gaagcgcagt ccttcgctgt atacctgcac
                                                                       600
ctgtcgcgat acatgcgtac aagcctgtgc aagttgcctc ggagcagacg cgtatttccg
                                                                       660
atacattgct ttcgtactcg ttcgaagttt gattgccatg caggggcctt tgcatttctt
                                                                       720
gatgtgatac tgcaggcaga cgcggtccgt ccttgtcgga ttttctcctc tctcagatcc
agtttgcagg tacngtcgga tagatctctt gtcacaaggc ggagcatccc tttggcaatg
                                                                       780
                                                                       840
agtggcccgg ataggggccg aagtattcgg atccgtcctt tttgatgtcc cgttggcgaa
tatacgtggg aaaggttccc gtttgatcac tatgctgggg tagtcttccc atctttgagg
                                                                       900
                                                                       960
aggacattat accgaggttg atactctttg acagtgagtt ttcgagcagc agggcatccc
                                                                      1020
cttcgctgtc cacaactatg atttgatgct cctgatctgt ctgaccagta tgcgggtttt
                                                                      1080
cctgtctgct gctccttgta aaaatacgaa ctgaccctgc gccgaaggtt tttggcctgc
                                                                      1140
ctacatagat taccttccca tcttcatcga agtactggta gcaacccgtt tttccggcag
                                                                      1200
ggtggggagg atgatgttca gttcgtcggg ggtcatattc ggttcgatat tttgtttcac
                                                                      1260
gtgaaacgtt atcttccgca gagtagagaa ggatgcttac gtcgtgggga gagactcccg
                                                                      1320
gtattcgaga tgctgcgcga tggtttccgg ccggatgctc gtcagttttt ggcgtgcttc
                                                                      1380
ggtgagaggg actgcatctg catataatct acatgctgcg gaagtcggat acttcgagtc
                                                                      1440
tgttgatctt gtcggccaag gctctttctc ttttgatata gcgtcgtatt tgatcaggat
                                                                      1500
ctctgcagct tccacgattt cctctcgtct gatgccggga tctcttccac gattctttgg
agagagggca ccatcgaacg acttcattca ttcctatttg aggacggagc agcaggtcgt
                                                                      1560
                                                                      1620
acagtttgtt ccttgcttga gaggaaggtg gccggccgac tccagatgcg ggttgataga
                                                                      1680
tccggtttga gggaaaactt gtgcgtaaag tcgatcagct tatcgcaaat acttgctttt
```

ctcggagcaa	ttcgctgcgt	ctgctgtctg	ccagccgatc	gcttccgcct	tcggtgtgag	1740
					tgtaaacatg	1800
cggtagggct	cgtcacgccc	tttgcttcac	caagtcatcg	atcagtaccc	tatgtaagcc	1860
tctcccgtcc	gagtgtgaac	tcgctgcgca	tggcat			1896

- (2) INFORMATION FOR SEQ ID NO:1019
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 412 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...412
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019

gggcattacc tgctggcagg aaccatacac gtcgcagtta ccgtaataac accgaaagca	60
cctacggaag atataatcat attgtatcgg gcctgactga tggctttgtc aaccttaggc	120
gcgcatcgtt gaaccacatc tgctccaggg aggaacgtag aaataggatt cgccgaagaa	180
tttcactttt ttgcttcttt ttcttccaga aagaattctg ctatacctgt cgtgtacgct	240
gtaaatagtt gatcgtacct gtgttcggag aatcgacatc cacggaataa ccggtatcgg	300
acattgtgaa ttcaggatat aaccatcctg aggacattaa ccaaccttgt ctcccgtcgt	360
agtagaggca taataactgc tgtatgcccg gaaaccagat agtattctcc gg	412

- (2) INFORMATION FOR SEQ ID NO:1020
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 547 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION  $1...5\overline{47}$
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020

ttgactatcc	tgccctgtcc	gccatgctcg	gtatcccctg	gttccgacgg	tgggacgaac	120
gggacaaggc	ctgccggaac	ttttcgaacg	cttatctcca	ttcatgaagg	acgaaacaaa	180
atcatacgtc	ccattctatc	aactatggca	gcatcataga	accggccgta	gaagctctga	240
ctgagaaata	aacaatcagc	tctctctacc	ctattctctt	ccggcacgct	atatgcagtc	300
aagctgctgg	aaggcgataa	ggagatgaat	cgcttcgtag	gcgacagccc	aaaggtcttt	360
tcatcctttc	ggcccgggac	ttcgctctac	ggagatcgac	gaacatctga	cagtggcgag	420
agatgccgaa	agcattatca	cgatcagcga	tatggattca	tcgcaggagc	cctcaaagaa	480
acataccgga	cagctacaaa	cagctcaaga	ccctgaccga	tagatcgatc	atatcgtcac	540
catcgcg						547

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 590 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...590
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021

60∤ ggcaaaatca ggataatcga cgctttcgga agagtggcat ccgaagtctt tgtcgtgatg 120 ccttgctctg caagccatgc ctttacgcgt tctttcaatc atatccggcg tggtcgctac aaataccgat tgtttccatt gtctgagtgt agtttgtaaa tacagattgc ccgaaagcta 180 tattccgatt tggaagcgct ttcgggcatc ccgtggttgg ttatcagtgg agtatttca 24Ö acactgttcg tacacattct ctgccgtaaa gccgagtttc tcgtccagca cctttaggga 300 36Ò geggagaate egaaagagtt caateeceag aeggeacege tttacecaca aggeetteea 420 ggttgacggg caatccggct gtcaggccga aagcctgata ccgatgggaa gcacttcctc ctgatactcg gcactctgcg acggaaaagt ccttcggaag gtaccgacac gatacgaagt 480 540 tttacaccgc tttgcgcagc agctctgcac cctcgaccaa tgtggacacc tcagatccgt 590 ggccaggaga actacttcga tattctgatc cgtattgacg atataagccc

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 555 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

#### (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...555
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022

gaaacttact	tggccaactg	tcgcatagct	aaagacaata	tcgctgtaaa	tctgtagcag	60
atcagatcaa	aatgctgacc	aaagagcaaa	aagaagagtg	aaaaaattcc	tctaaacatc	120
tttttccctt	atttcgtttt	caggagcgat	attatccgaa	tcggaatagg	gttactccaa	180
taggcaaggc	tgtccggtat	aaaaacttcg	gcagcctttc	ttttttaggc	aagaggagct	240
aaggaaatag	ttggtttctg	gaccaaagat	ccggtatcta	attattgctg	tccgtgaact	300
			cattggaatt			360
			gatgcagtga			420
gttctgtatc	gatagggtaa	atatccgcta	tctttggtct	aatgatgata	gccacaaacc	480
aaggatacag	gagttcggcg	actacctcgg	caggtatttc	cacactataa	agtccagaaa	540
taccctcatg	cagct					555

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 977 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...977
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023

aaggcggtta	cgaagaactt	gaccggggta	gaacttttt	acccgacggg	cccgcctctt	60
			cgtgcatcgt			120
			gacgcttgtg			180
			tataaacctc			240
			ggagtattgc			300
ctgcttgtaa	tcgggagctg	gacgtgcaga	cggtttttcc	gttgaagtaa	gcacgatgcc	360
			cgggaagtgc			420
			gatttttca			480
			caatgactgt			540
			gagcggcagt			600
			tggatttaat			660
			cggctccaat			720
			cgctttccgt			780
			tccggagctg			840
			atcatattcg			900
			ctccgaaacc			960
tgacaggtat						977

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 563 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...563
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024

gccagaacgt	tccatccggg	gatgaaacac	gtatggctgt	gccatctgac	aaggacaaca	60
accaccccga	cctgtgctgg	aaatccatcg	aatatcgctg	ttcagtgagg	ggattcgtgt	120
cggaaaagat	atggaactca	ccgtactaag	cgtacatccc	cctcatctct	atatactctt	180
ttagaggact	gacctaagag	actccccctt	ctcgcacttc	atatactgcg	gcaaataagt	240
accctcccat	aactgtgatt	gttacaggag	aagggtgacg	gataagatta	taggattcct	300
ttttcagcgt	ctccatccga	aaggatgaga	ggccaggggc	aaagtgcaag	ggggtggtat	360
tcgcccttca	gtcctacggg	agaagcattg	cgatgtcatg	aacgatctga	atgctgttgc	420
			caaaatccgc			480
cttccgtaaa	ccttcactga	actcgaatga	ttcgccgtcg	attctatcga	cgaaaggtcc	540
ttctctcctg	tacgcattct	cgg				563

- (2) INFORMATION FOR SEQ ID NO:1025
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 580 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...580
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025

gaatctttct atctttaact	caataagaat	cagattggaa	caatgactag	atgcagtggg	60
agcgattgct ctccgacaaa	agggtgggca	tggagcacac	caccaaccga	aacaatcggc	120
tcagccatgg gagagaacgg	acttcgacga	gattatgacc	gcatggtctt	ttcttcacct	180
tttcgccgac tgcaaacaag	gcacaggtat	tcccccttgc	aggcaatata	ttcgtacaca	240
atcgtttacg cacagtctcg	aagtgagctg	tgtgggacgc	tegeteggea	ataaatcaca	3.00

cgcggactga	aagcgcggta	tggcgaattg	ccatgggagt	cggggccatc	agtgccatcg	360 420
teccatttce	gcttatttcc	ggaaggaaag	ggtagggtat	gggaggacgc	gcggcgagcg agtccgcaag	480
gaaggaggtc	ctgggaagac	ttcctgcact	tcgaaggcaa ttgccttacg	tgcaaacgct	ttccgtctgt	540 580

- (2) INFORMATION FOR SEQ ID NO:1026
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 576 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...576
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026

оосаарарср	aataagaggc	aatcacctct	atttattccg	atgtattgaa	caaaaacttt	60
ctatttctta	tgattttctg	ttacggagag	taccgatcgt	tctctcaaag	gcttggttgt	120
gateteatea	agacccaatt	cgtcaaggcc	ttttcggcca	aaccgttgtg	ataatcgatc	180
agatetteca	cgatcgacga	atccccagac	gattataaat	acctgtcaca	gctcggatct	240
tttctcacac	tgcacatccg	gcatcaaaag	ggattctctg	aggagattca	attctctccc	300
tgagccatct	caagggcttt	gatcagaagc	atcgtctttt	tatacaagct	atatcatcgc	360
cgattttctt	gccgaggata	atgggatcgc	caatacatcg	aggaggtcgt	cctccaattg	420
разарасаар	ccgatatgta	tccgtagcga	tagagaatat	ctgctttctc	aatatccgct	480
cctccoocta	agcccccatc	ttaaggctgt	agccaagaga	actgctgtct	tcaaacgaac	540
		ggcaacaaag				576

- (2) INFORMATION FOR SEQ ID NO:1027
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 566 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...566

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027

gtcttcttga	taaaaatcac	aaaaaaaga	tttggccgac	atttgaaagg	attgttttt	60
ggaaaaagta	caaactaatg	aggttattcc	aatattccgg	atgacaccaa	gttcccaggt	120
atacctaatg	acattgcttg	cattcgtatg	aagagaagca	ggaagataag	aagcgatctg	180
aaagagtgca	gcgagaataa	ttgaaagaat	aatttctaag	gttcaatagt	taattataga	240
aaggggattt	attattttaa	tagattttat	attgttgtat	ttgttgtcgt	aagggatgca	300
aatatttata	ataatagctt	ttttatagca	tgatagtttt	cctattaaag	ctgcgcagtt	360
gatcctcgca	ttcgccattc	tggttttcgt	cctgaattgg	gacattactt	ttttgctcgt	420
ctcttccgag	tcagggtgga	cagttctacc	ttttcttcga	ttggggaggt	gccatcttcc	480
gttcaagccc	aacggagcga	aacggaattc	ggatcggtgg	cttcctctcg	tggctattga	540
gatcacggga	tgatagacga	atccat			•	566

#### (2) INFORMATION FOR SEQ ID NO:1028

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1013 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1013
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028

tcagggattc	ggcagcgatc	ggaccgatcc	tcggatgtac	tcctctccaa	caaaagtaat	60
atatcccgta	ctaagccctc	ccatttcgct	cttgatagat	cgatacgatg	aaagagatgc	120
gtgcgcatgc	aaggagttgg	tgtcgctctc	cccgagcttg	atctccggat	agcaggggct	180
taagaaaagg	aaacggtgag	atcgtgaaag	atgaaacacg	aaccaaaaaa	cgccgggttg	240
cggttgtatt	ttctgaaaaa	gtggcgtgag	atctttttcg	ctgtggcgcg	taaatttta	300
cttcccgaac	caaaacgaaa	aaattctcgc	gccacgtttt	tggagcatgg	aatgagaaaa	360
ttttgggctg	taaactcccg	aacgatgaat	aagtgatctg	tgccgaaaaa	cttcctgtga	420
gcaggggggc	gaaagattgg	gtctccgcac	agagcgaata	agagagggc	tgaaagccac	480
tgcggatctc	gcccctctct	ccttatgata	gtattcgtca	ggcgtctctt	tattcgagct	540
atgtgcgaca	gtgaagtgtc	agacgatagc	cgctacaatg	gttgctgctc	cgccggcaac	600
atttgctgct	ctcccgtcag	catgttttc	agattcattg	cccggccgct	cgttcgtttt	660
ctccgacgag	tgccacgtat	ggaatgtggc	tgcattggca	tagctcatct	gtttcttgat	720
cttggcaggt	tcgggtacag	ctctgtgcga	aggccttgct	ccctgagctt	ttggatcagc	780
gggacaggct	gtcggcatcc	tcttcgctga	aattgacaaa	gagcagctgc	gtacggtcag	840
cttctcggca	gggaagaggt	cgagctgcat	catcacatca	taatacggtc	tgcaccgaaa	900
gaaatgccca	caccggacat	tccctccaga	cgaatatgcc	ggtgaggttg	tcgtagcgac	960
caccgccggt	aatgctgccc	tctcggcgtc	gagtgctttc	acttcgagaa	tgg	1013

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 796 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...796 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029 tgcatcaggg taaagaaatt gccgagcaga tcaacatcct cggtgatgag gtgtacccgt 60 tagctaccac gtagtcttct ggaaagcaga attgatcgct ttgtgatcct tcagcaagat 120 getttegaeg atgtegattg caacageege tegagegtea ggagetgatg eteageagaa 180 taacggacat ctgtcgacgg aattcgattt cgaagacttc ctcgaggttt cggactattt 240 caagcaatga tcaatacctt caagcaggtg aactattctc agttcaaaag tgctaatttg 300 acaaatacaa taaagagttg gacgctattc tggccgaacg cataaataaa ttaagatagt 360 tatgtcaaaa caaagctttt cagaaaatat atcgaagatt accaatatca ccaaggcaac 420 480 ctgctctttg cgtgccaccg ggtgggtaat gaagagttgg ccactatcga cggccgattg gctcaagtgg gcgtattcag ggcgaagatg taaccctgca ggtatttgcc ggtacggagg 540 600 gattcccacc gatgccgaag taatcttcat gggcaaggct ccctcgctaa agtgggagat 660 cagttggccg gccgtttctt caacgcttat ggcgaactat cgacggaggc ccccaaccgg aaggaaaaga agtggagatc ggcggtcgtc cgttaatccg gtccgtcgta agcagccttc 720 780 4 agagetgate getaeggtat egeeggtate gacetgaaca ataettiggt gaegggaeag 796 aagatccttt cttngg (2) INFORMATION FOR SEQ ID NO:1030 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 970 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...970 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030

agcgtggccc gaatgctccc atcagaatac cgatgatgat agggccgccg ctaatcccag cttgataggc atactgacac cgggcagata gaaggggaca tgccgaaaac acatcccaag

acaaggooto ogaacaaagt ggtoaaagag gattgtocaa otgtttgaco toatcacoca

aaatctcggc cacacgtcta cagccttgcc ttcgccaacg acggtcaggc ggtcgcccaa ctgcagcgaa gatctctatc cggcagcaat tctactccgg cctgtccac acgatgatat

'60

120 180

240

300

```
tgaccccata caggttgcgg attttcagca tgccgaggcg tacccgttga gcttagggcg
                                                                       360
agttattacc agcctgcgtg atacgagctg ttgtccacac tgttccagtc tatatcggga
                                                                       420
                                                                       480
cggttccaat ccttcatttc ttcttgccga agagtatttc gagctgtgag gtatcctctt
caccggagac gcgaggatgt gatcgccgaa atagaggatc atatcagagg tagggatctg
                                                                       540
                                                                       600
actitaccgt tgtgccagac ccgtgtaatg acgaaagggc gcttgagcgg agtgctactt
cgcgaacgct tttgccatcc aaagcaggat tgcagattca tactcggaga agaaagcttt
                                                                       660
                                                                       720
gggagcctcg gaatcgtctc gttcctgacc ttgggcatca taactttcag cagggccaaa
                                                                       780
gcaataataa caccccaacg cccaaaggat aggtaacggc acaggccaga cctttttcgc
                                                                       840
ctattcggcc gtggcatcgg gattgatctg atggagggtc gtttgggctg caccaaagca
ggggtattgg tagtggcacc ggccacgata cccatcagat tggcatggaa atgccaagga
                                                                       900
                                                                       960
tataataaag gaggatgcac aggagaaatg tagtaggact aatcccaagg agataagatc
                                                                       970
tggcaatgcc
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 817 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...817
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031

```
60
gtcgtacaat tcctgaaaat agtcggaagc atagtagata ttgccccagg gaagccaagc
                                                                       120
cattctatat cttctctgat ggcatccacg tactccactc ctctttcacc ggattggtat
                                                                       180
cgtcgaagcg caggttgcag acgccccgta tcgctgagct atcccgaagt ctatgcagat
                                                                       240
agctttggca tggccgtatg gagataagcc gttgggttcc ggagggaaac gtgtctggat
tcgacgtcat tcttcccttc ggacaggtct gattccacaa tttgttcgat gaagtaagac
                                                                       300
tottotttto ctotatgccg ctgttcttat tttcgttcat atcatccgtc ttgcttgtcc
                                                                       360
                                                                       420
ttatttacat tagtgaacaa aggtaatgat atgggacata aaataatcac ggggcaatcc
                                                                       480
gctcaagcag gagccaatgc cagtttgtct gtttggtacc ttgaatgatt gtgtatgaca
                                                                       540
acgaaacggc taaggacgat tatgacggag tgtcatcatg cgcaaattac tgcgttgctg
                                                                       600
cgacattcgg cttcagtcgc gtacttgtaa gttcgctcct ttctacctag tcttagtacc
                                                                       660
ttgtacttta cacattcttg cacacccaaa aggggctcga caaaaccgaa ttttgacaca
                                                                       720
gccccaaacg aatcagcgtt caacgggaga gacctttata tccgcgcgct aaatcatttt
tccttctttc ggctagcttt ctaaacagcc ccttcttggg cataggcctg ttcattctcc
                                                                       780
                                                                       817
tctcgatgaa cctgggatcc tgaatcacaa tagcgtt
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1137 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1137
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032

tatcaattct	tcccgaatct	attcataact	tcacaagcca	atcgattttc	cctttttgca	60
acggcaagca	aacggttagt	tcatgagcca	ggcctgtccc	cgaatcagtt	cggctgtgat	120
ttgtttccca	ttgagtgtta	catatatcca	ttgccgaaag	tcaggtggca	tgccacggtc	180
tettctctat	ccgataaata	tcctgcacca	gcagacagga	gctaatctct	ccccaaggct	240
ttttcccact	tgtcctacag	gcatttcttc	ccaccctttg	gttaagggta	gaggatggag	300
tcgcctcgaa	ggatattgtc	tggaatcata	ccgaataccc	caccacttgc	cgaacatagg	360
gtttgcccca	tgacaagccg	tcgtgcgaaa	tcatacttcc	tctgatttgc	ctccttccaa	420
tgtaatttct	cgttcctccc	tccgacagaa	agccgtagtg	tcttgccggc	ttccatgtcc	480
gtatatataa	agcacgcgga	gcagaaaccg	cttgccactt	catgcccgtt	atactcttga	540
gcccgtatag	tagtcccagc	agctatggcc	gtatatccga	gagctattgc	catatgcagg	600
ggatagcctt	gaggtcggcc	tgcgagtaca	aaatcgttct	gtcaaaagcc	aaagccagca	660
caagaaaaga	ctcaggcata	cttgcagcat	tcggatacga	acccccgtct	tgcgaatgtc	720
catattgagc	ggtgagcgtt	ggtcaaattg	ctcacctcct	ccaaaaattc	tccattcacc	780
ggaagaatac	ctccttgccg	gccatatccg	gacgaacaaa	cagataaagc	atgaatcacg	840
aaccgaaact	tcgccaaagg	gcaagagttc	aggaaaagga	gacgttccgt	accgtaaata	900
ccttctccat	acatatcgag	aaattcgccc	aggttcgcag	cacttcggat	tcataaggca	960
atatggagcc	attgccttca	gaccgatgtt	cagcagataa	ttacccccac	gacacaccac	1020
tcgcaccaat	cttcgaactt	ctcgcgagct	ttgtcccgaa	tagagcctct	ctcctgcctg	1080
agcgatagcc	ccatgtctca	gggaacatag	atgccgccgt	ctgccaagat	ggcaatc	1137

- (2) INFORMATION FOR SEQ ID NO:1033
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 960 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...960
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033

acgcgagtta ttacctctc	c gaagcaaggc	tgtacataat	cgaattgagt	gtaatacagc	60
agttgccaat agctaagaa	g tatttgtcct	tattagtggt	gctttcagtt	gagaagtagt	120
cagaagtgga tcagcccat	g cggtctcgat	ccatgcgctg	tatagtttgc	aaagctgact	180
ccggtattca aatgacgta	g caacctgtat	aaggggcttt	gagatagttg	tacacgtcgg	240

tataacatgc	tcttggttgt	agtagtactg	cataccgtat	ttaatggttg	gctgcctacc	300
tgggaattcc	agctataatc	tgcacctgca	atcaagagaa	cttctccaaa	taactcttat	360
ctggcatagt	agccttttca	tacatcaata	cctatcaatg	atgttcgtca	gttcttctgg	420
ggaagaagca	gacatacgga	agtatacatt	tcagggaaat	agtcgccatc	gactgcactg	480
taatacaagt	ggtaactttt	tttgttttct	ttcctttttc	tccgctaata	acgtcagtgc	540
accaaccaaa	gccaagaaga	ccggagcagc	actagctgcc	aatccatctt	gtatttcttg	600
		ggcgtttgtc				660
		tgagcctcca				720
ttttgcacct	gcaacacaag	catacgaacc	ggcgtattat	acaagtcgcc	atgatctgta	780
		tgtttataag				840
atacaaacgt	tgtgtagcta	cttcatcagc	tccttgaaag	ctacttcaat	ttcgatgttg	900
		tgcaaccaca				
960						

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 405 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...405
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034

caaaagctta	gaaaggattt	ccccggata	aatatagtag	gataccgagt	ggctatctta	60
agggtaacga	tgatgaagtc	ctgattgaag	atattgctct	aaaaagcccg	atgtggtctt	120
tgtggccatg	gggtctccca	agcaagactg	ctgatggagc	gtatgcaaag	ggtacaccct	180
aacgctatct	atcaagattg	ggcggtagtt	tcgatgtata	tacggggcgc	cgtagagcgt	240
gctccgagtg	gtggattcgc	cacnatctgg	agtttgccta	tcgcctttat	caagaagccc	300
agtcgcatca	agcgttaaga	tacatttaag	ttaccgattc	ctgttagagt	atttaaccca	360
atagnaatat	aaatttccat	tgaaaaaaaa	gtgatgtttt	ggtct		405

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 613 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...613
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035

caggttttcc	tccatgagaa	gagtggcact	ccgatcatgt	tctcgactag	cgtgtcgttt	60
acaatacgca	gaatgagaag	atcaatggtt	ttatgcttgg	cgtatgttcg	agaaagctaa	120
ggatgggcgt	tatcgtacga	tgggcgaatt	atccgatcgg	ccaaacaggg	gatgctcagt	180
actettttcc	ccgattgatc	aaccagttga	gtttctttct	gatgggtgat	ccgtccgtgc	240
gtatgatctt	cctacccaca	aagtgcaatt	gaccgcaatc	aacgggcagg	atccgaaggg	300
cagtatggaa	ctattatgct	caagtctttg	gaacgggtag	ctcgaagggt	aaggtaaccg	360
atgaaaaggg	gacattcgac	gagacattca	gtgcaaggtt	ttcctgaccg	tcttcgatgg	420
cagaaagaaa	atgacagctt	tgaagaggag	ggaaacgatc	tctctcttgn	atattatgac	480
tatcctaacg	gatgtatgcc	ggtattgccg	aggtgaaaga	cggactcttc	gaaacttcgt	540
atcgtaccca	aggatgtgaa	ctattccgag	cacgaaggcc	ggatcaattt	tatgcttata	600
acgagagcac						613

- (2) INFORMATION FOR SEQ ID NO:1036
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 565 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...565
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036

ggacaaagct accggacgagagaccatac cacatcacga gggcgaagcagatttctg ctaccaagacatttccga agggatgacattgcatgg atcaggatcgatctt gccacagggggatctt gccacaggtgatccaatg gcaccagg	ctt catcgcgaac ccc tacgaggtcc aca gaacatagca ctc ggacatatat atg ggctacgaca tgg agcgcgatgg gaa acgcaccat	gcgacggagg gatgaaaccg tacgccaagc atctataatc cctatccgaa attgaaagcg gtaaacccac	aatgatcacc tggtcgggta cgcaagaaaa tggcttccgg gttagccccg atctgaagcg attcgattac	accggcaaag tcgaagattt cgggcatggc ccggcgcaca acggcaagag tcttttcgtg aatgtggata	60 120 180 240 300 360 420 480 540
tgatccaatg gcaccgga atctggggga gatcacg	aca gtaagggtat	ctatttcctt	gcctgtaagg	agcagagaca	540 565

- (2) INFORMATION FOR SEQ ID NO:1037
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 618 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...618
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037

tttccgacct	tttgccccca	tattccgcag	gtctttatcg	aaagaaagct	ttacactgtt	60
			tttagaagca			120
			aagtacactc			180
			tgatttccgg			240
ctatgcggtg	cgaatgacac	ttgtgccccc	ttaccaatcg	gcacaccact	cggctacgca	300
tactcgcatc	ccgatgccaa	caaactcgaa	ccgccgaaaa	aagaatcggg	caccttcctc	360
ttcgacaaaa	acacgaacca	taaatggaca	aacatggttc	gtgaatttcg	agaaactcga	420
gcctaaaaat	tattcttttg	gtcgcaaaaa	tttcacttct	caaaccaaaa	gcaaaatttt	480
cccgcgccac	tttttcagaa	ccacggatca	caatcttttg	gcaccacaaa	taaaactctg	540
gagccatcgg	tctttttatc	tcagcaagga	tggtaaaatt	cgacccgata	caacaatgcc	600
ctaaaccttt	ttcggctt					618

- (2) INFORMATION FOR SEQ ID NO:1038
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 512 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...512
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038

ctttgggcta aaaagat	caa aaggctggtc gattt	ttgtc tcgcattgat tttttagct	a 60
		atttc ctgcaagacg ggggggctg	
		gcctt tcatgctata taagtttcg	
tcaatgaagg tgaatga	gaa gccaacaatc agcct	cagct attccagaaa aatgattcg	a 240
ggctgcaaag ttcggtc	gtt tcctgagagc ttctc	acttg gatgagttac cccattctg	g 300
aatatcatca aaggcga	tat ggctatcgta ggcta	caggo ctgaagggaa tattacatc	t 360
gccaaataat ggaaaag	aat ccggactacg cctac	tgtac gaaataaggc cgggtctgt	
ttcctatgct acgctga	caa cgctatacgg atacg	atage aaaaatgetg gtgegtetg	g 480
agatggattg tatactt	gca aaaatcagtt ct	1	512

- (2) INFORMATION FOR SEQ ID NO:1039
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 930 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...930
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039

```
60
attggatcga tacgagtatc ggtggcaata tcggattcta tatggcgaaa atagtctgag
                                                                   120
cggacagaaa gattctcgca catacgattt tggcggcatt atcaagttgc cctaacgctt
                                                                   180
240
gattcaagtc tggacgatgg ctttggaatg cttcgctttc atacagcttc ctccgtgaca
                                                                   300
aggccgtaca ctgcgtgtca atggctatga catcctcggt cagcggtcaa gtatagccgt
tctgcttcgg ccatcaatat agaagagac atgtccaata cgacggacgc tacgtgatgg
                                                                   360
tggactttat ctaccgattc aacgccttca gtgtggtgga tctcgcagcg atcatcagcg
                                                                   420
                                                                   480
tggcaatatg aatcgtccgg gccacctttc ggcggtggca gacgaccgtc ctgatcagac
                                                                   540
gccacctatc gcaagagaca aagtgtgtaa gtgtttttat aacgaaccga tcgaggggcg
                                                                   600
tgtcaaaatt tgattttgtc gcagccctct ttctttgctc cttgcagtgg ttaggcaacc
                                                                   660
ggcttcatct tggaggccct actttattag cttttcgaga catagaagcg aatcaggcta
agattgtatt tattctgtac agacacgaaa aacagtcaat tgacaatgaa atcttcccgg
                                                                   720
aaaatgccat gcgacatctc atctatcggt ttaacaggct cacacggaac ctcccactcc
                                                                   780
ccgacctgcc atccgacaca gagcagatag catcttccat caatagacca tagatcctct
                                                                   840
catgtgagac catagtatcc tctcatacga gaccatagta tctctcatgt aagaccatag
                                                                   900
                                                                   930
tatcctctca tgtaagacca tagtatcctc
```

- (2) INFORMATION FOR SEQ ID NO:1040
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 310 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature

#### (B) LOCATION 1...310

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040

gggcacgaat	gacacgggta	ttattcctga	ccagcatact	gcccgatgga	gtacttccga	60
taattgggaa	aatacggcat	cctttatctc	acccttgtat	aaacgagcaa	tttacaggca	120
tcgcgctgtg	gcaaagcatg	tttggcattc	gttcttcggg	caatggatag	tcgtagtcgg	180
caatggaaat	atccgtgtcg	taatcatcgt	ggtatgatat	tttgcgcggc	aaaattagca	240
aatacatggc	cgaacatgct	cttttctgag	tgtactgatc	ccattcgaga	tgttaaaatc	300
ggatttctac						310

### (2) INFORMATION FOR SEQ ID NO:1041

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 596 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...596
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041

gaggaagaac	caatccctct	cggaaaacct	acactcaacg	aactgatggc	aacccactgg	60
aaggaggaag	cgaatacatc	gaactataca	accctacgac	aaacctgtcg	ttccctctaa	120
attcgccata	ggcatactcc	gcaatggagc	tacaccacca	caactgcact	gccgactgta	180
gccgatacac	tctatcggga	caatacatcg	tctttgccaa	gaagagtgag	ggagtcactg	240
acttcacccc	caagcgcaaa	atgttgtcac	gatgagcaac	ctgcctcagc	tggcaataag	300
ggatttacga	tcggactgtt	cgaagaaggc	cttgatcaac	ctctgaagaa	gtggtctatt	360
cacctaaaat	gctcggagaa	ggaaaatgta	acagacgagg	gggtatcact	ggagccgtat	420
ctccttcgag	actccggatt	cgattccgac	caactgggca	ggcggactcc	atcggcaggg	480
atatgctact	cggctacctn	aactnccaat	cctcaatgca	gatactccca	gtagggctac	540
caataacgaa	acagaagcaa	cggaaaagct	acctgncacg	gcagtatácc	gaagaa	596

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 546 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...546
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042

acagtagatg	tttgctattc	ggagattttc	ttcaagaagt	tggatacagc	ctcaaaggac	60
gccctatcga	ctatcttatc	gtcgatcaca	tggagccgac	catagtggct	cgataggcct	120
actacaccaa	cectatecca	atatgcaatc	gtcggcaaca	agaagactca	tgggatgctc	180
gaaggctacc	accacatacc	gaaggacttc	tagaggtaaa	agaaggcgac	aaactctccc	240
tcggcaaaat	gagettaett	tcattttcgc	tccgatggta	cactggccgg	aagtatgttc	300
acctacatec	caacccaaca	ggtcttgttc	tctgccgatg	cttcggtacg	ttcggtacac	360
togacggaca	tatattcgac	aaggatatgg	attctctttc	cgctgggagg	agatgtaccg	420
ctactacocc	tecattetee	gaagtacggc	agctttgtac	agaaagtact	caccaagttc	480
aaggaagcca	tetgeetgtt	caatatatat	gctctacgca	cggcccgttt	ggacaccgga	540
cacttc	2028000801		0 0	00 0		546
Cuccc						

- (2) INFORMATION FOR SEQ ID NO:1043
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2014 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...2014
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043

aagcaatatc	gaaagetega	teatecaect	tectategte	ggatggacgg	ctgatagcag	60
catattogga	tetecceat	otaatcoota	tootooacoa	cgagtgaatg	cctattgtga	120
tanagaga	tatatatata	ctctcgactg	toragraont	atctgtccaa	gtatccggag	180
Lgaagaggag	tatgtatetg	ccccgaccg	cacacttese	acetettaac	ttctttcgtc	240
gcttcctcgt	atcaactgct	gaaaagcccc	Cgggcttcgc	gcattttggc	atacataca	300
aagtggacta	tcccctccgg	ctgcatacac	gcctnccgaa	gagcatgcgg	accgatcgcg	
caatgtcggc	tccgtcctca	tcagtctgna	ctggctggat	atgatggctc	gcaagctgct	360
gatataaggc	aggaaggatc	tgcacttgta	tggaaaggaa	cacctttttg	gaccggaaag	420
cattcggaca	cagggccggc	catatgaaaa	tggattcgat	ccgctgtaca	cttccggatc	480
torreagog	gtctatctgg	tgaaagcctc	ggcagagcag	tgtgtactcg	aaaagaccag	540
ccaatacccc	aatacagtot	octocatota	tregatetet	tcttcctcct	cagcaggcca	600
teagagatat	aacacagccc	gotocachea	capprosec	gtggaaggcg	catoggtgga	660
rgccgggrgr	gcaggiacic	gatgegetga	cggcaaccc	5 c 6 c c c c c c c c c c c c c c c c c	agateggtat	720
tgcttccatg	cgttattcta	tagaccatcg	gttcataccc	tttctcctac	ggaccggcat	780
ggtcggatcg	atctgcgaaa	agctacaatc	gcttcttccc	ctataccgac	ggtgaccgct	
cgtacccgtt	gtttctgcct	atacctacaa	acaggatcag	gtggatcttt	ccagaagaat	840
gagcgcaagt	atatcgtctc	cacggatcgc	gccatctatc	gtccgggcag	aaagtccatt	900
tetteggeea	gtgcgaccgg	ataggttatg	cgtggaggac	gcacgcgcca	tcggtggatc	960
ggaagttgaa	atcatactag	agatoctaac	tccaappaga	tcggtcggct	gctatgccag	1020
ggaagttgaa	acceptate to	tccaataact	traacctccc	gacagggatc	ttgaatggct	1080
gcagatgagt	gggacgccc	cccgcagcc	togacticce	Stangagate	caarcaacet	1140
gttcggacta	cgagtgggag	gggatacata	tecetttagt	gtggaaggta	caageggeee	1140

```
acattogaag toggootoog gagtoocgao gotgoaatgo tatgggogao accotoogoa
                                                                      1200
tacgaggcga agccaagacc tttacggaat cggtatgcga ggagctacgg tgaactatcg
                                                                      1260
gctgagcctg acccctatac gcgtcggtgg tggggtagac ctgtggccga tagggtcgta
                                                                      1320
cagcoggtga ggcagtggta gatgaatogg ggtacttogt catacotgtt tootgtotog
                                                                      1380
                                                                      1440
gccggaagga cgggaagact attcctactg cctctacacg catcggcgga tgtgaccgcc
cccggtggcg agacgcaggc cgccgtactc gaatacccgt gggaaaagaa cccaagaggg
                                                                      1500
tggacgtcga agtgggtaat acattcgtgc caacgaagac aactggcttg ccacctctct
                                                                      1560
gccggatcga cattctccct taccaatact tccggacaga cggtggaggg atccatccct
                                                                      1620
acttcctgtg cgatgccgac aatgaacgta tcggtcggct ttatacgcag cttcaggtgt
                                                                      1680
ggtgacgcct gctccggccg aatggggcaa gttgcttcgg gacagtaccg attgcgtttt
                                                                      1740
ggcgagagtg gcggagagga ttccactttg ttacgaagga cgtttatctc ttccgtccga
                                                                      1800
aagatogtoa gtttogaato cotoccaagg cotttggaca tatgtggogg aggagaaata
                                                                      1860
cgcagtcacc gccctgcccg catcctggtc ggtgctactc ccaaggatgc gatgctcagg
                                                                      1920
agttgtatct gttctacgga cctgactcag gcaggcncga tcatcgaaag gaagatgatc
                                                                      1980
                                                                      2014
cgcttgccgg ccgggtgaga tcgtcgagaa gtgc
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 653 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
    (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...653
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044

ttttgacctc	tctgcggcta	tggggggaga	ggctgaaacc	gacaatggct	. 60
ctgatgcata	ccgatcatat	acattatagg	tgggtggata	tacccgtcat	120
tggccgatgc	cttactcgct	ctattgtccg	tggcaaaatg	gataggagcg	180
actctaaata	gccttacaaa	ccctgatgat	tacgcttgat	ttccggcata	240
cgaagctatg	ccggtgcgaa	tgacacttgt	gcccccttac	caatggcaca	300
tacgcatact	cgcatcccga	tgccaacaaa	ctcaaccgcc	gaaaaaagga	360
ttcctcttcg	acaaaaacac	gaccataaat	ggacaaaaca	tggttcgtga	420
actcgagcct	aaaattattc	ttttggctcg	caaaaatttc	acttctcaaa	480
attttcccgc	gccacgtttt	tcagaaccac	ggatcacaat	cttttggcac	540
ctctcggagc	catcggtctt	tttatctcag	caaggatgta	aaattcgacc	600
gcctaaacct	ttttcgctag	gcattgtata	gagtcatgtt	ttc	653
	ctgatgcata tggccgatgc actctaaata cgaagctatg tacgcatact ttcctcttcg actcgagcct atttcccgc ctctcggagc	ctgatgcata ccgatcatat tggccgatgc cttactcgct actctaaata gccttacaaa cgaagctatg ccggtgcgaa tacgcatact cgcatcccga ttcctcttcg acaaaaacac actcgagcct aaaattattc atttcccgc gccacgtttt ctctcggagc catcggtctt	ttgatgcata ccgatcatat acattatagg ttggccgatgc cttactcgct ctattgtccg actctaaata gccttacaaa ccctgatgat cgaagctatg ccggtgcgaa tgacacttgt tacgcatact cgcatcccga tgccaacaaa ttcctctcg acaaaaacac gaccataaat actcgagcct aaaattattc ttttggctcg atttcccgc gccacgttt tcagaaccac ctctcggagc catcggtctt tttatctcag	ttgatgcata ccgatcatat acattatagg tgggtggata tggccgatgc cttactcgct ctattgtccg tggcaaaatg actctaaata gccttacaaa ccctgatgat tacgcttgat cgaagctatg ccggtgcgaa tgacacttgt gcccccttac tacgcatact cgcatccga tgccaacaaa ctcaaccgcc ttcctctcg acaaaaacac gaccataaat ggacaaaaaca actcgagcct aaaattattc ttttggctcg caaaaaattc atttcccgc gccacgtttt tcagaaccac ggatcacaat ctctcggagc catcggtct tttatctcag caaggatgta	ttttgacctc tctgcggcta tggggggaga ggctgaaacc gacaatggct ctgatgcata ccgatcatat acattatagg tgggtggata tacccgtcat tggccgatgc cttactcgct ctattgtccg tggcaaaatg gataggagcg actctaaata gccttacaaa ccctgatgat tacgcttgat ttccggcata cgaagctatg ccggtgcgaa tgacacttgt gcccccttac caatggcaca tacgcatact cgcatcccga tgccaacaaa ctcaaccgcc gaaaaaagga ttcctctcg acaaaaacac gaccataaat ggacaaaaca tggttcgtga actcgagcct aaaattatc ttttggctcg caaaaaattc acttctcaaa atttcccgc gccacgttt tcagaaccac ggatcacaat cttttggcac catcggagc catcggtct tttatctcag caaggatgta aaattcgacc gcctaaacct ttttcgctag gcattgtata gagtcatgtt ttc

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 758 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...758
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045

ccacccatgg	gagagtagtg	agtgcattct	tgaacatctg	ttcgaaacca	ggaacttcag	60
		gatggaacgg				120
		atgtttactg				180
acggaatgtg	aatacagatc	cggctctacg	atacgctcga	tgataccgtt	cttttcgaac	240
tcgggtgttg	gttgtacact	tcttctacag	agagaagaac	ttccttcact	gcttgaggaa	300
ttcgctttcg	ccggggtgct	tagcctccag	cattgtcata	attcttgggt	cttcatagag	360
aactctaaat	aatagtaaga	gattactccg	gcaaagtagc	taatgtgttt	ggaactttca	420
agccttttct	caaaaataaa	gttagtaaga	tccttgtagt	ccaaatcaca	aactaaccct	480
tccgaatatc	gctttttcag	tacataaatc	agtatccgaa	tacgtcgcca	aaagattaat	540
atattgactt	gattcaaagg	cagcatgcat	cgatggttta	atggaggtgt	tgtcggtatc	600
gaagcctcgc	caaaacgcat	accgaaacat	cctcaaagca	tagcctttaa	tctctatctc	660
attatatcca	aatgtgtctc	ggatgacgaa	cactcaccgg	ccggccttgg	tttttgaggt	720
cggacccgat	ggatagggga	gctttatcat	cctcgaca			758

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 682 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...682
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046

gcccttggac	tctccaggat	ccnccgaatg	ttctctgcca	cgccttgttc	tcattcgaca	60
cagagaccga	ctcgaaagat	gcacttnggg	ccaatatcta	tggcatagac	gccttttgnn	120
gggggacgcc	acacggcccg	aatagacaaa	ttcccatccg	gaagtagtac	ttaacccaac	180
aaaaaaccaa	gaaataagca	atgaatatcg	ataattcttc	cacaacgatt	cagggaaaga	240
ccatctcgtc	agggcttgac	gcattaaaaa	cagctttcta	agtacttta	tagtgttaaa	300
gccccgttag	ttatgtatca	ttctctattt	gaaagcctct	gcaggttccg	gacccacgga	360
tagagcgtaa	aaaaatttat	cctcttgatt	tttactgctg	atcgttttcc	tctctacact	420
ctcaggcaat	acctcttggt	agagattgaa	gattatgccg	aggaatacga	agaagaattg	480
aaaagtctat	cgaaatgctt	accggccatc	agcttatgca	taccatgcct	tctcatgatc	540
tctcaacagg	agcatcagct	ggtggatgta	gaagettttg	aggggcttta	agcgatggat	600

- (2) INFORMATION FOR SEQ ID NO:1047
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 645 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...645
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047

cagccagtgt tcccagttat	ataaaacaac	cccagggatg	cctttactaa	cccctgaggt	60
tctttaaat aacttgttcc	attoccopat	ttcgtctatg	ttcagtcatc	cgttcgtcgt	120
tgaatcggtg aaatcttttt	acaboogge	ааарардсса	agaagccaca	gacaatccct	180
gggaagttgg ctataagatt	acaceatect	tettettace	aataaaacca	tatcctaccc	240
gggaagttgg Clataagatt	agecaattee	ctgaagcgaa	tcacctttat	gtccgagaga	300
acagtogoag ttgatacotg	cgaccaccgg	tacatorcoa	tagtottocc	gtggcaatcc	360
ttggaaccaa tctgtggaat	ataagaaaca	tatategeca	ccatatttag	ttcttgtgtt	420
aaccgagaac tgacaaaaat	ttttcttgat	ctecatatt	ccacgcccag	aatatatoao	480
tagcaaagat agtattcgca	attaatcaaa	gtaggtattt	aacaaagaaa	tataccaact	540
gtcgatgatt gtttaaacac	tgtatgttgc	gccttctctg	acgetatete	attattatta	600
agctctctga ggttgtacga	gtgcagattc	gattctcaaa	tatecatetg	actactgcta	645
cacttgtgaa aattttcatg	gccgacatcc	gaataaaaga	atacc		043

- (2) INFORMATION FOR SEQ ID NO:1048
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 749 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...749
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048

ggaaattacc	ctttaatctt	ttctatttag	gcaaacactc	aaaaaataat	tttatgtatt	60
tgtccataac	ggagaatatg	cttatggcca	agataccttc	ctactgtttc	aaggccaata	120
ggtaagaata	ttcgcaaagt	gcttcgtaaa	ttatgcggaa	acagcccaaa	tatttattgt	180
tctgtccaga	attggagaga	tgaatacaat	cctttatgta	ctaaatgaca	agatatatgt	240
ttacaagttg	cacaaatgaa	agaatacgag	ttgagcgatt	attttaaaca	cttcctcgtt	300
gaaattgtag	tatacctcaa	aggagggat	tgttcgaggt	tgcctatttt	gggactttat	360
atgttttac	tctgcctcaa	aaaaaaaga	ataggtggtt	atggtgctgc	agtcgtatac	420
gaaagctaga	agttgaatac	ccgcaggaag	taacgaaaaa	atcaaaaaca	acacaaaaaa	480
acagaatcgg	gactagagcc	gggggcatag	ggaatggtta	ttttcccact	catggggatt	540
cctgcgccaa	aagctatatc	tttgtaatga	accaatcagc	gtggaaggtt	tgtaatgctt	600
gcaaccacga	gaaaaaatgc	taaaacattt	cttcttaaaa	gctcttcgac	agctattctc	660
caatggagtg	tgcaagccct	tctgtggaag	gaagttttac	aaattaaaag	cntaaagata	720
tgagctatct	attcaatccg	aatcggtgt				749

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 651 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...651
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049

```
ggctccactt cacaatccgg ctaacctcaa aggcgtcgta gccatcgaga gttgctcccc
                                                                        60
ggtattcgtc aggtgggtgt attcgataca gctttcttca aaccatgccg gaacatgtgt
                                                                       120
accgatatge ettgecatat gatatgteaa caageatggt gtaegteget atggatteea
                                                                       180
eggeaceage categeatgt eagtgeeegt gettgtgaaa tettngggtt tggaetaega
                                                                       240
caaaatcgca taatcacggc acatatcggc aatggagctt ccatcgctgc aatcaaaacg
                                                                       300
gcaaggettt ggacgtatea ttggggatga caccegtaga aggettatga tgggtacgeg
                                                                       36b
cagtggagac gtagaccccg gtgttcttac ctcctgatgg aagcagaagg cctcgaagca
                                                                       420
gcaggaatct ctgaactgat cataaaaaga gcggtgtact tggcgtaagc ggtgtgtcct
                                                                       480
ccgacatgcg gaaatcgaag atgccatcaa gaatggcaac gaaagagcta ctctggccag
                                                                       540
accatgtacg actacaggat caaaaaatat gtaggagctt atgccgctca tgggaggagt
                                                                       600
cgatgtgctc gtattcaccg gtggagtggg tgaaaccata taccacgaga g
                                                                       651
```

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...3\overline{7}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050

actatatata	ngtttggggn	acccggatac	agctttctct	atttctgcca	aagatcaatt	60
atcatcacat	tagtttgttc	tatcagggat	ttataaaaca	aggactctac	cccacggtat	120
accecace	agagactttc	caatcttgga	gacgtttaag	ctcgccatct	tggattagga	180
cgaaaacttt	castgactga	cattgaatga	caaagctgct	ttcccttcgc	tatcgttcac	240
aaaacgccgg	ggagtgtacg	cottocatto	teccagaaat	acaagtcctt	gtcgcagaaa	300
tgtgaccaag	ggagcgcacg	ttattacaat	gtcgttgata	caggctcgct	gttcttttac	360
		cegeegeaac	844844	00 0		377
caaagaaggt	gaccatt					

- (2) INFORMATION FOR SEQ ID NO:1051
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 756 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...756
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 424 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...4\overline{24}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052

ggcaacgaaa	aattccgtgt	aaacaaataa	ttcgcctcga	caaaaaatag	gctatcataa	60
aaccattcaa	aggagtacgt	cctccgaaag	aactcgtaag	caagtagcat	ctcgccccta	120
coacotcott	aattcagaag	aagctcgaaa	gaagcgaagg	gcaacgaaaa	gtcgctctat	180
catattatcc	etccgggatc	gatttccctg	taggaaaaga	tgaacacgat	gcggacgtgt	240
atgaaaagct	gccgagaact	tcagaatgtt	ccaagaaaaa	ggctggctcg	tacagacaca	300
gaagaaaact	actacgttta	tecccagacc	atgaatggca	aaagcagtac	ggncttgtcg	360
taggtgcata	totagaggac	tatatgaacg	gctgatcaaa	gaagcatgag	ctggacacgc	420
CECE	-8-6-66		0 0			424
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- (2) INFORMATION FOR SEQ ID NO:1053
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 622 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...622
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053

gacatgacta	tctccgccaa	cgtgtcttgc	aactctttgg	caatatagag	gtcttgcgat	60
ttttcaaggt	gttgcgacag	atgaaaagcg	actcataaca	cctttatcag	cctttcgcct	120
ttctcttctt	gggactcttg	aaaaatcttt	gacattggtt	cttcatttgg	acgttccgat	180
tcaacacact	gctctttaat	tgagagcgtt	ttatttcgct	ctcatttctt	ttcatgggaa	240
taccceteaa	acaagttccc	ggatggcaac	aggatctacc	ttgccgtttt	ggtttctgtc	300
atacttactt	aattttnatt	gntatacaat	tcactgttca	ttttttgccg	gtatatttac	360
ctgcaaagat	gaatacatcc	actatctaag	attgcccgat	aatggggttg	taccagcagg	420
ectacatect	ttcgttcata	cctttttgtg	ggagatgttc	attgatgtcc	atcaatacaa	480

tcgttcgatt	tatctgcttt	cacacatttc	cacgttcaag	tgaaaagaat	caaaggacgg	540
ttcttcgata	taccccctcg	cttatatcgc	tcatcgaatc	gtgatatctc	gaagacacat	
tcctncaccg	acatattcga	cg				622

- (2) INFORMATION FOR SEQ ID NO:1054
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 464 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
    - (ix) FEATURE:
      - (A) NAME/KEY: misc_feature
      - (B) LOCATION 1...464
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054

gtaatagtgg	ggcgcattcg	gcaggatttg	gctaatccca	gcggtttggg	ttttggtgcg	60
tatcggatca	gatccggaaa	ggggctgcac	tcaacgcttt	cagatagccg	aatatctcat	120
cgccaaagga						180
aaactccgaa						240
gttctttcca						300
tatcttgaat	ttcctaactg	cccaagtttt	accgatagca	atagaaaaag	agaccattgc	360
acaataactc	ttctatccct	tcatattgat	cagacagaca	caagcattga	ttcgacgaaa	420
gtaaggagtg	cttcatgcag	ttttgcgaac	cctcaagtat	ggga		464

- (2) INFORMATION FOR SEQ ID NO:1055
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 847 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...847
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055

gattatagat gagaat	tggga taaaaactta	cgaactctcg	tgcggaactg	cagctcatag	120
tagtgtagta aaagca	aagaa gtcttgttag	ggctaacacg	ttgccaatag	gagataaaag	180
aagtggggcc ttgaga	aaaa aagaatctgt	cggtagagat	atgtactgaa	atagagtgtg	240
acagtgtgag gatago	ccatc aaaagccctt	attaatcggg	atagtccagg	tctttaggtc	300
ttataagatt tattaa	attca ttggagagaa	tcagatatag	cacgtattga	agtccgcttg	360
acttttttca aaatct	tccta tctcataata	. tgaactcctc	taccattata	cccaaggatg	420
tatttatcgt ctaatt	tctat tcctgagaat	agtctttaat	cgcttttta	taccatcctt	480
tottagaata goatti	tcctc taccatgata	cgcaggggcg	tatttatcgt	ctaattctat	540
gcctgagaat agtctt	ttaat cgcttcttca	tatgatcctt	tctcacaaat	gcatttcctc	600
taccataata cgcat	gggcg aatttaccgt	ctaattcatt	gcctgagaat	agtctttaat	660
cgctttttta taccat	tcctt tcttagatat	gcatttcctc	taccatgata	cgcaggggcg	720
tatttatcgt ctaato	ctatt gccttagaat	. agtctttaat	cgcttcttca	tacgatcctt	780
totocaatat gcaact	tccta taccattata	cccaaggtgt	atttatcggc	taatctattg	840
cctggag					847

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 569 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...569
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056

gcgaattatt	acaacgtcca	agttgttcgt	acgtgcagcc	acaacagcct	gaggtaataa	60
				tgctcggttg		120
				ccgaaagccg		180
				cgcccaattc		240
				ctcgttaaga		300
				agcttttgga		360
				tattggtata		420
				cttttgagca		480
				ggtctggctg		540
	tacctagatt					569

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 608 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...608
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057

cgacaacagc cg	actgcaca tcaco	tatat gaacgt	cgcc gtaccgttt	t gatgaagaag	60
tgccgcagct cc	ttttctct ctatg	ccgct ccggtg	ctaa gttcaagac	g gcttccagct	120
ctaaggtgtg gt	tgccggac aacaa	igatca ccagaa	acac ggtcgcgat	c tgaacctgaa	180
tcctatcgtc ct	cgaactcg tgtcg	gtato aattac	agtg ctttcaatc	t ctatggttct	240
tataccttac gc	ccctgttc cgcag	tggaa aaggac	ctga tacacgcat	g ttcgcatcgg	300
cttcggcttt gg	tttctaaa aacga	aaaag caatga	aacg tttttttg	a ccaccgctat	360
actgctgtcc tc	cgtgcttg cctct	tacge egeage	cttc cttcggccg	t tcgcgatacg	420
gtgattcgtg cc	ggggagaa accat	tatga tcaagg	atgg tgaggacca	a tttcgaggta	480
attatacagg gt	ccatgcct tccgg	agata cgatcc	gaaa cgaaaagat	a ttcagaggtt	540
ctatcgcaat gg	tcgcagca tcgaa	caacg ctttcg	gaat actttgata	a tcggccgaca	600
gggataag					608

- (2) INFORMATION FOR SEQ ID NO:1058
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1130 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...1130
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058

acggtcctgc	ttgagcatgt	attgcgctgt	tgcaaatgcc	gattgtacta	atgagagccg	60
			gctgatcctg			120
			gaaactatta			180
tgatcgctca	gtcgttatat	tctttcttat	tccgacgcag	taccttgtgc	ttccccggac	240
gaataaaagg	agcagctcta	tcccatcgcc	gctttcatcc	cgataaagcc	cctgaacagg	300
gccatttctt	ctccatgtct	gacaaccata	ttgtccggta	cggaagatga	ctgcgacaga	360
aagagaggaa	atgcagcgca	tccagcagat	tatcttgccc	attccattgt	tccccaccag	420
acagttcact	ttgggcgaaa	acggcaatcg	gcagctgcga	tactcttaaa	attgacgata	480
tggagttctt	tatgatcatt	ctcgttgggg	taagatagag	ggtggaggac	tgtctcgcct	540
tctgtcaaac	gaatacctac	ttccgtgata	cctgaaagag	tcggtacctc	atattgtgct	600
ttaactctat	cttataaaga	cccgaatagg	gaaaacggcg	gagatcggca	ggcgaaaccg	660
gttttgctgc	ttggcaaccc	cttttcgttc	cactgttgcg	gcttgtcggc	caaagtcaga	720
tccacagagt	ccgcaagatc	agacgctctc	ccactgaaac	ctcgtatgcc	aatgccaaat	780
cgcgtattca	taccgattgt	catggcggat	cagcagctcc	aaagaatatg	agcagtatag	840

tccggtatga g	ggatttcgta	gtcgagcaca	tcgcgcttct	gcaccttcca	tgaggcacct	900
gacgatacag 1	tattcoctco	tecttacnet	agtgcaagac	acaagccaag	catatcccca	960
atgcaaccag	aaaaaaacto	ttgcgccttc	ggacttgctt	tcgtaccggc	aagcacccat	1020
ctccctttat	ccttctttct	cttttcctgg	tcggctttct	gacgtggaag	tgctttgacg	1080
cggtggtctg	coccectooc	caccacacet	ctggcttctt	tcatacgtcg	_	1130
CEELEE .	CEECHCLEE	0000000	. 30	0 0		

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1373 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1373
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059

```
agccataaac tgcggccgta tttcattatc tttgttccat aatcatggat attatgaata
                                                                        60
                                                                       120
acgateteca atttactatg gtagetaaga ceetttatgg ttggaggatg tettggetge
cgaactaaca gccttgggtg ctgaggagta accgtcggcc ggcgtatggt cagttttcga
                                                                       180
ggagataaga ggatgcctat cttgctaatc tccggttgcg tacagcactg cgcatattga
                                                                       240
aaccttaata actttccatg cgaagacgac agatgaaatt tatgaaaggc tcagcttttc
                                                                       300
                                                                       360
gattggacga ccgttatctc atcggatcaa actttctcca ttgttccgtc gtttattccg
                                                                       420
attcgttcaa gaacagtcag tatataagtt atgtaccaaa gatgctttgg tggatttctt
                                                                       480
cagtgatcgt gagggcaaac gccctctgtc cggctctcca atcccgatat tttactgaac
atacatgtgt gcacgaggaa gtaaccctgt cgctcgatag ttcgggcgat agtctgcaca
                                                                       540
gcgaggctat cgtgtggccg aaacgactgc tcctctaaat gaggtgttgc tgccggtatc
                                                                       600
ttgctcaaag ccggttggga cggtagtacg gatttgacga tcctatgtgt ggatccggaa
                                                                       660
cgttcctgat cgaagctgcc ctgattcatg caatattgct cccggtatct ataggcgagg
                                                                       720
ctttgctttc cagcgtgggc ggatttcgat ctcgatctat atgatgagtt gttccatgac
                                                                       780
                                                                       840
gacatgcgga acgtgtattc gatcatatca tctacggttc cgatattttg ccaaggccgt
                                                                       900
ggctgcggcc agaagtaacg tggagcgagc cggtcttggc agtatatctc tctgagtgtc
                                                                       960
cttcccatgc agcagcgtcc gaagcctgaa tcaaggctat gctggtgatg aatcctccct
atggagaacg tatcaaagtg aggacatgca gcagttgtat accatgatcg gagagcgact
                                                                      1020
                                                                      1080
caagcataat atgcaggttg ctctgcatgg attctggctt tcaagccgga gcatttcatc
atatcggcct tcgtcagtct catcgagaaa agttgatgaa tggagcttgg aatgtgagtt
                                                                      1140
                                                                      1200
gcgaggttat gaactctttg agggacgacg cgattctttg ccgaaagaaa aagtcgtcga
gccgaaggag aacaaggcgt aggacgagaa tcgaccgtcg tgacgtttct gccggaaggg
                                                                      1260
                                                                      1320
aaaaacgctc caacccatgg atcgagaaaa taagtctcct tatcgttctc ctcgtcctga
                                                                      1373
taacctttca gaacttccga taaaaggaaa aaagagcata atgatgagca gca
```

## (2) INFORMATION FOR SEQ ID NO:1060

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 770 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

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- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...770
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060

gcattccact gtacgggatt ccgtgacggc cattccgta cattcccatg agagtgccga ctaccgacta cgatacgggg cagcttgaat tgggctatgc cctcgtatgc cggagattga attcctaaga ttagaggtcg tatccggtca ggcctcgcga gcacgcgagc ttattgccaa tccaggttgg aaccggtcgt tatatatata	gtgggagtcg aaacgacttc cgtttggttt tgataggatt tttgatcaac ggaggggtca aagagcgatt gcatggtcat acatttgatc	tggccaaact ttgaccatga tagttaactt taatccctca gtcatgatat gtccgaaata ccgggccgat ggggaaagcg agttcgaagt	atatcgacca gtccggacgg tttgatgaaa tcggccatac tgttgatgtt cgtattccac tcggaaaggt actccttcgc gaatatccca	categeatee gegageatee tgageatagg egecategtg agatgaatag tteettgtaa aegateagge agaegaacaa tegttgtaet	60 120 180 240 300 360 420 480 540 600
tccaggttgg aaccggtcgt tatatatata gcggaatacg gatggagtcc ctctcacgat ttcagcacgg gaggcctttc	ctctcctgaa tgaacagaaa	aaccgccgaa ccttccatcc	gtgagactgt tgacgttgat	tgaagacata	

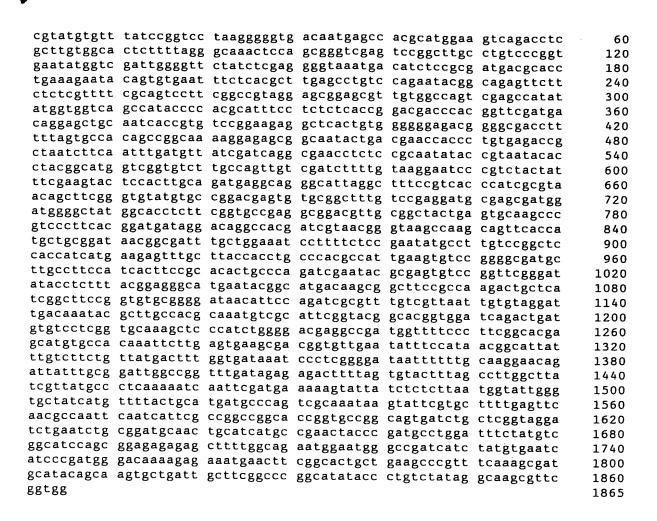
- (2) INFORMATION FOR SEQ ID NO:1061
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 504 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...504
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061

tatatccatg	caggatatag	ggctctttcc	caaaacaggc	aatactctcg	catcggtcaa	60
gaatatgccg	atgtcgtgca	gcatggcagc	ttcttcgaga	agagacgatc	cgcctgaagc	120
tcgggatgga	tttcgacgat	acgaagacca	aggccgccac	atcacggcta	tgctctacta	180
aaatatggta	ttggttgttc	cctcagtgta	gtacttattg	atgatgctga	teggatecat	240
catttgggaa	agagagttag	acgggaagtg	cccggagccg	ggatcgaacc	ggcagaattt	300
gcattcattg	gtgtttgaga	ccaacgcgtc	taccaattcc	gcctccgggc	aattgtcttt	360
tcgaatacgc	gcaaaggtag	aaaaataatt	catccgcaaa	tacttcttga	taaaaggagg	420
tctatgggtc	aaaaagatgg	atagtatcga	agagagaaag	tetctcttcg.	atgctgcccc	480

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 661 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...661
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062

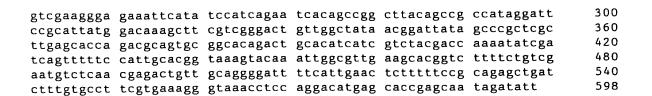
gttcgttcgc	aaaccacagt	gacaggagta	caacccaagc	tatctctcgc	tttgaccaaa	60
tgagcaattc	gcccaagcga	tttaccatcg	tgggcttggg	ggacggttta	ttcttaaacc	120
traaaragag	cottattcgc	atctcccgaa	ttggaggatg	tgtcaatgca	ccttgcagag	180
attoccaaga	tagaaaagtt	cctcatggac	teateceatt	tagcgatggc	gaactatgct	240
attactage	cacatagacc	dascadaca	200002222	ctcccaatgg	aagaatgtgc	300
						260
cagctctcag	agcgtctgac	cgaatataaa	tacaaaggct	caccgagcag	gtagccaagc	360
				aagtactggg		420
				attactcgct		480
anaanaa a ta	atatcaactc	actccagctt	aceacctect	gtctacggca	cttgtattct	540
						600
gaggatacag	aagaacttgc	attgaccctc	tgtggcaaaa	agcgcaaatc	actcgccaac	600
				tgtgtgacaa		660
7						661
<b>x</b>				· · · · · · · · · · · · · · · · · · ·		

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1865 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1865
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063'



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 598 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...598
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064

ggctgtatct	ctgtcagact	gttccgatgg	attcgccaca	gctgagggac	agccagatgc	60
aaggccgtat	ctatggtacg	aaggagccga	tcgttgtcca	tggcttgcct	atgaagtcga	120
aagctccaag	cctcattccc	tccactgcag	tggaatcgaa	gcccaagccg	tcatcagtat	180
gacagggcag	gaagtgatat	ctgcatcttc	tccagtagtt	ccaatccttc	cctgccggag	240



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 547 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...547
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065

gcgaatagcg	aggcaacttt	gaatgaatgg	tgcgactatg	cacacccggc	ggcatcgtga	60
gggtagaagg						120
ccggattaca	ttcgaaaatc	aagaaatgaa	ggaacgatcg	tcttgatacc	caagcccaaa	180
gtctcgctgc	ctcatggtcg	gaatcggtgc	cttgcatccg	aaccgaagcc	gggagggaat	240
ttatctttgc	gaagaagacg	acacctttgt	gtctcacgat	ggtaacgaag	taacataggc	300
ggtaaacctt	tcttgctcaa	taccaacgta	aagattgtgg	gggcgtatct	caaaagtatg	360
ccgtgggggt	aggagaaatt	cgattcctgc	agtttgtgcc	caaacagtat	cacaacaaaa	420
atgaacacaa	gatgaaacaa	aaatacttgg	catacagctg	tcacaatgga	caaagtgttt	480
tctttcattc	tcctgattgc	aggatgtaca	ggagcattat	cggggcagtc	ttccatcaca	540
tcgagag						547

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 970 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature

#### (B) LOCATION 1...970

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066

```
gccgcaagtg tcgttttcgg tgcagaggca caggtcacag agtcggggct ccatattgga
                                                                        60
aggatattcg tacggtaagc gtaaacaaag aaccggcggt tcgtccttta tgacctatgc
                                                                       120
cgaccgaagc gaagctctca ccggcaatat gagaagagtt cgtactaccg tcttctgaac
                                                                       180
ggcacgtggc gattetttat geegagageg aggeacatet geetgeegge ataaeggata
                                                                       240
gctcgcaaat acaaagggat ggcacgacat ccaagtcccc ggcaactggg agatcaaggg
                                                                       300
cacggtgtgg ccatctatac caatcacgga tacgagtttc agctcgcaat ccgcagccgc
                                                                       360
ccaaactgcc ggaagccaac cccgtaggtg tgatcggcgc gagatagaag tacccacgga
                                                                       420
ctggatggag cgcgatatct actccatata gccggagcca agtccggact ctatgtctat
                                                                       480
                                                                       540
atcaacggac cgaagcgggc tacagcgaag actccaagaa tccggccgaa ttcctcatca
                                                                       600
tccctatgtc catgccggaa aaaacacgct cacgctcaag gtctatcgtg gagtaccggc
togtatotgg aatgtoagga ottotggogo atoagtggat ogaacgogat gtattootot
                                                                       660
ttgcacaacc caaggcggca gtgaagattt cagcatcaaa tccacactcg atgatagcta
                                                                       720
ccgcaatggt atatttccct gaaagccgac ttacgcaacc gccgtggcga agcctccgag
                                                                       780
ctattctgac atacgaattg ctcgatgccg aaggaaagac catcgccacc gaacccgttc
                                                                       840
gacceteata getgeeggeg gagagegtae cetetette gageacagee gggtaeggta
                                                                       900
                                                                       960
catacatgga cgtcggagca tccctatctc ttaagctctt gatgacggta cgagagaaag
                                                                       970
ggaaagtcac
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 885 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...885
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067

					+ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	60
ggaactcacc	atcgacgaga	ttgtggaggt	gaacggtgag	aagiggatai	LECEAGGE	
cacaagacac	aggtgccgta	ccaagtgaaa	ctgctcgagt	acccttgcaa	atcatcgaca	120
gataccgacc	gttccaaaag	gacaactcat	attcggggac	atcaactact	ggacggtctg	180
caagaagctc	aaaaaatcat	cagcgagtgc	ggaataacaa	aagacatctc	cttccattgc	240
gcaagcacgg	ctttgcgaca	ttggcactca	gtaagggcat	gccgattgag	agcggagccg	300
tgtactcgga	cacacgaaca	togtaaccac	gcaactctat	gcgagataac	caccgagaaa	360
ctcgacaccg	acctctccat	gctcggcagc	aactcaacgc	ctcatttggc	tatatcaaaa	420
toocatoaca	atgaaaggga	appcataaac	agcaatgtcc	gtcagataat	cacggtggac	480
naacatnaaa	catcaccuta	cccaatgaag	aaatatooat	gagogagtat	gagattgcca	540
gaacacggga	cattactgta	. t t		0-0-0-0-1	caggataga	600
cctgctgggc	gtattcggac	ataccatccg	cacgcaggtc	aagaagatta	Cagggacgga	
ctgctgcact	cctgcacggc	agagaggaac	atcagggggc	ggagggtcgc	tggcttgatg	660
tgtacagcct	tgaaatggtc	atagccttgc	gttccgcatc	aggtcgcaaa	gggcaaaaag	720
gcttcgaaag	catgtatcgc	aatgctgacc	gaacgacacg	gaggctttat	catgttcctc	780
CCAPAPAARC	aggttgttcc	tgctaaaaca	gcctgacagg	gtttatagag	gttgtcccca	840
			tttggtggct			885
LIBACACAAA	999 caaacc			00-0-		

- (2) INFORMATION FOR SEQ ID NO:1068
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 962 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...962
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068

60 ggattgatgg agtggatggc aatgctgttc cactgcccaa tgtattggtg accatctgaa 120 agaccggaat gttttggggc atggtgctct gttcttttag caaatggaat agttgctacg ggaaaatctc ctcaagaaat tgctgaagtg tggctgtcgg cgaagtagat cttacctctt 180 240 1 accepttetg ttetgeaatg teattgeaga tacattggea cegeteataa eaggagggat 300 gcaaaaatag ctgccaacag aaagagaaga gaggactaca tcgagactct cggaaagggc ctagacctta tototacgtt attgttgcta ccggcaatat atagaagacgittgttcaagc 360 420 ( acaagcaget getegeeaag gageegatat tatgeegtaa taegtaetae gggaeagagt 480: ttgctcgact atgttcctta cgagctacga cagaaggatt cggggggtact tttgctacac aagaaaactt cgtatcatgc gaaaagcctt ggatgaggtt ggagaagagg ttggtcgatt 540 atcaggetet geaactattg tteaggtett tgeatgeegg aaatageeta atgggageae 600 660 tcgaaggctt ggatgtaatg ctcaatgatg ctctctagga attctttcc gagacattaa tatgcaacgt actttggtgg atcaatcatg agtcgtgtta tcaatggatt tgccggcgtt 720 atcatcaata coggtaggat aactacctaa ccactgotga tgoogtagaa gaagcacata 780 ccgtcttgcc tcggatttga tcaatgagca gctggctctt acagccggat tgcttcagaa 840 cagatggggc ttggacatgc atttgaaatg gatcccatgc tcagaatgga ttccttttcg 900 aattggctca agcacaaatg accagagaaa tttcccaaag ctccgctitaa gtatatgcct 960 962 CC

- (2) INFORMATION FOR SEQ ID NO:1069
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 623 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature

## (B) LOCATION 1...623

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069

gaactcacot	taaagtagat	tatagaaaga	cccagtaacc	caattgtaga	ctatcccggc	60
ccaactggtC	aactttttc	agtacacgnt	caaactttcg	gtttggcgcg	ggagcgaaaa	120
aattotoace	ccactgcgaa	aaaattccgc	gccgcttttc	gggaaaacac	gcgccacaat	180
coonscettt	ctggttgtat	ttccgaggct	gtcagttgta	gactttccga	caatggtgta	240
gctctactcc	tccatcctac	aggctcggcc	aacagacaag	cacgacatcc	ccaccattgc	300
cctcgcatca	gactgatgag	atcgtgactg	ttgatgcagg	aaccataaaa	aggaatttt	360
ttcggattca	tttggcgcat	aacaaaaaa	gctacctttg	cagcgtcaaa	atcagaagga	420
ectttccttt	tgatgggtat	tactccgtag	ctcagttggt	agagcaaatg	actcttaatc	480
atteggtcgt	agttcgagcc	tcaccggggt	cacaaaccaa	tagcagaggg	ctgtgttgaa	540
tagtttttt	gacacggccc	tttaactttt	ggatcggggt	tcgcctttgt	gaaaggatat	600
	tgtcaaatgc					623

# (2) INFORMATION FOR SEQ ID NO:1070

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 930 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...930
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070

ctttcatttt gtattcntga tacattcaat ctcctccgtt ttatttcaaa ttatgccac atagacaaca cacagaaggg aatgtctatt tacgctttat ccgtggcgac cccagcaacg	tctgtcgttt gcgatgcaga tcgtaaccct tgatgctcgt tagttacatt aagatgagct aggcaagcca acgcagttcg cggagatcaa ccaagagtgc atccgcatca tgcctggct	ttttctaaat aaaatgaaga ttttgctttt tcttgcttac ccctgcattt tagatttacg cgtgccaaga ttttctctga acgtaagttg aagaacgaga tcttcgttct atccaccacc	ttgatacacc	gcaaaggtac aaacctatga gttacgattt gtaagaaaat ccctaattct tggagaggta ctattaccag tataagcccg atcacatcca gcaatggtgg tgggaaccgg	atacgaacaa cacagttgtt ggtaacggaa gctaatgata taatgactga ctcggatcat aagttcgatg gaggagaatc tcgcatgaag acgccatgaa ggtgtcaatg ttcggatttg	60 120 180 240 300 360 420 480 540 600 720 780
ccgtggcgac cccagcaacg gagcacgcaa aacaagtncg	atccgcatca tgccctggct cgggcgttgc atgtgattat	tcttcgttct atccaccacc cgtgccgtaa	acttcgatgt ttgatacacc gggcaatatg	tgggaaccgg tttggcgtcc attgccaagg	ggtgtcaatg ttcggatttg agttgcggat agttcaattt	

## (2) INFORMATION FOR SEQ ID NO:1071

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 537 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...5\overline{37}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071

tcgatattcg	tcagttggta	cgaggtgcag	ccgatatgca	agccatgacg	cttcagacat	60
		ctttacgata				120
		ggccaattcc				180
		gcgagggcaa				240
		ttccatggga				300
		gaaaatcaag				360
		ttctggccgg				420
		tatgtagatg				480
		ataggggcag				537

- (2) INFORMATION FOR SEQ ID NO:1072
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1801 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1801
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072

tcgtggaacc gacttctcg	g ccaaataggc	aagcgccgat	aatacctctt	ggganccaac	60
atctccatcg atggtatgc					120
cacgggagta gatcggtct					180
aatgaatncc ggtatcact					240
gancgggcat ctcatccgt					300
ccaagcaagg gtctgctcc					360
cctatgtggg gaagggatt	c aaagtgtcca	aggcggggca	tccattcata	cgggaataga	420
cttcctgcac aacaaaccc					480
catgccagat tagcgatca					540

```
gatgcagacc ttttccattc aagacagcaa atcggatcag ctcgtcaaga gtatgaagag
                                                                       600
acctacaact ccaagtattt gcgttcttct ctttcctcga tgccaaagtc cgcttttcgg
                                                                       660
gtagttggct caatagtata gactggttct ctctgccgac tatacttccg atctgctcaa
                                                                       720
aaggaagaaa tactaatcag tacgagtggc ccgaagagta tgcccgtagc taccgaaagc
                                                                       780
ggagacatga aggtgttttc ctcccttcgg cctactatgc ctactatgaa ataacaatca
                                                                       840
gccgctctat ttcttcagcc gtttcaaagc caataccgat ataacttcac cgaacgtcat
                                                                       900
caccatcatt tgctgtacgg gctggaagct ccagcagtaa gaatatcggt aggggagtgg
                                                                       960
tggccgatcc tactcgtccg cttatccggg aaacaacagc tatatccgcc ctcgtcccaa
                                                                      1020
ctataatatc cggcttcggt ctatgctgca ttctttgtcg aggacagggc ttctgtcgat
                                                                      1080
ggggagccaa taggctgggt attcaggccg gactgagggc tacgcattat tcaatctgcc
                                                                      1140
ttegteetat geeetetete ggaagatget gatagacege gtateaagge caactggeag
                                                                      1200
tacagagccg aacatctgtc gataacctgc gtgccggata cggtatggaa aacaagttgc
                                                                      1260
ctacactgga tcattgtatc cggacaagat ctaccgtgac ttcatggtgc tgaatgccta
                                                                      1320
tatcagaatc ccgaactgga tcatctcatc acttatactt atatccacaa tccgagaatc
                                                                      1380
ctgctatcag ggagaaccgc aatgtcaaaa aagagatcgg ctagatatga cgtacaagcg
                                                                      1440
tttcgacttt tctttgacac tcttccacga gaatcgcgac gcggtttcga gtatttcgac
                                                                      1500
tectatetge etatageete gaeegetata ecaagetgat ageeeetett eeteegggae
                                                                      1560
                                                                      1620
acaaaccgag aaggaggatt atattcagga gcatcacaag gatttctttg ttatcccacc
                                                                      1680
gtgcagaatt ctgccaaagt agtcaagcgc ggtatcgaat ttcgttgcgc acaccttatc
tgaaagccat caatacccaa gtcgaagtca atggacctat taccatacgc tctacgcttc
                                                                      1740
gggtatccct atcatgttcc gaccgatagt gtcggagtac gagcaggctc tctatcctta
                                                                      1800
                                                                      1801
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 611 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...611
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073

```
agttgtaaat cccccttgag gagctgcttg cacgagctcc tcaagggtgt tataccttat
                                                                        60
cctagagatg aggacataat tatccccggg gttctgtaaa attaaaggcg atgctttcaa
                                                                       120
gaatgttttg agtatgggtc ttggcaatcc ccggtatcga catcgtccgc catgaaacca
                                                                       180
ccggcgaata ctgccaaggt gcgttcgatg gtgctccgta tctccacaag gcttgcatcg
                                                                       240
acaagaccct ttccctgacc gaaatgtgat ggcgggaaag ttgtttgtta aactcgccaa
                                                                       300
tagtttgtcc atgagcccca actctgtcag tgccgaacga aatgactgat ggtgctgtgg
                                                                       360
tcgggagata cctcttccat agccccaaga atgggaaaag gtgattgaat cattgatgcg
                                                                       420
ctcctncaaa gcacaatcac taggttgtac catgtcttcg gaagcaacat cttgaataag
                                                                       480
agaatcacgt ataagccggg cgccgatggc attttgtcgc ttcgtgtatt tcttgttgac
                                                                       540
aagcgtcctg atcggacgcc aatcgataag cctgtcaacc tgattgagaa gtcgttttgt
                                                                       600
gctttgcgat a
                                                                       611
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 842 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...842
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074

caatgagtgc	caatcatgac	ttatagcgga	atgaaacttg	gtcatcgttc	gggcatggcc	60
gaaggccacc	ggaacgctct	atcccctgtt	ggctccgcca	taggtgccgt	aggaaccttt	120
totcacaget	agcgatactt	tggtccatat	cctctttcgg	caagttgcag	gcaggagtag	180
ctcatcagat	coototoato	cccaetgect	ggctgcagcc	aatacggcag	gagctacggg	240
aggaagatca	tttcgccaca	gagcattgcc	attgctacgg	catcttgcaa	ccaaagggcg	300
aggaagacaa	catectecst	tctgccattc	cttatgctct	ctttatgtgg	tggtcgtagg	360
tctgatggtt	tacttcctgg	cctaaggcta	tattataatc	gtataatcgg	cggtttgcag	420
tcagtattta	caagaggtet	togaacggct	tctccttacc	ggagaccgtt	gcacaataac	480
cttccacctc	tcatatcgat	caagacagac	acaagcattg	atttgacgaa	gaaaggaaga	540
tttcatgcaa	tctcttcaaa	gctcaagtat	acctctgatg	gaaacttggg	aaatttctgt	600
ttacttaata	occatatett	gaggtttgat	ctttcctaaa	aacacttaag	aatcagctct	660
acaacaaaa	acttcaatga	aagtccataa	aatagttgca	aatagctgat	agttagcgca	720
ttastaggs	cagaacaget	gacaatcgcg	tcctgcatcg	tgcaggaagc	aagaatcagc	780
taacatcaca	tectacatea	tocappagea	agaatcagct	gacaatcgcg	tccgcatcgt	840
	cccecacca	-666-6	-630-6-0	G	5 0	842
gc						

- (2) INFORMATION FOR SEQ ID NO:1075
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 267 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...267
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075

taacgctttg aaag	gagtgc gtctgcaaat	gttacatgtc	atcggtattc	ttggattggt	120
atgccatggg agga	atatta tgctgnttta	atactcaaat	atacaaaata	actccctact	180
	cagcaa aatacacaco				240
ttgaaatgct acaa	cccaaa gagctat				267

- (2) INFORMATION FOR SEQ ID NO:1076
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 593 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION  $1...5\overline{93}$
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076

gcaggaagca	agaatcagcc	gacaatcgcg	tcctgcatcg	tgcaggaaga	agaatcagct	60
		tgcaggaagc				120
		tgacaatgcg				180
		cacctatcgg				240
_		acctcaagta				300
tgtttgctcg	atgtccatat	accggaggtt	tgatctttcc	caaggcacta	agaatcagct	360
		aaaaatcccg				420
		ttatataaat				480
gagtgtagat	ttcattgtca	tttaatcatt	tgtcaaagag	ctttacaaag	ggaccgaagc	540
tctatccatg	tatataaatg	ctcgctgaaa	gcaagttcta	tcggcattca	atg	593

- (2) INFORMATION FOR SEQ ID NO:1077
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 467 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...467

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077

ccggtgagta ccgtttcgct ggtggcatgt accatggctt ctaccatatg c	ccgtctttga 60
ggaactggac gccgtcgatg cttgcacccg gtatggtgtc tgctcgaacg t	tttcggggtg 120
catgaagttg tatcccatct cgtcctgtag aggtactgat agggacgtcg t	ttctattctg 180
acctettega cettgageeg etgtteeagg tettategag gataegteet g	gtagccacgt 240
tettggtttg gtgeggaega aageegggee tttgeeggge ttgaegtgaa g	ggaatcgacg 300
tottggtttg gtgcggacga aageegggee eeegegge tagaaagtet g	eccettetae 360
atgaagtagt attgtccctc aatttcgaga cacatgccgt tgcaaagtct g	60060060
ccatttgggt ataatcgctt ttttaatgat gagaaagggg taggggggggg t	467
actgccgatc cttcgggata tggcaaagcc tcctgttgcg gaggcaa	407

# (2) INFORMATION FOR SEQ ID NO:1078

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 479 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...479
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078

ggcgatataa	ggtttgagaa	aagccttgcg	ccggatctcc	gccaatccgc	tgaatcggaa	60
ggaatctctt	ccegtacgat	ctgctcgatg	gccatccctc	ctcatttccg	atcataaact	120
ctatotccot	aagtgaagta	atcttttggc	ataggaaata	ctgtcgagca	tctcgttgga	180
aagacgacga	atcagcccag	attttctttc	gtgaaggtat	tgtcacagtc	ggtcaataca	240
gcagctagtt	atcattgccg	aaaacggatt	tgaactcctc	cgtcttgatg	atcaaggatc	300
atcetegaga	aaatagteet	cccaagaggt	tttgatacta	aggaacgcaa	tccattgaat	360
ecceegaga	одададаода	aaaacctccc	aaacaatcca	acgcttgcgg	ataatccatt	420
caccacaata	actasaccac	cottaatoco	ttctattttc	attgctttgt	ctcgttgtg	479
LECCALEALE	gctaaaccac	~6~~~~6~6			0 0 0	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1708 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1708
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079

```
60
geggggtace eegegacett etactegtae gattactget tgategeeet atgtaattet
gataatctca tgatagcgca aaaatactaa ctaaaccatg aataaacgag aaatacaatt
                                                                       120
tattattaaa gagactgttg cacaataccc tctccccctc tcatattgat caagacagac
                                                                       180
acaagcattg atttgagaag aaaggagaag cttcatgcaa tctctctgca aacctcaagt
                                                                       240
aatctaaaaa cacttaagaa tcagctctgc ggcaaaagac ttcaatgaaa gtccataaaa
                                                                       300
tagttgcaaa cagctgatag ttagcgcatt gatgggagca gaacagctga caatcgcgtc
                                                                       360
ctgcatcgtg caggaagcaa gaatcaactg acatcgcgtc ctgcatcgtg caggaagcaa
                                                                       420
                                                                       480
gaatcaaget gacaategeg tetgeategt geaggaagea agaatcaaet gacaategeg
                                                                       540
tectgeateg geagggagea agaateaact gacaategeg teetgeateg tgeagggaga
agaatcaact gacaatcgcg tcctgcatcg tgcaggaagc aagaatcact gacaatcgcg
                                                                       600
tcctgcatcg tgcagggagc aagaatcaac tgacaatgcg tcctgcatcg tgcagggagc
                                                                       660
aagaaacagc tgacaatcgt ttcttattct cgcctatttg acgaggaaag gagtacttct
                                                                       720
ctgatggaaa cttgggaaat ttctatttgc tcggtaccca tataccggag gtttgacctt
                                                                       780
toccaagada ctaagaatda gototgoago aaaagagoto aatgaaacto ccagcaacag
                                                                       840
                                                                       900
tottacogoa gatacgatti otacaagaaa taatatgoga aggoaagact cotatatooa
                                                                       960
aggagtotgo goottotttt ttotaaacot cactttttag gototgotta gtgtoggaat
ttttttacag atgagtcgtt tttctatttc ctttccgaaa accgcgtcct gtatcgaagt
                                                                      1020
caaaatcatc tcatcacctt cttcccaacg attgcgaatc ctgctttcgg; aacgaggttc
                                                                      1080
ccggcattgc gttgcgacgg aacctctttg tgttgtttag gacgcggttc tttcgctttt
                                                                      1140
catcctgtct gccttgattg gaggcggagg gagcgaccgt tcctcatatt tgcgcaggga
                                                                      1200
                                                                      1260 <
gatttcttca cgaatgagat ccttgtagga atgtcaatat catcaagaag aacaatgtct
                                                                      1320
ttttcgcaga ccaatccgtt aagcgagcga ttcgaccatt gattttcact cttccttcgg
                                                                      1380 ~
tgagtatttc tctgcttcgc ggcgggagcc gagtccggca tcgctaatca gctattaatt
ctcagtttca tctgaattca aatcagtaag tgtggaaact atttgttaat gataagttga
                                                                      1440
ggttcaatct gagtacggca tgcataatcc tgcggaagca gggtttattg ccgaaaacgg
                                                                      1500.
                                                                      1560
agcaaggccg gcaatccaat ctgctccgat acaatcttct atgcgctgac catatccgag
aaatcctgtg ccggatgcgt ggcacaccag atggagataa ctcgtgtacc taccaatatg
                                                                      1620
                                                                      1680
cgaagtgcat attggcacta tccattgaaa ccatacagcg caaggctgaa taagagatag
                                                                      1708}
ctcttccgga gcgacagcag accggcaa
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2419 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...2419
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080

ggcgtatcgt ggagcaagga cgccacgatg aactgtatgc cctgggaggt actacacgaa gctatgcgat atgaacgcag aatgagaaaa tgatactttg tgaagaaaag aaaaccgatg

```
gactacaaga ctcgcatcat atatgcctgt tgaaaagcag gctgaaaacc atcgacacct
                                                                       180
atgcctctcg agctgagaaa tacaagaccg ccagctcagg cgcatcctgt cgagtgcagc
                                                                       240
                                                                       300
ctacaatcca ccggtatccg ctacgggttc aatcgcataa gctcgaaaga gtgtttgctc
gcaacgtacc tgttcgcgat tacgaatcga cacaagccga aatgaacgaa tgcttcgtgg
                                                                       360
cgaaaaagac gtgctctgtc cggggcgttg taatggtttg ccaaaagcag cggcaccacc
                                                                       420
aatagcaaaa gcaagttcat cccgttccat accgccacct gcactattgc cattatcaag
                                                                       480
                                                                       540
gggggaaaga tooctatogt tatacotaog caatagacot gacagtogtt tottcaogat
                                                                       600
aaagggttgg tactgggtgg cagtcacgcc cctgtatcca tgaatgccat atacaagtcg
gcgacttgag tgccatcctt gtcgagaata tgcctgtctc ggcaactgca tgcgcgtacc
                                                                       660
ctcgaaagaa acgctcttga tggacggtgg acggagaagc tcaaagccgt agttcgcgaa
                                                                       720
gtggcgcatg tacgatcgga agcttgtccg gcgtaccgtc ttggatcctt gtcttgatca
                                                                       780
aggagtactc gcagctacag gccgagagac tttgtcggat gtatggccgg aatggaagta
                                                                       840
tttttccacg gcggtatcag ctttgctccc tatcgagcgc agatgagaag ctgatacctt
                                                                       900
cttcacggat gcagtatatg gagacgtata agcttcggaa ggtttcttcg gtattcagga
                                                                       960
tgatccgaag gatagcggta gctgctgatg ctcgattacg gagtttacta cgaattcatc
                                                                      1020
ccgatggaaa tttcggccgc cccgaagcgg aagccatccc actcgaagga gtggaaaagg
                                                                      1080
gcgcaattat gccatgatta tcagtacgct cggaggactc taccgtttgt actgggcgat
                                                                      1140
                                                                      1200
accgtacgat tcacatcggt gaaaccatac aagatatcat caccggtcgc accaagcact
atatcaacgc attcggagaa gagctatggt agacaatagc gacaaggctt tggcggcgac
                                                                      1260
atgcaagcga tttgcgtgca ggcagtggac tatacggtag cgccccactt tttttcggaa
                                                                      1320
gaggcaaagg acggcacgac tggctgatcg aatttgtctc tgcaccggct gaccgaatgc
                                                                      1380
gtttgccaaa gcattggatg ccgagttgca aacgctcaat tcgactacga agccaagcgg
                                                                      1440
                                                                      1500
tatgcagaca tgactctgct cccactctcc tgacgatcgc tcgctccggt ctcttccacg
attggcttac ggagcaggga agctgggagg acagcacaaa gtgcctcgtc tgagcaatac
                                                                      1560
accggaaaaa tgaggtctat cctcgaaatg aacagttaat cgcatcttcc cgattatggc
                                                                      1620
                                                                      1680
agggggagat gtttccgaac aaaagaatca atgagtaaaa agaaagtaaa agcaagacta
                                                                      1740
aagcccgcaa gggagacgct cctcgcatca accgtccggc cgtaggaaca agcgcatgac
                                                                      1800
caaggaggag atgcgcaatg ccatttggac atattccaaa gcaatcctca gagcgtgatg
                                                                      1860
aactacaagc aggaagccat ctgatgggag tagaagctgc accacaaaag ctaatggtga
                                                                      1920
acccctgatg gaagacatgg ctgtggatga catcctgcat gagatagagc gggacgctat
                                                                      1980
cggtacaatg ccttgggatt gattgtcata ggcacttttg gcgtcggttc aatggccgca
                                                                      2040
attogtttat toocgaaggg ggoggaacgo cattttoatt googaaagaa attoggoaca
tgccatggac ggtgacaagt gaaagtacaa ctctttgcca aacgtcgtgg tcgcgcgccg
                                                                      2100
gaagccgcgt gatcgagatc atagaacaga agcaggccac tttcgtcggc aagatcaaat
                                                                      2160
caatagagac tttgctttcc ttgttacgga agatcgcacc ttagcaatga tattttcatc
                                                                      2220
cccaaggaca acctcggcaa cgccaaaaac ggcgtaaggt aatagtccga atactcgaat
                                                                      2280
ggccggagca atccaagaat ccctcggaga ggtacaagcc gtattgggac cggccggaga
                                                                      2340
caacgatgcc gaatgaatgc cattttggcc gaattcggat tgccttatgt ctatccccaa
                                                                      2400
                                                                      2419
gggtggaaga ggcagccga
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 426 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...426

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081

# (2) INFORMATION FOR SEQ ID NO:1082

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 574 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...574
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082

cgtaacggct	catgacttat	ccacacgacc	ggccgtatcg	acaagtttgc	cttgcctgta	60
agaacggaat	gcgacgtatt	ggagatttcc	actttgataa	agggtaagta	acgccgtcga	120
tctcgatcgt	ctcctttgcc	tccatcgaga	gcgtgtgata	aagatgtctt	cgttggacat	180
atccttaaac	accaccgacg	ataattttcg	ggatgaatac	cttttttcat	tgctgtctat	240
ttagtttgtt	cttgttttcg	ttcgctattg	acgtactctg	gattggtaac	cgttgtttat	300
aatcggatag	agatttccgg	acggcaaagg	tagggatatt	atttacttgg	caagcagtta	360
ggccgagtca	aaaatgagtt	cgatcattca	tgcggacatt	catgctctta	agataagcag	420
gaggggacgc	atgctcgtgt	agtcgatgaa	tcgtgtgtcg	gatttacgaa	ccgcaatcgt	480
tetaattete	cgcgagaatt	ttgaaaaagt	ggaacgtaaa	ttatttcgtt	ttggttcgaa	540
tttttttgt	tcccgaacca	aaataaaaaa	attc			574

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 796 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...796
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083

ggcagatgat	gatacacggc	aagcgcaaac	aggctgcggt	ggagaccatg	aggagaccgg	60
ttggccggtg	ctattcagtg	ctctcaccac	ttttgttgtt	tgctttcttt	tctggctatt	120
cccgtcgtac	cgatgcactt	tatcggttcg	ccacttctgc	cagtgtcctc	ttctccttta	180
tgatcgccat	tacggtatgc	cgactacctt	gagtttcggc	aaagaccatc	agccgaaagc	240
atcaggcgaa	aagaaggaaa	gcatcggctg	gatcgatggc	tcgaagcctt	cggtcctggg	300
tettegatca	tgagaagtct	gtctggggtg	cttttatcct	tatacagtgg	tgatgctctt	360
tggattcttg	aaaatggaga	cggcattcga	catgaaagaa	caatggggcg	acggatagaa	420
tacgtcagca	atatccttec	ctgagcgaaa	gcgaattggg	ctctctttat	tcctatgata	480
ttatgatcga	ttgggagagg	agggaaaggc	caagaccccc	gaagcacttc	gtgctctcgc	540
agcatcgctc	gccatgcaga	ggcatattcc	cttaccaagc	gtaccactcg	atattgaata	600
tcctcaagga	tctgaaccag	accttgcacg	atggggacag	gcatactata	gcattcccgg	660
				gaatgcnggg		720
gcccgaaagc	tggatgactt	acgaatacca	gaccggttgc	taccctgaaa	gttgggaaaa	780
tgacctcttt		J	2 20 0	_	<del>-</del>	796

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 385 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...385
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084

gttacaacgt aatcga	cttc gtagcggagg	gttgttacag	cagctccctt	gcaattatag	60
gtacaattcg agatgc					120
gtttttagac catgct					180
ttgcttccta tacatt					240
tgctgccata ttatca					300
agttctacat cgggat					360
tgcgaccatc tttccg	-	-			385

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 874 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...874
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085

********	agcgatttga	ggaataccgg	catgagcatc	aggatttgtg	ccaatgcgtt	60
actgicgica	agegateega	66aactcaat	accaccgaga	gcgtctcgct	caaataagtc	120
ggcaaactgt	gcaaaacgaa	Claccingge	accaccagaga	000000000000000000000000000000000000000	aatacatogo	180
atctcacggt	tggccttggc	tccttcctat	aagccttttc	gagagaagac	cotcaacaca	240
catagacagc	actcttccgt	tcttacggat	ccagtctgcg	aatgetettt	CCCCggcacg	300
cttacaccta	tcacgtcaag	acgagcgaga	ccgcggttca	taccgatcga	attetteaat	
agttagcact	ctgagcatac	ttgctggcat	atttgatacg	ggtgcctgat	ctgcgctcat	360
agitageace	cogagocata	acttaatacc	gcaacttcga	tacgaggatt	gttctcgttt	420
ggcttccttc	Cagatgeett	gcccgacaco	gatagagata	cotactoccc	gggaaaccga	480
tcgatacgat	cttccacacc	Caagaagcga	ggtagcgatc		200	540
tggtcatggc	tagtcgtcag	ccttgtagcc	ttgcatggat	acggcagcga	agcadacggc	600
ttatagggtt	tattgtcctt	gctgtattcg	gccggccggt	tgtcggcacg	gcatacacgc	
ggaatacgct	gaagtcgccc	gtgtgacgcg	gccacatcag	ttgtccgtat	Cgccccgaa	660
ottacctaca	gagetggggg	pagcaatacc	atacgaacgt	ccttgaatac	atcgtagacg	720
CCCacca	6460066646	gaatagaag	octctacoat	gcagagttgg	ttctcgtctg	780
atgaggaagt	attegegeeg	gaacagaaag	atactacgat	ttacacaaac	potcatotog	840
catttcttt	ttggccagtt	cttggcatac	CLCCLBaget	ccgcagac	gctcatctcg	874
tcagtgatac	ccttgagctg	tccttctacc	ttgt			0,4

- (2) INFORMATION FOR SEQ ID NO:1086
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1314 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1314
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086

otoccc	+202002202	accogacat	ttgctgttta	gccatttgcc	tcaatagctt	60
gaactcccc	nacatagaa	catcatccag	ctateccatt	accacacacc	caatgttggg	120
agtocogaag	togotagage	tenegactos	tocacoacat	caacaactct	gccgaagcga	180
ctagtcgtca	ccgatggtat	tacaataaac	tagagagaga	aacatccaca	ttcaaaccgt	240
ccaatcttat	gggcgactga	tecaatggat	cggagagaga	t*doucacaga	actgacaaca	300
tctgctctca	acaaaggaga	tgacaatgct	cgcggacaca	Laggeacaga	20-8	

aaacggaaag	tgtcttgctc	atcaccaagg	acaacagtga	tgcgacagga	gcgttgtctc	360
agogtocato	attcgctcta	agcctttccc	tcctttgcgt	ttaggctcac	cgaagtagac	420
aacatctocc	tacgcgagtt	aacacagact	tcacggccaa	agacgcacag	cctttctcct	480
accasosact	agtggtgagg	agcatcgcac	agccttgcga	gaagcctttg	gccaggcttt	540
gagttgggct	atggcgacct	attgaagcga	ctcagctcat	catacttagt	gtcagtggtc	600
gaccttatoo	acagacgaag	ctcaaagaat	tgctccgttt	ctcgtgaaca	aacgtatgct	660
catcaagact	agcagaggac	gctatcgttc	aacccagact	tccattactg	acacatcggt	720
tcaatcaaac	gcaggtatat	ateccteacc	aaccgaccaa	ccataaataa	agaatggtcg	780
CCEECCEE	tgcctatagt	aaacgtccga	ccgaccaaag	aagaaccgcc	aaaaaaaac	840
accatacaac	tacacgacat	caagcaagtc	tccatcgtgg	acacttagca	caagctggct	900
ttgaagcaaa	gctcatcaag	ggcgtgaact	ategtattec	tcccctctac	gctcagagct	960
cacacatta	tttaaagtca	tecapagege	aaccaatggt	atgacttcgc	cacaggagac	1020
cacgcccccg	catcgacctc	gtttgcactc	tccagcattg	ctccacagca	gaagctataa	1080
acagetatet	gcgctgaagg	gtgtacggct	agcaccgtct	ttttctttgg	aggaataact	1140
acggctatec	tacaaagatc	ctccatggag	ctcatcgcgt	acaagctgtg	aagcatccca	1200
acetettact	gtatctctcg	gagggggg	acagecetet	gatgcctctc	ccttcttatc	1260
agetetatet	tacaagtctc	taggaagtgt	ttctttgccc	ggggatcctc	tana	1314
ggaagtetat	Lacaagicic	Laggaagigi	cccccgccc	9999		

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 393 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...393
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087

			•			c io
gccgccgatg	cattaagagc	agaagccaag	gcttccgtac	tgattacaca	tcagcgattt	60
tgagatccgg	aagatttatt	ttcttccctt	ttactttgct	tcgaaggtta	agaagagttc	12/0
actcttgtcc						180
tcatagctga	ctacacctca	ttgccaagta	ctttttctcc	ctgaaaaagg	aatgaaggtc	240
cccatattca	cctgtagcat	agcgcagcac	aggetteact	gtaagttcgg	ctttttattg	300
aaccatttgg	caggaaaagc	gatactcacg	gtcacaggca	cttgcttccc	acgacttcag	360
tggttgtggc				•	_	393
~00~~0~00~			-			

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1343 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1343
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088

```
ggttatgagt ctgcgtcatt tctgtgggac tgttggtctg attcgttctc atcccccact
                                                                     60
caagaaaccg atagccatca agaggaagaa aaagatttac tttctcattt tctactcggt
                                                                    120
attagtgaag agaatcgaat ttctcgttgt aaattatcgg gaacttaagg taatggaaaa
                                                                    180
tectatacet titgittee tataaaacag caettetate gacaaegata igaaagnang
                                                                    240
                                                                    300
360
tctgcgaatc aagtatctaa gcaaaaaggg cgaaatagcc cgttgttcga tgacttccgg
                                                                    420
ctggtaccgt ccgaagagaa aaagcaaatc ggcaaatgct caatgagctg aaaaacaagg
ctcaggagca tatcaactcc ctcgcgagcg ggcacaggca ggctctgcac aagcttcggc
                                                                    480
                                                                    540
agaaaccgac tgacacgaac atcatacccg acgagactcg gaacacgcca tccgatctcc
                                                                    600
tggtgaagca ggagatctgc gagatctttg cccgcctcgg cttcagtacg ccgacgggcc
                                                                    660
ggagatagag gacgactggc atgtattctc ttcgatgatt tcgccgaaga ccatcctgct
                                                                    720
cgtgatatgc aggacacatt cttcatgagc atcgccccga tgtcatcctt cgcacgcata
                                                                    780
cgtccagtgt ccaaaccggg tgatggaaaa gacacaaccg ccgattcgcg tcatttgccc
                                                                    840
cggggtacct accgaaacga agctatctcc tatcgggcgc attgtttctt tcacaggtgg
aagcactgta tgtggacaag gatgtttctt tcgccgattt gcgcaggtgc ttctttactt
                                                                    900
cgcacaggaa atgttcggag ccgaaaccaa atacgccttc gcccttctta tttccccttt
                                                                    960
                                                                   1020
accgaaccgt ctgccgagat gacatctcct gcaatatatg tgggggtaaa ggttgcaact
tctgcaagct acgggatggg tggaaatact cggatgcggc atggtggatc ccaacgtatg
                                                                   1080
                                                                   1140
gacaactgcg gcatagacag caagaaatac agcggctatg cgctcggatg ggtatcgaac
gtatcaccaa tottaagtac cgagtcaaag acottoctto ttotoggaga acgacotoaa
                                                                   1200
cttcttggaa cagttcaaga gcgtgactaa ccctctgatc agtatcgaat gcgcaaggaa
                                                                   1260
                                                                   1320
gagcgataca aagcgttatc gattggtttg ccgagaatat gccggtggcc gaaacggagc
                                                                   1343
tgcgtaccgg gatcctttcc agt
```

- (2) INFORMATION FOR SEQ ID NO:1089
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 647 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
    - (ix) FEATURE:
      - (A) NAME/KEY: misc_feature
      - (B) LOCATION 1...647
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089

catctacgcc	cttcttcaga	aggtcgcaga	ttccatatcg	aatttgattt	cttttgccat	180
agtetttatt	atttatattt	atttttttc	ttttttggag	gattattgtc	tcttccttta	240
agicticatt	tcctgttttt	gaaggccaac	ctocaptott	aacttgttct	ttgattcttt	300
ccactgggtt	tttattattt	2++++++	ttttggagg	attttgtctc	ttcctttacc	360
tgccatagtc	cotattatta	200000000	taaatattaa	cttottctoa	ttttttgtt	420
actggggttt	cctgtttttg	aaggccaacc	ttaccacata	atratatat	tttcaccctc	480
ttgcccatta	gatgattgcc	agacateget	Liggiguacg	tatatactac	tttcaccctc	540
cagctctatt	cagtgccggc	atatttgccg	tagagtacgg	tgttttttt	cttgagcaca	600
tctcttcgtc	tttcgtgccg	ttcccgacag	cgattacttc	accettgaag	gtttctcttt	
ggccgaatcc	ggaataatga	tcccgctcac	tgtttttctt	ctgctgc		647

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 289 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...289
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090

tgacaatccc	tcatttttc	aaaggtctct	atatcngttt	tactcgtcgc	gttcgattgt	60
tttctttccg	gccggggaaa	gtttccccga	cagccgacaa	aataatttt	ccggccggaa	120
aatctctatc	caaaggtttc	ggatatgatc	caaagccttt	gaatacatat	ccgaaagctt	180
catttatata	tccgaacctt	tgaataaaga	attegattat	ggcttttnca	acttttccgt	240
actocatata	aactttttc	ggccgggnac	gattatttct	ttttataaa		289
accecaaaa	440000000	667766611	0			

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 897 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...897

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091

			_			60
acgatcggca	gagagaccag	cccgacgaag	aggatgggca	tcaggatcgc	atcacgagga	
aggatttctt	tcggacgcga	atcatgtatt	cgcgttgttg	atagtgttaa	tgttgttcat	120
aacatcaata	tetatoggte	gtttctttg	tgcttggatc	ggattctctt	cctctacgcc	180
atagactaca	atettataaa	tatotrotor	atgctcggga	tctcttcgta	gaaggacacg	240
gragectaca	stoccescaa	teacacacaa	gatcgcggtt	gtgcgccgtg	gttttttgcg	300
agccgaccga	Ctcgggcagg	tegegeacga	Baccacabac	toostatoos	antecaacca	360
cactctcagc	ttcgtcatgg	aacccggtag	ctccgtcttc	teegtateeg	gatteggetg	
aggragects	ccggcagctc	gccttcgact	acatgcggat	aatgccgagg	ctgttctccc	420
teerestts	acacacaact	COTOGAGCAC	tacgcgcgat	ttgttgatca	gtgcgaagtc	480
tacgcactic	gcgcacggcc	0606666	tecatogram	anathachnt	acortectte	540
gtcgcatact	cttccaccga	ctgcatgttg	tgcgtcgaga	agatgatggt	acgeteetee	
cggccagctc	cagtatttca	cgcttcagca	ggtcggcatt	gaccggatga	atccgctgaa	600
agattcatca	aatatgagca	attccggttc	gtgaatgcgg	tgcacacgaa	ctgcaccttc	660
REGULCECCE		atattaactt	ttttgttcca	ccaaoocato	atetogaact	720
tgctgcatcc	ctttggacag	Cicicacic	LLLELLEL		******	780
tctcgaacca	gtcgggagcc	gcttgcgcgc	ttcgtgcttg	ttcactccct	taagttgcgc	
tagaagatgg	cctectcecc	cactttcatc	ttggggtaca	gcccccgctc	ttcggcaagt	840
	accontatet	tecactacat	gggatggccg	tcaagatcac	ttctcct	897
ageegatgee	gugaauguuu	CCCECCECAC	00000-0			

# (2) INFORMATION FOR SEQ ID NO:1092

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 605 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...605
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092

acacatecta	cagtctgcgt	рарсраасда	tgcgagcgca	ggaatccttc	ttatccgcat	60
gcacgccccg	cagcccgcgc	acttccaaca	agtccaatct	togoggagea	gattcacccc	120
ccagaatage	Cacaagcgaa	acticeggea	tetteestes	+ 1000000000	ctccaccata	180
gatgagtgca	tcgtagaccc	ccttgcgagg	tcttccatga	Lacguacacg	techange	240
tccacatcgc	tgtgtagtag	ccggtgctga	taccgtggcg	tagcaggtat	tegetaaget	
cctctccata	cgtttggtca	gggtcgttac	cagtacgcgc	tctttcttt	cgatcagcgt	300
gctatctcct	ccatcagatc	gtccacttgg	tttgccgtcg	gctgacgtcg	atgatgggat	360
ccagcagtcc	ggtcggacgg	atcagctgct	cgcgatcacg	ccttcgcttc	tgttcagctc	420
ataagtagta	200001000	coatataaao	ggtccggggg	gtgagagett	cgaactcgtc	480
acaagcegge	aggegegea	cgatataaag	66000000	atocatatto	gaccagattt	540
gaagcgaagc	gccgattgtc	gagagcggca	ggcaggcgga	accegeacce	gaccagaccc	600
cttgcgcgaa	cgatcgcctc	cgtacatggc	acgtatcttg	cggtatcgac	atggettteg	_
ctatg						605

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1539 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1539
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093

```
ctttggggaa agaaagaggt aggaaaacgg ctatcaggtg atcaggaaaa agccaagcgt
                                                                        60
                                                                       120
ttgcttcttc cttacctctt tatggggacg gtggcattct gcctaaagtc ctactgagtg
cctacacata ccacccgatg aggcctcttt ttcggatatg tcagcagctt tcttttccg
                                                                       180
gcaacgaatg ctattccttt ctgtggtttt tgccctgctt gttcagtcta ttttgcctgg
                                                                       240
                                                                       300
ttgtttttat cctcggaagt ggatggaggg accgaagatt ttcggagctt acctatcgcc
                                                                       360
tgccttctgc atatagtcac cgaatacatc cctgtggcat tcgggatgat cctttctgta
                                                                       420
ttatagcagc ctttaacaat tttcactact tcttctgggt atgatgttat accgctattc
                                                                       480
cgatcgtata gtttccagac ggtatcggta gccctgctta tcgctttcca tgtggcactt
ttctcccgtt ctttatgccc gagcagtcat cgttcttggg ggtattgaac tggtcttata
                                                                       540
                                                                       600
taccctgttc atcgttgtcc tttatggcgt gtcggtaaaa atcggagaaa ggtgatgcct
gctccattgc ttcacggtat agggttgtac agctatccat attcatttt tcatggttcg
                                                                       660
                                                                       720
tgctggtcgc attgagaata gtccttatga ccgctatgag ctgagcacca tgatgatcaa
                                                                       780
tggagctatt gccatagttt catagccggt ttgttcatac cgctttacct gtccaagttt
                                                                       840
ttggcaggaa acttccggtt tctctcaagc cgctggtcgg attgtaagca gaccagagga
gctgcgcaag aagggaaagt taaggttcga acttacgaag agaaaactat cgataacgaa
                                                                       900
                                                                       960
cggacttaac gacatgattc cggccgaatc aggaagcctc gcaaatagcc atagacacgg
ctcacactcg cagagtccgg actgaagttg tcagcatatt tattcccgga ttcacaggtc
                                                                      1020
                                                                      1080
ggctgaccga agaacggtat tgtcggtgca aaccaattgg agaaacatct ccatcgttca
tcaggacgaa gttgtagacc tctcagcctc gtgacaaatt ccaatcggtg ccttccttat
                                                                      1140
                                                                      1200
aagctgtacc tggggtgatg atgaaagacc tgttcagaat ggcatctccg gccggtagaa
acacgtacta teteeggeea geatatgate gaateeagtt egtagaaega accategage
                                                                      1260
                                                                      1320
atatccatcc ctttttctca cgctccaacg taatctgctt gtccagatcg attcgctgct
                                                                      1380
tttcagttca tcccgaacgc tttggcagat ggcgatatac tcttccaaat caggcgacca
                                                                      1440
taccacatca gcgtgctgtc gtaatccatg cgagtagtgc ctacttggca aacagattgg
gtgtaaaccg cttcacgaac actatccgtc attncggatc gtatatatta gcaaagtgac
                                                                      1500
catcggccac ataaagttca ccatcagatc cttcaactt
                                                                      1539
```

- (2) INFORMATION FOR SEQ ID NO:1094
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 605 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...605

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094

cagaatatet	tottoaatca	tgttcgcaat	cggatcgatt	tcacctacaa	ggcacagatt	60
tastatacac	caacgtatcg	aaagaaatga	gaatattcgc	tttgaaggac	aagcgaatgt	120
ggtactgcct	tacggctttg	gttttcggct	tcatattcct	acacttatga	tegatggaag	180
ggcaccgata	aggccgaact	gagatgaagc	tctcaaacac	ccgccctcat	gcagctactg	240
ccacttctct	tatogacata	atttttcgaa	gaattacaga	ctagcctcca	actttccacg	300
cactteett	ccgatctgaa	aacagggcgt	atgaactccg	acggttgttt	gaggaaataa	360
catatecaga	ttatacgatc	tgtcgtttgg	atttgaaaat	cattttttatt	ggaactatac	420
cgtatetggg	getecegaga	actgttcgat	tataaaccca	aagcattggc	attcaattcc	480
ccgacatcac	cogacgtate	atatacgggt	tggttcggat	cactttttaa	Lacgactiat	540
tacaacagaa	atataatttc	gccacgatga	agaaaaaata	atttatcttc	ggtagccatc	600
	acacacaca	8	J			605
ttatg						

## (2) INFORMATION FOR SEQ ID NO:1095

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 590 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...590
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095

aaactaaaca	ottoctests	tcaggtcttc	ggatcgctta	caccgaatgg	caggaggcta	60
tt cagtatat	gracaataca	ctgaatattc	cctatcagtg	gaagtcctgt	gcatcatcgc	120
tetagrange	Popogggggg	acagggaccg	cecctecat	cggaattgaa	gtgggagaac	180
tateggacae	adagecgage	cattoocaca	otototopca	tgattgatcc	tgtaggactg	240
gtttttatag	gcgaaccccc	atacttatca	gcagtggaaa	tctggctacc	caaaggctct	300
cccgaacttt	Cgcgcgcata	gtgcttgttg	teaggtatag	agragaatar	cgagcatgcc	360
ggccttgtcc	gaageegeea	gcccgcccgc	reactaces	tcaaacaaaa	cgagcatgcc	420
gaacggttgg	cttccatgct	gccgggagca	acgctaccga	ctegacagag	gagctactct	480
gcgatgcaga	gctttatctc	ctgcagtgag	cgaccatgct	ctcgaatccg	tagctgctac	540
ccttccgccc	catcgggaat	atgggcacat	acggctggca	gtatgccgat	ggataccctc	590
gcccttatca	tgcgcagatc	ggggtcttct	atcctcttca	gacattcacc		390

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1104 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1104
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096

cggtgtaagt	cgccaattag	gttcttctat	gaaatctgtc	ggagaggttt	ggccatcggt	60
cgcaccttcg	aggaggctat	ccagaaggga	ttgcgtatat	cggtcagggc	atgcacggtt	120
tcgtagagaa	caaagagctc	gtgattccaa	tatagacaag	gcactgaatg	agccgaccga	180
cagacgcatt	ttcgtctaag	caaggcattt	cgtcaaggtt	acacggtaga	taaaatacat	240
gaactactaa	gatcgatcgc	tggtttctgg	aaaaactcta	tggtatcgtt	accctgcaga	300
ggaaatggaa	gagttcgaca	agctcgaaga	tctttcacct	gctttttggc	tgaggccaaa	360
			cggctgtact			420
tggaaagcgc	aaccaatcag	gacgtgccat	gcgaaaggag	ctgggaatcc	taccggtggt	480
taagcgtatc	atacgcttgc	agcggagtat	cctgctcata	cgaactatct	ctacctgact	540
atagtggcga	tcgtcatgat	gtagcctatg	agacgacaag	cgttccgtgt	tgtactcggt	600
tcgggtgcat	accgtatcgg	tagctcggtg	gagtttgctg	gtgtggtgtc	aatgctctgg	660
ctaccatccg	taaggaaggc	tatcggtccg	tcatgatcaa	ctataatccc	gagacggtga	720
gtacggacta	tgatatagtg	acaggctcta	cttcgacgaa	ctgacattcg	agcgcgtaat	780
ggatttcttg	aactggaaaa	tcctcatggc	gttattgttt	ccacaggggg	acaatcccga	840
acaaccttgc	agttcgtctc	gatgaacagc	atgtgcccat	ccgggtactt	ccgcacagag	900
tattgacaat	gccgaggatc	gtcataaatt	ccagccatgt	tggataaatt	gggtatcgat	960
cagccccgtt	ggcaggagct	tcttcgatgg	acgacattga	cggattcgtt	gccgaagtcg	1020
gttatcccgt	ttggttcgtc	cgagctacgt	cctttccggt	gcagctatga	atgtgtgccc	1080
_	aacttcatcg					1104

- (2) INFORMATION FOR SEQ ID NO:1097
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 4902 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...4902
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097

ggcttcgata	ctcgcagctg	tgggatcttc	tccagcattc	acgagcagat	gcggacatca	60
					gtatgatgtt	120
				cagtggatct		180
				tecgatgeet		240

```
ctgatccaag agccaagtga cgatcgaaca tgacgatgaa ggcagacccg tccgatagac
                                                                      300
acgatogtga tttccaccca gcatgacgaa tttgtccaag catggacggt atttcagaag
                                                                      360
                                                                      420
cagaagccga ccggatgatg caggagcgca tcatcatgac atagctacca tactgatccc
ccgagtgaaa atgctgtaca accggagatc gcagccctat tcgacgaaaa ggtacgccta
                                                                      480
ttcgtcaatc tacgggtaag tttgtgatag gagggccaca tggagacacg ggcctgacgg
                                                                      540
acgaaagatc atcgtggata cttatggagg cagggcttct catggcgggg agcattttcc
                                                                      600
ggcaaggacc cgtccaaggt agatcgctcc gcggctttgc cgcccgacac atagccaaaa
                                                                      660
acatggtggc agcgggcgtg gccgacaaat gcttgtacag gtagcctatg ccatcggtgt
                                                                      720
agcagagccg gtaagatata cgtcaatacg aaaggccgga gtcatgtggc tctatcggat
                                                                      780
ggccaatagc ggagaagatc aagaagattt tcgatatgcg tccttacgcc atcagcaacg
                                                                      840
                                                                      900
actgaaactc cgcaatccga tatacgaaga gaccgcagca taggccactt cgggcgcgaa
ccctacgaag catacaaaac ctttgtcgat ggcacggaac ggaacagatg cgaatcgtgg
                                                                      960
agctattcac atgggaaaag tggattacgt agataagatc agggccgagt tcggtctgtc
                                                                     1020
gtaatcacac ctgcctcctt ttatcgcaag acaaaggctc tgccattgac ttcgcttttt
                                                                     1080
gctttactaa agcttggcag acagaagctg cttgttcctt tcttagggat gcagagagga
                                                                     1140
agtttattct accggttttt cacttcatca gctacaagac gaccaacggg gcagcagagg
                                                                     1200
atagatagat cgtatcgctc actgctcgtt gagcgttccg caccacaact ccggcagagt
                                                                     1260
ggtattgcga agcgccattt cagcccttcg gccgtgacgg ctgatccgct gaaactgaat
                                                                     1320
atagaaattt gtctccctcg cttccacttc tatgcgagcc ttcccgttaa aaccaaaaaa
                                                                     1380
                                                                     1440
cattccgtaa tccgtaggca tcacgatctt ttcgaaaaaag cggtatatcc gggcagatgt
gccagattgc cgacaaaatg atcttcacga gccccgatgt ccccagcaga cagacctcgc
                                                                     1500
gaggggaata ggtctcggcg agaatgtaac tgtcttcgtc agatcattgg tatcctgctc
                                                                     1560
gtctatgcat gtagtttttc tgcaggcaaa atatgtcgcg aggctgtaaa agaatccagt
                                                                     1620
cgcccactac tgcatccggc tctgcaccat agtccagcaa attctgatgg;ctccatcgca
                                                                     1680
acagacgatg gtaccttcag gatgctccga tgctcccgga ggatagcaag ggggaggatt
                                                                     1740
ttacggggaa attccccctt agccgaataa caaaaagcgg agctgtctcc ggagtaagcg
                                                                     1800
                                                                     1860
agggaaagaa aatataggto gatgotgatt gtggcotgto gttgcatott gcgccacogg
                                                                     1920
aatatcccag aacggacata acggtattga cggcaaagac gacagtggtg aatggtcgcc
                                                                     1980
ggatttatag aaaagggata agctgatgat attggctacg accagcacac ccagtgctgg
cggatgcgac gcgccaacca aatcatccca caaagctgat tacagtggca agcgtatcgg
                                                                      2040
cccacggcac aagactatcg tatagtggga caacacatag aacatcggga gaaaagccac
                                                                      2100 /
cgtagcccag caaggctgat ccacaggaca cgcggggaga tggatacgat ggcacctctt
                                                                      2160
                                                                      2220
ccgtcccttc gcggtggcga agccacatca cccagccgat aatacggtga tcagatagta
gacattgatg agcacattgc cgtagaactg cgcccgatcg agagataaat gtagaagagc
                                                                      2280
ggcaggacga tccccacagg ccaagccaga cactcgcctt atattcgaga tagacccaaa
                                                                      2340}
taaaattgac gatgctgctg ccagctcgat gggatgagcc acaatgaatt ggatcaccgc
                                                                      2400
ttcatcatcg gattagaaat cgattgtcag actacccagt gcattaaatc ggcctgagga
                                                                      2460
taataacgca gatcggcata tgcacttagt tctccggatc ctgtacgtaa ccggcatcgt
                                                                      2520
agatgtaggc attggacgca tacatgagtt gaagagatta ttgagctgta bgcccagtgc
                                                                      2580
cactetetta acgaagtaac eggeageaca tageegagge ggaggtegtt tacceaatag
                                                                      2640
                                                                      2700
gaggaagcat gcgatcgctg cgctgtgtat tgtccagata ttgcttgctg acgaacggct
                                                                      2760
cgtccaagcc atttcgaaac cggcatgaga gagggtaagc atgcgccggc aatgacattg
ggcgagtagg ctatatccgt gctttcgagg gtccctcctt gagttcgagc cagttgtagt
                                                                      2820
ccgcatcata tacggatgta tatgtacgta gcggtcgatt ttgttgcgac tcatagtgaa
                                                                      2880
agaagcatcc cacgcagcaa acgaggaagg atctgccaac cgagagtcag ctccagtccc
                                                                      294D
tacggtaget gteggggaeg ttgettgtga geatetgtee cacategeta aacggeeate
                                                                      3000
                                                                      3060
 cagcacgagt tggtccttgt attgcatata atagagacta ctccggccga caagaggggc
gaagcatage ggtageceag etcatagega teagtegete aggegtagga taetgteeta
                                                                      3120
                                                                      3180
 ttccggcttc ggtgtattgg ttctgttagg ctcgcggtgt gctaccgcaa cagaagcata
 3240
 tettgtecaa ategatgtge tgeatactte cetgtacete atetattegt eegtgatgee
                                                                      3300
                                                                      3360
 gtttatcgtg tagccgatgg tacgatactg gagtcggcat acatgttcag ttccggagtg
                                                                      3420
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                                                                      3480
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                                                                      3540
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 taagcgaacc gatgagtcct ccgaagtcat tgtccagtac ttctgacgga tgagatccgt
                                                                      3600
                                                                      3660
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 cggtacgata ttcgtcgtat agccatatcc ggccgtgtag tgtgccgtga ggttgaggat
                                                                      3720
                                                                      3780
 aacgaaggag agaagctgtg cgtcatgatg gcatggtagt gacgctgctc gtattgtcgg
                                                                      3840
 tattgtggta gtagtgcggt actccttgcg cgtccacgta caaagaccgg cactgttgta
                                                                      3900
 tcggcggcca tatttggctt catcctctt gaaagaccgt tccatgcgat acccgtaact
                                                                      3960
 tetttteete egaaagtgat aacetgagag eegtgttget aeegaaatag eecacetgtg
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casstsaat	ttcagatcca	cgcttcctct	atccacgtag	ccgtccgaac	cgattttgac	4020
aggraggeat	ccactaccca	atggcgaccg	atgcgtccgc	taccgagttg	accgatcggc	4080
aggegggeac	gaacgaacct	ccgctcaaat	cgacacgcca	taaggagcca	gtcccaaatt	4140
atccatacac	atattgacac	ttgcccaaaa	gctccggcac	cattggtgga	agtacccaca	4200
cctcgctgca	cctgaggtct	tcgatggaag	aggcgaagtc	gggcatattc	acccaaaaga	4260
coocteagat	toggagtogt	tgaggggtac	tccattggta	gttatgttga	tggattggca	4320
toggtgccac	gcacgcgaaa	gccggaatat	ccgatacccg	tccggcatcg	ctggtggcta	4380
ccacggaggg	agtcagcatc	agcagatagg	gatgtcacga	ccataattgg	acttggaaag	4440
ttcggccttg	cgaacgttgt	gtaagcgaca	ggggttttcg	ccgtggcgcg	agtagctacg	4500
acctgtacgt	ctggagctgc	acattgctaa	gactatctat	ctcgctgttg	gagacggtgc	4560
ttgtgccgtc	aggcagaaag	gcaggacggc	taaggcggca	atcatggaag	ttttttcata	4620
aatctcttat	cattgaagtt	ggacaaagaa	gagagggggg	aatgattgct	tcgccgtgaa	4680
gatagtcaga	cggagagttt	cctagccggt	attatccggt	tcaggtgatg	agggtttgtt	4740
ctcagccatc	caccattccg	attgctacag	gaagcacccc	ttctcccaat	tttatgggac	4800
aagataagaa	aacgttcgtc	cttcagtatt	cgggacgata	ccgctcggca	tttcatcttc	4860
gagaatgctc	aagtagctga	tatagcggct	ctcggctatc	cc		4902

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 310 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...310
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098

ggggatctac	tgcattacgg	aatggctgct	cgactgaggc	gaagaggtgc	tattcgacct	60
cccaantgcg	ctcgaaaggg	aaaatettga	tttcgatett	cggcgcttgt	ccatttgggt	120
cacttgaaan	cccbaaabbb	catacacaac	tatatrarrr	acatogogoa	gttcctgctt	180
cacttgaaan	cggaatgget	Cgcacacgac	LECALOGOCO	00000000	gaaaggattt	240
gatttccaag	aagagccact	tagcgtatct	acctegeece	CCHattcatt	gaaagcaccc	300
tccggaggtc	nagatagtgt	cgaacatcng	agacatacgt	ntntccttca	anaaataact	
gcnatccccc						310

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 700 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...700
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099

		ccasatatag	acattccaca	gctaagtaat	gctccgcctt	60
agtctgtttt	ttagaacctt	ccaaacacag	ttgagtctca	tagagcatcg	agacaaacaa	120
tgatgggaca	gtcgtatctg	caataccigi	ttgagtctca	actoccota	cttttccctt	180
taacctcccc	aaaaagaaaa	gggggggcga	ccacatgccg	gccccccg	ananchtono	240
atonggetet	+otttttag	aaatgaacat	tgaatgtagt	Caaggetgeu	aaaaccco ₀	300
	tatatrarag	tagetectge	cccaagggta	LLEBABALEC	gacaccgcag	
accet acces	caccaagget	aaatttgcca	ttggcatacg	LECTECTATA	gcacgcccac	360
gccatgcgag	catcatataaa	taattattot	tttataagaa	agacctgcct	gaccggctaa	420
tgtctacatc	Calalacaaa	+++000000	accttoatoo	poctgaaacc	ggcaacggcc	480
aaccaaatca	tgacggctgt	CCCCaaacc	tttccaagt	ggcatcctca	tactececac	540
ataaaggagg	agaacttcca	gaattaagac	LLLLLaage	ggcacccca	tactgcgcac	600
++000000122	tootatogaa	gagcagttgc	ctccgcatag	gagaatttta	ccgagaccgc	660
tocoggggag	tttcattgag	ctcttttgct	gcagagcgat	tcttagtgtc	ttcgggaaag	
otcasacctc	cggtatatgg	acatcggcaa	acagaaattt			700
50000000	- 00					

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 962 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...962
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1357 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1357
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101

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60
accatatcaa agccgcaagg tccgaaccca tccggtacac ttcgcgatac cggaagaaga
cgaaagatga aagtacggct ttggggagtt tgtccaagtg gctctctata gcccgaacca
                                                                       120
gcgcagaagc actctgtccg gaaaagaagt accctctcct gctgaagcaa tgtcacggca
                                                                       180
catcttttcg tcgaattggt aacgacagga ttgcccgttt catctttgag gtatccttct
                                                                       240
                                                                       300
tcaatggtat aggtgccccc aaggctgttc cgagaccaat aacattgacc cgtagcctgc
                                                                       360
ttcatgggct tgctgtgccg cttcgatggc atttccttca tgatttctcc atccgtcagg
acaatgatag tottacogat ttoottatta togaaaaaga tttggaggca agttogatag
                                                                       420
ccgctccgat agccgttcct tggctgtaac catattggga cttatatctg caagaaactg
                                                                       480
tttggctgca acaaatccgt agtaatcggt atttgcgtat aagcattacc tgcgaataca
                                                                       540
ccaatccaac cttgtcgttc tgcaagccgt caaagagctt tcccaacatt gcttggcaaa
                                                                       600
                                                                       660
actcaaacga ttgggcttga catcttcaca gagcatgagt tggaaatatc caaacaaatc
atagcctcga tacctttctc ctctttggca catccacacg aatacttatt tgcggacggg
                                                                       720
caagcatccc gatcagaaaa cgatggcaag aagaagaaat ccgttgcgcc agatccgacg
                                                                       780
tttgtacttg cttccggttt gagagcctta gcagcggaag ttcgggcaaa ccgtctttct
                                                                       840
                                                                       900
tgcgcccgtc ttttgcgata agcatagacg cctaccccca cagcaatggg agcagcagca
                                                                       960
gtaagtataa gtattcgggt gaataaaatc taacatggga atctttttac gggttggaac
                                                                      1020
gaagaagtgt attgcgaagc aaaactctgt cagcaacaag agaaaagcaa taagggcata
gacaaagtat tttcctcata agccttgaag ctcttggtca taagtctcgt cttctccatt
                                                                      1080
                                                                      1140
tgtcgatttc cttgtagatt tcattcagcg tttcattatc gacagcctga agtattttcc
                                                                      1200
accegatace teggeaatte egteeaatgt gggtteteta tategacagg cacattetga
atccgaactc cgaattccgt ctgaagggga aaggagcttc tcctcgtgtg cctacaccga
                                                                      1260
                                                                      1320
ctgtgtacac acgataccga acgttctggc aatatcggct gccattcggg gtgtgatgtc
                                                                      1357
gccatgttgt ttgatccgtc cgtcagcaga ataacca
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1381 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1381
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102

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gctatcatgg cttcttctgt gtccatcctg atcttcgggt agcgtacccg aatggttgga
                                                                        60
gcttaatccg aatcagggtc aatccatatg aacagtacgt tggcaattaa ggcctaaaac
                                                                       120
agcaagaatc gttttcatat aggctttgcc taaggancaa taccaagggg tgcaccgaaa
                                                                       180
tcaattttcg atgcaccttt ctgcataatg cttaggaagt gaggattata tttctataag
                                                                       240
aacctccgct aataccgcta taagtagtcg tcccttaaaa gtcctttaa gggagattag
                                                                       300
ctaaacgcta aacgcaatat acacaggtcg cacggttatt tccgtcagag attacgtaaa
                                                                       360
                                                                       420
gcgactgcag agtaaccccc atacaaatcc ggacggcaaa aggggagagc ctcttggcca
ttatgatatg cgtccgacag atggatgtat ttattctgac gaagctgatg acagatcttc
                                                                       480
                                                                       540
aggaggtcgt ggagctgtgc acaagcagat ggatttgtcc ctcgaaaatg ccatctttgc
cgtaagctgt atgtgcttga tgccgacatt gaaatcttcc gaaataactg tgtcacagcg
                                                                       600
gtgaggatac cggtggagtc aatgcccttg agtgcgactt agcttcgaac gaggtacgac
                                                                       660
tgtgcaagct ccattcggta gagaggtgcg gttgccaaag ctgcttttca aacgcatggc
                                                                       720
aatggggcaa gatcgttgtg tacgaccaca gtattatcgt cgttgataaa tccgaaagca
                                                                       780
tcgtgcccgg aatcggtttg cagcattcgg caatctgata gttacgggag aatcgtcctc
                                                                       840
ttgtaggata taagtotttt tggtgttgta agotttotta tototttoto tgcgggotta
                                                                       900
ccggatggag aggaggtttt gttgcttttg ccgctttcaa tgccgaacgg atagccctca
                                                                       960
tcagaaagtt accgctatgt ctccctgaag cagttttttg aagctttcgg gcagagatac
                                                                      1020
cgtacccgtc cgacggcgta gaagaatgtt tcgcgattga ggaaaccgaa ataggctgga
                                                                      1080
tectatecaa aageteggea gagaceatgg atteggatgt cegtatacae tgaceaeteg
                                                                      1140
ttcttcccca cgattgatca gctcccgtct tttgcgcgga gaaaagtatc tactttcgat
                                                                      1200
                                                                      1260
ttggctcgtg ccgtagtcac atagccaacc actcttcggt cggttgctgg cttttgctcg
aaagtacctc caccgatcac cgctgttgag cacataactg agcggaacga gtttgtgatt
                                                                      1320
cacttggccc cgatgcaatg gtctcccaaa tcagagtgaa gcgaataagc aagtccaaag
                                                                      1380
                                                                      1381
```

- (2) INFORMATION FOR SEQ ID NO:1103
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 575 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...575
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103

cccgatttt	atcaggacag	caaggttact	tgccggatgc	gaacaaaatt	caggtgaaag	60
ctgaaaatta	tgaacaggca	gtagccatta	taaaaactgg	caaggtgaag	acgtgatgaa	120
			gaaggagaaa			180
			cgaccataga			240
			atcagaggtt			300
			aacctgaaaa			360
			ccaatctttc			420
			tattgaaggc			480
			tgttaggtcg			540
-		tcgaccttac				575

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1010 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1010
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104

gggcgggtgg ctatccgtct cctacaacct cgcggcggat tattcctggt ggaaacggga gccaacgctc atcgccggtt gccccaatac cggcatacgc ccgtctgacc ttgctgccga tccccgtct gtcgctgcgc atggcagcga atataacgcc acgactctgg agccggggca tgtacatgag gatgttttt cgactgcgaa gcacgctaca gtttcgataa ggtttgggaa gtatcgtttc gatgcgcaat ctgttcgatc gtcgcatgta tcttatccgt caacgacgga gtacaacgct ttttccaccg ctatccccat tcgcggtcgc gaatgcttgc cacagtcttt ttccgctact gattttcttt attcggtata gcgccgagga tcgtattgag attctttctg aatttcggta cgatttttct ttcggcgagt aatttcgtcg acgaaattac tcgctgcagc tatgcaaggc aaatcttggc aacaaaattc atagaatccg acctgcaaac atgaatttcg caacaaaatc gcttcctgca agctgcaaac atgaatttcg gcaacaaatc gcttcctgca agctgcaata agcaattttg ttgccaagca gacctttgca agcttgcagc aaggaatttc gtcgacaaaa ttacacaatg cataccgcgg caaggaattt cggcaacaaa atcatcaaat gcatatttca gccaaaattt cgatagagaa atttcaaata catgctttcg gcaatcaatc tttgacataa aatttccatt gccgaacggc gataagaaac tttgccaccg aagtgatatg tattcccctt aatctttatt ccaatatata tgattggcag gaaatagttt catccactaa attacaataa togtatgact gotttoggat aagottaaga caagaaatat ataattotat cggttttcta tccacaacaa attatttact acttttatcg aagcaaacga 🦫

#### (2) INFORMATION FOR SEQ ID NO:1105

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 741 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

60

120

180

240

300 360

420

48D

540

600

660 720

780

840 900

960

1010

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...741
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105

ctotoagaag	aaactgctgc	gcagggtgga	cctattcgat	gtgtacgaga	aagaacttgc	60
ctgcgagaaa	gaagagttat	gragtgaget	tcttcctggc	aatgatgaga	agacgcttaa	120
Cigciggaaa	atagageeta	tratagrasa	atacgggacg	actctggagc	aaaagctcgg	180
cgacaaacag	acagaggeta	ccacggcaag	cgacaaaata	agaatogaca	tatcattate	240
tgcgcaactc	cgccgaaacc	aaacgaaaac	anatanaaca	ctooogcaat	atggccgcgt	300
ggacggcatt	tgaatatcgt	aaagcaagga	adatgadatg	CCEEEECCCC	atggccgcgt	360
cttcaccaag	ttaggaaagg	aaatcaccat	cgctgccaaa	gaageggeee	cgacgcggag	420
accaatccgc	gtctgcgtat	cctcgtgcag	acgccaagaa	ggagaacacg	CCgaaggaga	
acgtggaacg	cgccatcaaa	aagctacctc	caaagactat	acggactaca	aagagatgaa	480
ctatgagggc	atggtcctta	cggcatcgcg	atcttcgtgg	agacagctac	ggacaataca	540
cacgtaccgt	ggccaatgta	cgcagctact	tcaacaaaca	tggcggatgc	tcggtacttc	600
coocaectte	gaattcctct	tccagcacaa	atgcgtattc	acatcgtcaa	gaaagacgat	660
atggateteg	aaagccttga	actcgactga	tagactacgg	tgtggacgaa	ctggaagagg	720
	gagtcaggtg		0 00			741
	a-aaa-a					

- (2) INFORMATION FOR SEQ ID NO:1106
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 540 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...540
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106

cappagacca gcgt	aggeet aeggtgetea	ttacaacatg	ctaattatcg	tgcattatgg	60
ccaattaaag taaa	acgaga acgaccttag	aaattttcct	gttttgcgtc	ttcaaaattc	120
gtttcccccc ttgt	ttggga agttcagctc	aatagcagat	cgacgacctc	gactcccctt	180
gtcgtatttg aagc	atattt cttataatag	aaagaagaca	cgtgaagatg	gtgatgatgt	240
cattttcagt acac	atcgct tttctttatc	tttgtagagc	atggtttcga	atttggaccg	300
gcttttgaaa tcag	atactt ctaagaaacg	tttcaaagaa	ctagttattc	gaatcgatta	360
cccctgtgca atgg	tggctg atagcaggta	tctgctcttt	gtttttgaga	tttttacccc	420
gggtttcttc ttgg	cttgat cgtatgggag	cttttgctgc	cattataccg	gcggccttgg	480

ggttgtctat gtgtggcana ccggtttttt atcgtggctt cgctgctctc gctcttcctc 540

- (2) INFORMATION FOR SEQ ID NO:1107
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 896 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...896
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107

gattaagaac	caagatgaaa	aaagtatttc	aagatcttcc	tttggggtgt	gttggccgtt	60
gcagtgatcg	gcacttttat	gttcctctgg	caaaagtcaa	agccaaaccc	aaagagtacc	120
aaatcgaaac	ggtaaccaag	caagacagat	cgagagcaag	acggtgatca	ccggtacggt	180
		catcaaacca				240
cacgagccgg	agacgtggta	cagagcggag	acgtgatcgc	ccgcctcact	gtcgtccgga	300
aatgatccag	cttagtcagg	ccgagagccg	tgtccgtatg	gcgagatttc	atacgagcaa	360
		cagcaaagat				420
		atttcgccaa				480
		aggtgccagc				540
tgcgcagcac	ggtaacaggt	aagatcctga	atgtcccggt	caaagtggta	attcggtcat	600
tcaggccaat	acgttcaacg	agggaacgac	catcgctcga	tagcggatat	gaacgatttg	660
atttttgtcg	gcaagataga	cgagacgaag	tcggtcgcat	tcgactgggc	tctcccatgc	720
gcatttcggt	gggagattgg	ggaaagaaag	ttttcctgcc	acagtagaat	accttgcgcc	780
		gagctgtact				840
agcgacagag	taatccgtgc	cggctatagt	gccaatgctg	aaatcgtact	cgaagg	896

- (2) INFORMATION FOR SEQ ID NO:1108
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 429 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...429

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108

tccacattca gatccg ttgcaaacag ccggtt cgagagcatg gcatcg agcactttga gcttct; cgaaggcacc tctatt cccgtcttac gcccca	caga tccggaccga atgc ggtgcgaatg gcga atgtcagcaa tccg acacattgac cggt ctgtacttcg	atagtttgtg ggctggccta ggacttcgtc tcccagtgcg gggactgaaa	gcgatattgg tttcgatatt tttggaacga tgctcgtcca gcagatttct	cgcgcgtacc cacacccggc tccttgagga gttcgcgcgt tctgccatac	60 120 180 240 300 360 420
gcccattct gtcgct	ttcc tccagcgata	tgccggtaga	agtgcttacg	ttgatggtga	420 429

### (2) INFORMATION FOR SEQ ID NO:1109

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 507 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...507
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109

gagaaaatta	caagagcaag	tcctgatatc	caaaagacga	agggtttgaa	cgatcatcat	60
atttatctgc	aaggaacatt	accecaaega	aaccaaataa	acgaaataag	gtaacatgat	120
tatctatttt	ttctatttgg	atgaggcgat	tcgatagcgg	aattaccgat	attaagcagg	180
gtaaaatcgc	tatccacaga	agttcgtaca	cattacgacc	gtcgatgacc	aaagatgcag	240
ccatctttga	cacacacta	accastcaco	cattetgaat	tccttccatt	ccgtacatgg	300
aacagagcct	gagagagaga	accaaccagg	nacetatoco	togatattcc	aatttggcgc	360
aacagagcct	c t go t not c	gactggattg	coartegas	acccasactc	toraaccaac	420
ccaatctttt	ttgtgcctct	ttcatcgnca	cagaicggac	accegaacte	antaccaat	480
ttccaacagt			ggagetteat	gcatattatt	ggcaccgggc	507
ttgaatgaca	cccccatatc	gctacac				307

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2681 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...2681
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110

```
gccaaaggat gggccggcgg tattctcttc aatgagcaag cgaaagccag ctggatcgtt
                                                                        60
tettegeacg accegatacg eteageeteg gtatetgeac ggetgeeage tgatggeega
                                                                       120
                                                                       180
gttggaactt ctataccccg aacacgactc aagcacaagc ttgtccacaa cgaatcgcag
aaattogaaa goacatogto actotogaaa tooogoataa ogactocato atgotoggoa
                                                                       240
                                                                       300
atctgccgga agcaagatcg gtgtatggtg tgctcatggc gagggtcggt tcagctcccg
tacgaggaga aagcctacca tgtggtggcc aagtacgaat acgcggctat cctgccaatc
                                                                       360
                                                                       420
ccaacggatc gccacaccgc atagccggat tggcagcgcg gatggccgcc atctgacgat
gatgccacat ccggagcgga gatattcccc tggcagtgcg gttattatcc cgaatcacaa
                                                                       480
cgacacgaac tcaggtgaca ccttggatgc aggctttccg caacgcttac gagtggatac
                                                                       540
caagcaggtg aaaaatggat gatcgtcgcc cccaactgac agaggagcac tgcttttccg
                                                                       600
                                                                       660
catcgcactc acgcatgtaa aaggcgtggg tagcgtgtgg caaggcagct gctttcggct
atgggcagtc ccgaagccat cttttcgaca ggaaggagct ggtacagagg ctaccgaaag
                                                                       720
cacctegeeg cetgeegatg ceatettete teetteggte atggaggaag cacgeegaaa
                                                                       780
gttgatcaag ccctcaaagc cggtctgaat atgtatttca tcaccgatga taatatcctt
                                                                       840
                                                                       900
accgcttgaa agaatgtgtc gacgccccca tccttcttta ttcaaaggca atgtcgatct
ctcgccacgt agggtgctga gcattgtagg tcgcgcaata tcacggccta cggacgtaca
                                                                       960
                                                                      1020
gccacggagc gaatcgtatc ggattggctg aaaccatccc cgatttgctt atcgtcagcg
gactggcgtc ggcgtcgatg tcgcagctca taaggccgct ttggacaatg gcttgcccct
                                                                      1080
gtagctgtat tggcccatgg attggacagg atttatccga gcggtcacgt tccattgcta
                                                                      1140
                                                                      1200
tggagatgct ccgaaacgga ggcttgctca cggattccct atggggactg aaccggagcg
                                                                      1260
attcaatttc gtcggtcgca atcgctcgta gcaggcttgt cggacgccac acttgtgatc
                                                                      1320
gaatcggccg aaaaggaggc tccctcatca ctgccggact ggcattcggc tacaatcgcg
                                                                      1380
aagactggct ctacccggac gagccacgga tagccgttcg gccggctgca atccttgata
                                                                      1440
agggatcaaa aagccgcgct tgtcagctcg gctcaagatg tctgacgctg ctcgattgga
gttctaccat agacgccaaa cctcagacat gaatttccgt cccgatagtt ggccggatac
                                                                      1500
ccccgtagcc gaatgtcttt cagagcaggc acagcctcgg tggacgagct gacacgcgct
                                                                      1560
                                                                      1620
accggacted tataaacgat gtttetgete agettttega eetegaattg gaeggaeggt
acagtotoag cooggtggca tatactoogt tatataaatt gtacgagaag atgtotocca
                                                                      1680
ccttgtccat actcataccc gtttataaaa gggatgtcgc agactgctgg aggaactgta
                                                                      1740
taagcaggcc gaagaactat ccgtggctac gaaatcattc ttggagacga ctgttccggc
                                                                      1800
gaacettaca ettteaatat ategettaeg aacaggaggg aetgtgeega ettgteagtg
                                                                      1860
                                                                      1920
ccaagagaac atgggagccg gccgtctgcg caatcgctta gcagaagaag ccaaggcgag
cageteetta teetegaete egataceetg eeggeateae egaetteate gaaegetate
                                                                      1980
tgcgacatgc ctccggcaca acagtcgtag tggagggttc gtctacccgc ccaaatcgac
                                                                      2040
caatcccctc cggcaacgta tggcgccgaa gtggaaagtc gatcggcgga agagcgagca
                                                                      2100
cgaaaaccca ctccggattc atctcaatgg ctttcatgat cccaagaaaa cagatgttgc
                                                                      2160
                                                                      2220
caccggette ceteceaata tgggtatggg gtatgaagae ateettegg egagegtetg
cgacaagccg gcatccccat cctacatatc gataccctgt agaacattac cactgcgata
                                                                      2280
ctgccgaggg atttttggcc actcgcgtag ctatctggac aatctctatt gtcaccgcga
                                                                      2340
agaattagcc gattggtaag cctgctcaga gcatacaatt tgctgaaacg gctacacctt
                                                                      2400
                                                                      2460
agcgaatggt agctgctttg tggccactga tccgatcctc attggaaaag agctcacggg
                                                                      2520
agctaagccc teteteetee tetteageet gtataagete tataegtage eteeetetet
ttggtgtgtg ctgaaaaaag ctgatcctag aaagatcaga aaaagcaata attatatcga
                                                                      2580
                                                                      2640
aatgtttgac ctcctctcga gtgtcaactt tttttcagta cacgtcagtt cgtaaaaatg
                                                                      2681
gcggttagcg tttggaaaaa cgtggctcgg gaatttttc g
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...601
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111

gtcgtatccg	aacaattggt	cggagccggt	ttcaatgaga	tactcaacat	tcgcttacgg	60
ccoottctta	ttacgaaggt	cttaagagcc	atccgagaag	atggcagtgg	agctgatgaa	120
tccgctgagt	caggagetta	actgcatagg	cagactctgc	tattcggagg	attggagacg	180
ctcagccaca	acctcctcgt	aagcatctct	ccctctatct	ctttgaatgg	ggtaaatgct	240
atcoctccat	gccgcaaagc	gcacggacga	gactcccctt	gcggcctatg	cagagacgat	300
cacctcaaca	tttggatatg	cggacaacgg	gtgcacaata	gctggcacac	cccgaagaac	360
cgacttcggt	atttgaactg	aaagctgtgg	taaacaggta	ctttgccgcg	tagggatcga	420
aaccooagct	tatacgctga	aacagctgac	aatgatctgt	acgcatctgc	catggaggtc	480
aagactcgtt	pppcaaactg	ttgggtacat	toggaacggt	atcaacggaa	ctgatcaaag	540
cttcgaaatn	gagcaacccg	ttactttgcc	gaatgctttg	ggatgcccca	tgagcgaatc	600
	6-6			<del>-</del> -		601
g						

- (2) INFORMATION FOR SEQ ID NO:1112
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 848 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...848
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112

ggccgaagcc	cagtacaata	tggctcgcaa	cggtgccgaa	cgcgaagaca	gctggcagct	60
totecctce	tcgatagagc	gagaggagcc	gtcgccgagt	ggagtcgtac	atcaacgaaa	120
cctacctcat	cgccccacgg	gcaggcgagt	gtcggagata	ttccccaaag	ccggcgaact	180
cgtaggtacc	ggcgcactat	catgaatatc	gccgagatgg	gcgatatgtg	ggccagcttt	240
gccgtcgtga	ggatttcctc	agcagcatga	ccatgggagc	cgttctggag	actgggtgcc	300
ggctctgaat	gaagaaaaag	tacgcttcaa	gatcacattc	atcagaacat	gggtacctat	360
gctgcctgga	aagcgaccaa	gacaacaggg	catacgacct	gaagaccttc	gaggtaaagg	420
ccacccttgc	ggataaagac	aggcacaaaa	gctacgcccg	ggtatgtccg	tgatcatacg	480

raadtaarda	gagragtaag	pocatgoacg	ggacagccct	tatagccacc	atgcgtagaa	540
caugcaucga	ctgacgagtc	gratectett	cctcttctgc	atggtgatgc	tcctgtcttt	600
tactatatat	tettecete	catcatogat	atggggtgcc	gcagaacctg	cctgcgggta	660
tgctgtctct	castcataca	caccacacac	caccatagca	cgccacctca	attcgatgga	720
ttgtggattt	cgattgtata	cagacgegeg	tacatagaa	tcgcttgcag	tacagogagg	780
gcaaacccaa	accgcaaaca	guicgaaggu	tancacagat	acctacacac	agagcagcca	840
• -	actactatat	accegaggaa	igacacggac	gcctacgcac	ugugeugeeu	848
agctctct						040

- (2) INFORMATION FOR SEQ ID NO:1113
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 303 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...303
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113

aaaagaaaca	aaaagatatg	tcccatttgc	caatccatag	aagttcgcac	tcaccgattt	60
topagtctat	ctgaagacaa	ttgtatctaa	aacatctgat	cttcagacag	atatgccttt	120
tctcatacco	acgactatta	tttcttcgct	tcatagaggg	ggggcaatgt	cgtctgaata	180
ttgatttcaa	ggatgactt	ttcgaaaagg	atagtctggt	tatcattcgt	ccgggacagg	240
tegaticcaa	attantactt	acaatctttc	ggcaaacttc	cttattattg	actctattgg	300
•	accgaigett	acaaccccc	ggcadacttc	cccaccaccg	2000000000	303
taa				•		505

- (2) INFORMATION FOR SEQ ID NO:1114
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 507 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...507
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114

gcaatttgga	caaatcacgc	atgaaaaacc	gttaacagcc	attatttcat	cagttacgag	- 60
tocaagagca	aaaattgaca	attttcacct	gaaaatgttg	tctgaagagt	gtttcaaaaa	120
attacaaaaa	tettttcae	acgagaccga	acagccgaat	acgtgaagca	ggggattatt	180
trattacctt	tgaacacaga	aacttagctt	tgacaatata	tgattacagc	cgaacgttat	240
caccaattag	catoggacac	cecetaetee	ggcacgatca	caagtgcaga	catcgcatgg	300
cacgaactag	catatroact	ttatttgcag	tgcaccggct	cttattcgat	cgggcgtgta	360
acacaaccac	ctattatcaa	agagttgcta	tecaeteect	tgaagatcat	tgggatcaca	420
gecgatticg	atacaacaa	atccattact	tectgetttg	ceteceacte	tgccggacga	480
			ccceanna	-6-6-66	-000-0	507
tctggttgca	taccgttcaa	LLLLALL				

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1866 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1866
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115

```
60
ggcggcgaag tagtccgaag ccgaggggat accgctcgct cctccgtaaa aatctccgaa
                                                                       120
ggcaggtcgg ctccgcttcg ggtcatttcg tcgaggaatc atcgatgagc gagaaggcgt
                                                                       180
ccggctcctt ttcggccgag gcgggttcag ctgctccgga tgcgtatatt gctccacgag
                                                                       240
caggtacago ttgcgctgtc cggcagatag ggtgccagcc ggcgcagctc cgaagcatag
cgcactcctg caccacatac atattatata ggtataggaa gacgaaggtg gagcgtaggg
                                                                       300
ataggcctcg tacagggctt tcatctcggg cagcgtgtca gccaaagccg cgaggggtgc
                                                                       360
                                                                       420
tccatgtagg cgtacagatc gttagtcgtc atgtggggga ggattaccag ttctctaccg
                                                                       480
tagogttata cacotgotto acaagtogto gaccatattg gocagoaggg ogtottgtac
                                                                       540
gtccaccage getegetget gtegaagtee gtggaagaeg taaagteeeg ategaagttt
                                                                       60¢
gttcgggagg ccttgttctc gtagtgcacc tgtatggata aggttacctg gtgcgtgcgg
ccagatogtt gtootgtacg gcgaggggag cgaagtotaa ttagtgatga ccacctogat
                                                                       660
gatcatgtcg gcatcgttgg ttcgtgcatt tcgagcttgg tacggcgcgt aaaatggttt
                                                                       720
                                                                       780
tggagggett eggtetagte tgegeeaaeg ggggatatae gegggtggee tgattggtea
                                                                       840
catcggcata taaagcgttt tgatgcggct atagtccaga gcacctccgt tgagctgtag
gagatgctgc atgccgagca ggtcagcagg acgataagca ccccgcaaga gcggaaaggc
                                                                       900
                                                                       960
tgtatcgccc gagggttcta ttccagtcca tctccttgat tttacggtat agtgtccgct
                                                                      1020
ccgaaatctt cagttcctcg ctgtctgctt gcgccttccg ccgtggcgtt ccaatgcaag
                                                                      1080
ggaaatcatt tottototac otootocago gaaaccggat cotoggtgta ttogotggtt
                                                                      1140
cctgtatcgg ctccacgggt tctgccgcgt tcgcgatggg ggccttggcg tgctgacgcc
ccacttegga tetgeggtge gettgtegte gttgcccaga egteegacee tacaggecat
                                                                      1200
                                                                      1260
gagggctgtt cgtggtgcgc caggcgttca tcatcccctt caaatcggct atctctttct
                                                                      1320
tcatatcgta tagccctggt agatgatttc gcgctcgtaa tgggggattt gtttgtccgc
ttcgtcgttt cgttccgtcg gatcacgacg gggtggaggt cttgcatccc ctagcgtcca
                                                                      1380
ggtagcgagt gatggtctct gccgataccg tccgctcctc cccaggatgc tcagcctgtc
                                                                      1440
                                                                      1500
ggttatattg cgcagctctc gcacattgcc ggccagcggt aacgcattaa tatggtacgg
                                                                      1560
gettegteeg ataggegeae ggaggeatee gataettete ggegetgteg geggegaate
                                                                      1620
ggcgaaaagc aagggcacgt cgtccggtcg catacgcagc gdaggcacct cgatcggacc
```

otattoaocc	ggaagaagag	gtcttcccgg	aacttcccgt	tcgctacgcc	tccttgaggt	1680
tracattrat	cgccgctacg	atacggacat	ccgtctctgc	gactggctgg	ctcctacggg	1740
gatgaactcg	cccgtctcca	gcacctcagc	agcctcgcct	gcgtgggcaa	aaggcagttc	1800
gcccacttcg	tccgaaagaa	togtgccgcc	ggatggcttc	ttcgaagtac	cccttgcgat	1860
ccgata	8	0 0 0				1866

- (2) INFORMATION FOR SEQ ID NO:1116
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 556 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...556
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116

atccccggcg	atacgctttc	gtatatccga	ctgtttgcga	tcggactcag	ggctctatcc	60
toggtggcgt	attcaatacg	ttggctacgg	atatgactct	tctatgagta	ttgtacctcg	120
gatcatcgtg	atgctgatca	ttttgctatc	ggtcatggtc	tgaacttcgg	tcttacgatg	180
atcagttcgc	ttgttccccc	attcgtttga	cattcgtaga	gttctataag	aacagcgaat	240
ttgaggaggg	ggcaaccagt	acacaccgtt	caaacgctcc	taaatcacaa	aagacaattc	300
aaaaaaatca	taacaactaa	acaacacaaa	agtattatgg	aacaatgtta	gcttatctcg	360
gtattgcatt	gatggttgca	ttgaccggta	tcgaagtgcc	attggcgtaa	cgatctgcgg	420
taacactacc	gttggcgcaa	taagaagaac	cccgattcac	tgggtctcta	catcggtctt	480
agtgctcttt	cgagttcaca	gggactctat	gggtttcgtg	ggcttcttta	tggcattccg	540
cttgatcacc						556

- (2) INFORMATION FOR SEQ ID NO:1117
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2307 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...2307

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117

gggcgtacca	ccacgacgca	gaggtatctg	tgccgcccat	tgcttcttcc	ttcttcgcta	60
agcacggcag	tcatatcggt	gatgataaaa	cccggtgcat	cgcattggca	cgcacgccac	120
		acactctggc				180
		gcctgataca				240
ccggtcgctg	tcccatcatg	atggggagtc	acgggcattg	gatcatgttg	aacgtgactt	300
		catcccattg				360
		caccaaaata				420
		acgaaatccg				480
		ctacgaaagc				540
atagccacat	cggcaccttc	cgttgcatac	ttataagcta	tggcacggcg	ataccgcgtc	600
cggctcccgt	aatgagagct	accttgttct	ccaataattc	atactttgat	tttaattagt	660
		tacgattgta				720
attcttaaac	actttacttc	caatctcttc	ttcaccgctg	tttactgccg	gagagagaca	780
gatacgtgga	agatcagatg	ctccacattc	tcactgattc	gctcgaacgc	gatgttccgg	840
catgcctaag	atgtccgctg	atatacggca	cttccagccc	ctgattgagt	ggagtaagat	900
cttggcggta	atatgggtat	cgggtataga	aacgcattaa	gccgaacacc	ttcgtccaaa	960
atggaacaga	tcagatgttc	tccttgaggt	cgaactcctt	acgagcagtc	tccaccttcc	1020
atatatcaca	aaaaaatcgg	cacgaagcgt	accattgcgc	acgacaatct	ctttgattct	1080
tccaaatgcg	tatagatgaa	gtgcatcagc	ttcttagtcg	gcggcatgac	acgagagcag	1140
		agttcgtcca				1200
ttttttgctt	ttgaagtaag	tatatgcgtg	cgtcgtccct	tgtttgccgc	atcggcgatg	1260
		acaccgatct				1320
tcagttctct	tgttttcgcc	acactcatta	aaatttttcg	attgccctat	atctatacgg	1380
cattctgttt	cggaacaaat	ataaggtttt	tggcgttgat	ttgcacgttt	gtttcagtat	1440
		cttagcctgt				1500
		aataaaaaag				1560
atcattctgt	tgtctcacaa	ggattcgaac	cttgacaaac	aggaccagaa	tctgttggct	1620
		tggcgaagcc				1680
tttttgtgaa	acaaacaata	aaaacacatt	tggatttaat	tggcatccat	atcttcctcc	1740
		gatggttgga				1800
		aatttttctg				1860
		catcaaaggg				1920
ccgcaacttc	tgcatcattg	cacatatcga	ccacggcaag	gtaccttggc	cgatcggttg	1980
ctcgaatata	ccaacaccgt	ctccggcaag	atctgcaaga	tccaggtctt	ggacaatatg	2040
gacttggaac	gagaagaggg	tataacgatc	aagagccatg	ccattcagat	ggactatgag	2100
		ctcaacctga				2160
		ctgcttgcga				2220
		atccaatctc	tataggcgat	cgaaaacgac	ctgaccatca	2280
tccctattgt	aaacaaagtg	gattgcc				2307

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 928 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION  $1...9\overline{28}$

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118

		cctgtgaact	atgtgcttcc	tccgggcgtt	tgcgttcact	60
aggaaaccgg	cgaccgcaag	gtactcagca	aaacgaacgt	ccatgagcct	gaaagtccgg	120
cgatccccag	caagcacaga	acgggcttat	ataagaacac	gggctacgac	ctgagacgtt	180
acactggcac	cgggcgatgt	acgggcccac	acacacttcag	gatgaagaCg	gcacgcatac	240
ataagcgttt	gcagatttta	cgcatgccga	ttaaaaacaa	actaccopaa	caatattacg	300
agggatggag	atctatccgt	cttcatccgc	teggggacgg	ttcaccaata	pcgaaagcga	360
aatactccat	accgttgcgc	ctgactcctt	cteggtactta	aactatctac	ccttactgat	420
tagagaaacc	gtttggccga	aagaaaatat	geegaeetea	tactaccasc	ttctatcgcc	480
attaagacga	aacgcaacag	gagaaagcag	Caggcaatte	ngcattatag	gaaatccgaa	540
ttttctccga	cccgaccccg	aaaacacagg	taatactgig	agegerates	gaaatccgaa	600
ctgagtgaag	tcaagactat	catgatcggt	attegtaata	acagcaccac	atcaaaagcg	660
constata	ootraatgag	ctcagactca	cggactagat	gagaaaggcg	84688866	720
0001000000	atcaatatgo	agcttacgat	ttgggattgg	LEGALALECE	CEERCABACE	720
ataaccacaa	gattcgtgct	ttggacgagt	ctctcacaca	gcgagccata	gaagacacgc	840
atacctcaac	ttctccacca	atttggagct	tggcaagttc	ttccccgaaa	aagicagaic	900
agcatacctt	tctattactc	ggtatcggat	gagaaagtat	ctcccaatac	aatccctttg	
atcaggacat	tctcctgaaa	gatgctct				928
	J					

## (2) INFORMATION FOR SEQ ID NO:1119

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 392 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...392
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119

tctgcgtgcc	ctgacgggat	topagegega	caagctgcgt	gcagagttca	agagatcatg	60
gcctccatca		agetettte.	actostagge	attactgatg	gagctggtca	120
gcctccatca	atcattigga	aguittite	becegatage	000000000	agatcatata	180
aaagcgaact	gctggagata	aaagagaata	Eggegalace	cgcaaaagcg	catcaccett	240
tgcttcggaa	gaattcaccc	cgaagacttc	tatgccgacg	atgatatgat	Cattactet	300
tracaatooo	ctacatcaag	cgtacccctc	tgagcgaatt	cagaacgcag	gctctggcgg	
agtaagagcc	aagggatcgg	atactcgcga	aagaagattt	ccgggannta	tatctactcg	360
gcctccatgc	000000000	tatactattc	ca			392
gcctccatgc	acgccaccac	catgetgete	Cu			

## (2) INFORMATION FOR SEQ ID NO:1120

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1952 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

.

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1952
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120

```
gggccgtgca tgaagcagcc ggcttcgccc gaacatatcg tccgggctac gcttcggttg
                                                                        60
tgatcgtagc cgagagggtc atatagccgc cggtcaatac ttgccaagac acagaatatc
                                                                       120
                                                                       180
cggcaccgtg gcagcgtgcc ggagcgcaac agttcgcccg tgcggccgaa tccggtagct
atctcatcga atatcacagt acgccggctt cggagcagag tctgcgagct tcgacgagat
                                                                       240
accgggatag tagaaataca taccgccggc tccctgcacg atgggttcga ggatagggct
                                                                       300
gccagctccg cccctttgc cgagaggagg tctcggagcg gcttatgtcc gccggcagcc
                                                                       360
attogocaco gaagogacto ttoggttgtg goggaaatac tgtacgggca atgotocoga
                                                                       420
gaaaatgccg tgcataccgg tacgggatcg catacgctca tggcgtgcca ggtatcgccg
                                                                       480
                                                                       540
tggtagcccg acggatcgta gcgaatcggg tacgtctgct ctgtccgcag gcttgctgaa
                                                                       600
ctgcaaagcc attttcatgg ctacctccac tgccaccgaa ccgctgtcgc atagaagatt
                                                                       660
ttattcaact cggacggcag gatgctcaga agcagttggc caattctacg gccgggcgat
                                                                       720
gggtgaaacc gccgaacatg atatggtcat ctcccgaagc tgccgttcta cggcggcatt
cagtogogga tggtttagco gtgtatggot gcccaccacg aactcataco gtogatoagt
                                                                       780
                                                                       840
togogoogto ttocagatag atgogtacto cotoggooog ottoacggga aatogggcaa
tggatctata gtcgatgtat agggatgcca aaggtggttg cgtccaaacg cagcatttcg
                                                                       900
                                                                       960
tcaatggtca tagcttacct cccagtctgt acgttagtca cttgaaatcc gcattccctc
                                                                      1020
acgagetgea tatecteage getttgette eegtegtggt gaggagateg eeegtgatgg
ctgcattgaa cctatatata tagctttgcg ctgaacggca gggcttagtt gtgcccgtct
                                                                      1080
cccgaaaagc gaagaaaagc tcgaggattg atgagccgga acagtgcaca gtcgtgaggt
                                                                      1140
attectette gettagagge agagteetet ceagegagtg eeggggateg getgeaggat
                                                                      1200
attgatcggg atggagtaga cattgtgctg tgcaggtaga aagcaaattc gatccgctgc
                                                                       1260
tccatcgtct ccccatgccg atgattccgc cactgcatac acgcattccc acacggcgtg
                                                                       1320
                                                                       1380
cagtcgaatg gtggcgagct tttcgtcctg cgtgtgcgta ctgcacaggg agggaagaaa
                                                                       1440
ctcggagccg tctccatatt gcagtggtag gtggtcaccc cttgtcgaat aatatctgca
                                                                       1500
gtttctcctc cgagagcagc cctaaagagg gcagcatttg atgtccgttc gttgcttgat
ggcacgataa ctttcggcct ctgtcgtatc tcgttcatag acgcagtgcg cccgctggcc
                                                                       1560
acaagagaaa gcgtccgatg ccttgccgcc tgttgtaagc ggcctgctcg gcacaaacgc
                                                                       1620
                                                                       1680
ggccgaaaga agtccgtatt tctctatcga agcggcataa tggcggtttg agcacaccat
                                                                       1740
ttacagtctt cgggacagtt gccgctcttg gcgttatgat ggagcaggtg tcgaacttat
                                                                       1800
cgcccatgaa ataccgggtg atccatgtgc agcctcgtag agtgcttcct tatcggcaga
ggaggccagc agagggcttc ctcaagggtt agttcgccac cgtttatcag tctgttttcg
                                                                       1860
                                                                       1920
atgtotgaat catatatggg aacggagcag atcotttoot gtotgcatoo ggacaaaagt
                                                                       1952
agaaagaagc tccggcaata gaaactaatc gg
```

- (2) INFORMATION FOR SEQ ID NO:1121
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 608 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...608
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121

```
ccccgacttt ttgcattaag ttactaccga caaagttagc atccagtcta gagcaggacg
                                                                       60
actctgagca tttgcaaaac cgattgttgc gagcagcaag tagctgccaa aatcattttc
                                                                       120
ttcatttttc gttcttttt gagttttttc tacaatgtaa cacactctct ctcgttcaaa
                                                                       180
                                                                       240
agtatgccta tacatacttc cgatgcagca aagatacaca atgaaacgta tctatgattc
aaatgaagat ttgcacttat caggtggaat ctgcaaaacg cgaaaaacgg acaaatattg
                                                                       300
gatgatataa aattattaca tacatttgca ccgcatttca aacaaaaaaa tgctactaag
                                                                       360
gctgaatcgc tagctcagca ggtagagcac atccttttaa ggatggggtc ctgggttcga
                                                                       420
accccaggcg attcacgaaa aaaaggggcc atgtcaaaat tcggtttttt tgaagtacgc
                                                                       480
                                                                       540
ctcaaaaagt ggatattaaa ttatccttgt gttatagaaa gagtccggta caataccggc
                                                                       600
tctttttcgt taatcttgcc ttaattctac tatttctata atnggtattc ctccaatgca
                                                                       608
ttgataaa
```

- (2) INFORMATION FOR SEQ ID NO:1122
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 778 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...778
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122

						•
tcttttcctc	ctcctgtaaa	gaagatcttt	cactatcaat	cacatccata	acccacatga	60
agtactgtgt	gcactaccat	ggtgagaaac	tttaattaat	caaagatgac	tggttttgtt	120
				cgggatctgc		180
agcagaatcc	gatgtcttga	tactcccaaa	taaaggcaat	agaagcgata	tigtigtcat	240
ccatttcgat	aatgggcggg	atgcatatcg	cttcaatatc	tgttcattga	tcgttcatca	300
tttacgttct	catcttttgt	ctcctcgcct	tcttctagtt	gtgaattctc	atcaaagcct	360
catagatagt	ttcctcccca	tcatagtctt	ctttttttgt	ttgtacagtt	gttgccaaaa	420
tagctttcga	tattttacat	cagtctatct	aacgcaactt	gggaaggaga	aaggaaaata	480
atcctcccca	attgttggca	agttgaatcg	caggagactc	atctgtaata	tattctcttg	540
ccaagccctc	ctccattctt	cttttctcaa	tatacattct	gccagggtag	cgccttttct	600
tcattgacat	tttgacttag	catatcaatc	acaatggcaa	ctgatcatat	aagcctatcc	660
acattcgctt	tcatctgctc	ccgtcctggc	tgctcattgg	taataaccct	ttggtagcag	720
ttatatatga	atatgttcga	ttataanggc	tggattttga	gttaagcatt	ttttatca	778

- (2) INFORMATION FOR SEQ ID NO:1123
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 740 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...740
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123

tacacactca	gcaatacgta	acopteteea	tggctacttc	ggctatcctt	cactccgcag	60
tgcgcactcg	gcaacacgcu	catagagag	catccatoga	tacgaccggt	atggttgtct	120
tctgaagtta	tggaaacgcc	catggaggag	categattat	aacaatacca	ecteteecaa	180
tgcaggcaga	gagcgaagtc	getgecataa	catggtttat	ggcggtgcca	actoactat	240
aatggtgatg	acctctcctc	cagcccgggt	atgagicita	agcaagaagg	agegageeae	300
tgtgcggtgc	cgaattgccc	tgcttgattg	taaatgttat	gcgtgggggt	cccgcccggg	360
aaccatccaa	cccggacagg	ccgactattt	ccaatctgtc	aaggtggtgg	acatggtgac	
tatogtotga	tcacattggc	acccaactcc	gtcaagagat	ggttgacttc	gttggtttgg	420
gactggagct	ggcattcaag	tccgcaatcc	tgcactcatc	ctttccgacg	gtatcatcgg	480
gactggaget	nanagatgat	attocctcco	ttcaaaaagc	gtcgtaccga	agatgaaatc	540
tcagatgatg	aaaaggcgac	actotoggto	02222222	togtcagoga	atatcattac	600
gcaaacaatg	cccgcgggca	actiticget	8000000000	tccaacttcc	aaaagaagta	660
ctctctcgag	cttgattcgg	ccgttatgga	gcagaacacc	toeggeeeee	aaaagaagta	720
tgcagagatc	gaagccaatg	aagttcctta	ccgaagagta	CCagacggaa	gatgccgact	740
atatcctcgt	tgcattcgga					740

- (2) INFORMATION FOR SEQ ID NO:1124
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 559 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...559
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124

gatcgtgtac	acagtctcgc	tatgttggtg	ttcgatgagc	aatacaggaa	aaaagtngcc	60
gaacatttt	cttcctccnt	anggagcggt	acttctacta	tgtctttact	gtgaaattaa	120
aacccggaca	gcgcgatttc	tttttcgggc	aaattttcct	ggtatgcaga	ctgccatggc	180
ttcgatcgtg	aacaaaccga	tatgaatcac	tttatgcagg	tcctcagata	tttggaccct	240
attcatatct	caaagcaacc	aatgataatg	gattccccat	gtcgagaatg	tattcaatca	300
gacggttacg	atcgggggaa	ccatcactca	gcctttacca	ttcagccgga	cggagaaaac	360
aatgtgaagt	tgcagcgtgt	ggttgcaaag	ttgatgtgaa	tatcgtggaa	ggagtggaaa	420
atctgcagaa	gattgaactt	ttaatgctaa	tgtccactat	agattggtgc	ccaaatcagt	480
cagagcctat	caagttttac	ggncccggta	gaactaaggc	gagtaggtac	cacgaaccat	540
ggctttggct	attatgccg					559

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 313 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...313
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125

atgatggcta	ccggcgacga	agctctctat	gctcgactgg	aggcctatag	gagtcgctca	60
aagaaaaagt	cgttaaggcc	aatcgcgagc	tggcagagtg	aagtacaact	tcaaaacgaa	120
ttaaagccct	gtcctgcccc	gttggtctcg	gcacaaaaaa	gatcggcagt	ctatagccgt	180
ggcttattta	tgagccctat	cggctgtagt	ctgcctttct	ttttctctat	tatcttttcg	240
aagtatgtga	agtcgttccc	gcttcgaatc	ggcaatccaa	agaatatagc	aaggctatgc	300
tcgatctgtc	gga					313

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 632 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature

### (B) LOCATION 1...632

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126

	annacattat	ccatacatct	tcgttttggc	attcgtccta	tcacgttctt	60
tcgaacagct	gaagcattgt	Cogcacgece		gaacccactt	cttttttcat	120
tgaagagttg	ctctgctgcg	gcaaactctt	cgggcgagtg	gaacccactc		180
- cactactta	geetetteaa	gtgtcagtga	ccttcgcgaL	gageeeeee	Backceage	
acgeeeeee	acttacttto	togaggetet	caaaagtttc	atttgttttt	atgacctgca	240
atacgeteca	acceacce	++	cotoctogca	octtatcaaa	agctattgtg	300
tgtttttgag	caattagtga	tgaataataa	cctcctcgca	bettette	taattttta	360
gaggtatatc	cactttcgta	aatataacaa	tctcagaata	tattttgttt	Lggttttta	
505500000000000000000000000000000000000	aagtgcatat	gctcattacg	cccaagcagg	atacgagcct	gaaatgctcc	420
CCgaggaaaa	a b = b = b = c = c =	Ganage and C	gcgagatttt	tttcgttttg	gtttcacttt	480
gattgtggtc	tgtgttttgt	gaaagcaggc	gegagaeeee	actttaggt	otcataaacc	540
ttttcttttc	cacgccaaaa	gcaaaaagtt	cacgtgccac	accicigge	gtcataaacc	
gaaaatttag	gcgtgtgaac	ccaatcggat	agggatgata	catcctatgc	tgaatcggaa	600
gaaaatttag	6060600000	anaaanacaat	ac			632
gtgaatatgg	tgcaaaaaaa	gagggacagt	50			

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2267 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...2267
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127

```
gcgttctact ttggctttga atataggcaa gcgagtcaac attggtaaca tgtggattat
                                                                        60
atctacagca acggtttcta caactccaac aagacgaagc catctcctac cgtttcttcg
                                                                       120
gcagctaccg ttccgaccgt tacgaagcta tgcttatgtg ggcaacaatt actatctgat
                                                                       180
gacggagaat ggggggttac gaatgatgac tacgtgatcc atccgggtaa ttttgccaat
                                                                       240
ggaacaacga attcgtatcg acggatattc cggtgaagtt tcccggcaat aatagttcaa
                                                                       300
ttcgcttcgg caaggaacgg ctcgtctgac ccatcgctac aactcggttt ctatcgtgag
                                                                       360
ggacagaccg agtattatga tggcaatgaa ttgaggctcc tcatttgatc gatacgatgg
                                                                       420
tattcgtgcc cgtgggtagt attcccacac tttcaattat accaaaagtc gccgtcgctt
                                                                       480
caaggicaag atcettigga caattegatt tateccaate tgittateaa aegaetgaag
                                                                       540
atgccggaga gatgatcacg ctgccgaacg acaccactcg tatggaaggt accacaatac
                                                                       600
gctggctctt tctttgcggg aaggtttcca tcgctggcta agttcggcct gacggcttat
                                                                       660
gtcaggttgg agaataggtt ttatacctac aagattcagt agtcggtgta ccccctacgg
                                                                       720
acagggagtt cagcattatg tcgggggaga gatcagccga cgagggggga aatatctcaa
                                                                       780
ctttcagccg atggagagct ttcggtcgtc gggagcgatg ccggagcatt caactcagag
                                                                       840
                                                                       900
gacgattaag tacagcgttc gatctccttc gtcggaagac ggaatggaag cttgggggca
actteteaat actegteegg getaetttet ggteateate atggtaetgt geaetggtgg
                                                                       960
gacgaatcgt tcgatttcat cagcaactca gatgggtggc tctcttcgtc tgaaggactg
                                                                      1020
gggtacgact tgacgttgca atccgctacg ctcaagaact atatattt cgaccatagg
                                                                      1080
                                                                      1140
ctttccccca acaggtctct tctcccatac aagtcctcga agggcggtag cacatgccta
ccgatggggt gctttgggat gggaagtgga agcggctatc aaacaagtag caaccgtacg
                                                                      1200
gctttgcctt taccgaagct ggcggttatg gcaatctcta tttggacttc cgtctgccga
                                                                      1260
gcagtaccaa ggtgtgcgta tacagacggg agtggatgct cgcattcatt cctcctacta
                                                                      1320
```

```
tgcccgtatt ntgaacccgc cgtacagcaa ttcaccacgc aacaagagat aaggtgggag
                                                                      1380
                                                                      1440
ggtctttccc tctgatgaat gcttatgtga atatccacct cagcgctcac gtttcttctt
                                                                      1500
tgaaatgtac aatctggctg aggctttcat gatagcaagc gtttctcttt ggtgcatacg
ccgtacaacc ctcgtggtcg cgtatgggta ttgccatcga cttcaataaa taaatggaaa
                                                                      1560
                                                                      1620
tgaagaaaag attgctctct acggcgtttt actgatctct gtccttatcg tgatggtgct
                                                                      1680
ttgcgccact gtggtggagg aggggctgcc ggtggggacg ctgtcgttcg ttgcgtgatt
atcctgatat tcaccgagaa ggagtgctga ggatcttgcc cgatacaatg acagagacta
                                                                      1740
ttatgtggga caggattcca ccgcggtttt gtttacgatg tagcacgtcg tttatcggaa
                                                                      1800
                                                                      1860
atcagtggca ttcgatagaa atcggtctgg aaaagaattg gaaagagagc cttgaaaggt
                                                                      1920
tggacggggt gcatgcgaca tcattgcaca ggacattccg ctgacggctg tacggacacc
gtccactacc gctttcttcg tccgatacac cttggacggc ttatctggta caacgtcgat
                                                                      1980
ccgatactgc tctgattcgt cgccagatca tttgtccgga cggacggtga ccattccgga
                                                                      2040
aggeteteeg gegaggtttt egteaaacae etgteegagg aaategggga tagtatatat
                                                                      2100
atacgaacga toccacttat totgoagago agttggocat gatggtggoa toggacacat
                                                                      2160
cgatctgacc gtctgtaacc aacatgaagc taagaagctg gggcactcct ccctgcgttg
                                                                      2220
gactgcagtg taccgctctc ttttcgaact gcgaaggcat ggttggt
                                                                      2267
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1794 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1794
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128

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cccctgggag	agcgatgaga	aagaaaagct	ctcggatgaa	gaaaaacgct	tctgtataat	60
tgctatcggg	gctttgtcga	tagcggagca	ctactcccac	agagaaaaaa	gaccggctgc	120
gtaccctgtc	cgaagagatg	agtatggctc	attgacattc	ggacagaatg	tgctcaagga	180
cgagaaacgc	tacaaatcca	cctcagcgat	ccggcggctg	tggccgggat	gcccgagacg	240
gctctgctct	cgcttcggag	aaagcccggc	gaaagggcta	tacggagggt	tggctttcga	300
cctttctgct	ccgagctact	ttgcttttat	gaagcattgt	cccatgggaa	cctgcgccgg	360
cagatgtatg	aagcgaaaat	gtgtgtcggc	ttgtagacaa	tgagtataac	aacgaagctc	420
				ctcctgggtt		480
cgcccacttt	ctcttcatga	caggatggcc	aagaacccca	aggcagtcca	agaactactg	540
acaaactact	ggatgcatac	aagcccaaag	cgacagatga	attggagaga	tccgcaaatg	600
ggcttgccga	caagacatcc	gaagtcgata	acttcacata	caaccatggg	attgggcata	660
cttctcggaa	cagtacaaac	aggcccctac	gatctggacg	atgagatgat	gcgcccgtac	720
ttcgaattag	ggcgatcaca	cgtggtatct	tcggcttggc	caaccgactg	tacggacttc	780
attttccgaa	cggacggatg	tgccggtcta	tcatccggat	gtaaaggtgt	acgagtatcg	840
gacgaagacg	gctcttatat	cggtctgctc	tacacggatt	tcttccacgc	gaaggcaagc	900
				atcagcaccc		960
				gctcctgaca		1020
tggagacttc	ctgcacgagt	tcggccatgc	cctgcatggc	atgctgtcca	aatgccgctc	1080
agctccttgt	ccggcacctc	ggtagcccgt	gacttcgtgg	aacttccagc	caaataatgg	1140
aaaactggct	gacagagaaa	gattttctcg	acaccttgcc	cgccattata	taacggacga	1200
acctatgcct	accgaattgg	tggaaaactc	ctctcggcac	gdaattacct	cgcagcaagc	1260

```
ggtgcatgcc gtcactcagc ttcggctatc tcgacatggc atggcatgga ttgtctgctc
                                                                     1320
cggggatgac aaattagaca tcaaggcttt tgaagaggct gcttggtcaa aactcttatt
                                                                     1380
ctacctcctt cgccccgaa tgccgtgatg agcacggcct tggtcatata ttctcgggag
                                                                      1440
gctatgcagc cggatactat ggttacaaat ggcggaagtg ctggatgccg atgctttcgc
                                                                      1500
agctttcaag gaagtgggtt tttcgatcgc gaggtagccg gtcgtttccg ccgtgagata
                                                                      1560
ttggagaggg cgatacggcc gatgccatgg agctgtatgt agctttccgt ggacatggcc
                                                                      1620
ggacattgct cccctgctga agcgtaccgg cttggtttag cctcattatg cggtctcaat
                                                                      1680
accacgtaaa acgtaagccc gaaagcgaca cgtcgtttng ggcttacctg gttttantcc
                                                                      1740
tggttttgga aacctgtgtc ttgaatacan gggatatgat ttactggcga atgc
                                                                      1794
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1366 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1366
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129

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60
ccgggccgat gctttcagct cgtcttccga ttcggaacga gtagcgcgct ggtgctggcg
                                                                       120
atccctccgc cgcgctccat gatactcatg tagctgtccc ggcgagccgc cattggaact
                                                                       180
catcttccct gtagccgccg aagacgaatg ggtgtggctg tccacaaagc ccggcagtac
gcagcgtccc gtggcgccag ctcccggcag ccttcggtca tggacggggc tacgtccgcc
                                                                       240
                                                                       300
atgcgccggc gaaggcgatg atgccgtcgc ggataactac tgcggcaggg ccttgatggt
gtgtatctgc cccatggctt cgcggccgtg tttggcttcg gagcttggca ggtgacgaag
                                                                       360
ctgggcgata ttcttgatgt agaggttcat tggtgggggg tgttaggcat gtgtgtcggt
                                                                       420
                                                                       480
aaggaagett geegatagaa eecaceaege caeeeggaag agggtggegg gtggtatete
                                                                       540
tatccttcaa caaaaaacat gctgacgttt actccatgat ccgtgattcg aggatctgac
catggagaag ttttcgatgc cgaggtagta ttcggcacag tcgatcaggc ctgcatgggt
                                                                       600
                                                                       660
acgagtccga tcacttcgct gcctacgacg gatacgcgta tcgggcggct tccatgcgta
ccatctcatg agcgcgatag acagcctctt ggtgaagtcc gtcaggttca tggacacctg
                                                                       720
                                                                       780
cacgatgccg cggtcgtaag ctctacgccc atggccttgc agaagcgcag accgccgccg
aggagogtac cttcttggcg atggcgtccg cgatggagag gtcgttcgta ttgggttcac
                                                                       840
                                                                       900
gttgtaagcg acgagcgca tgcgggcgcc gactgccacg gtccggctgt cgggtgacga
                                                                       960
teggeeggge egaagteggg atgecagteg gttegtgtat ettetetgee atgeettega
                                                                      1020
actcgccttt gcggatcttg ccaggttttc acggtgggga gcggtagccg atttctcata
                                                                      1080
gaggaatacg gcacgccgta cttctcgcct atcgtgcggc ctacctcctt ggcgaggggt
                                                                      1140
cggcgtcttc ggcagtcaca ttcttgatgg ggataaaggg gatcacgcca ctgcgcccat
                                                                      1200
acgggggtgc tgacccgtgt gtttggtcag gtcgatagct ctacggctat gccaacggct
                                                                      1260
togagoactg cotocogaag gggotgggtt ogcocactac ggtoacgacg agacggttgt
gatcctcatc gttgtatagt tcagcagctt gacgccttcg cgcgtgcgga aggggtttac
                                                                      1320
                                                                      1366
tatttttcga ttttctcttt gtcgcggcct tccgagaagt tgggca
```

- (2) INFORMATION FOR SEQ ID NO:1130
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1433
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130

```
60
ggaacagccc aaactgaatc cacatatacc ggatatgcag cgtgtcttgc tgaggtgata
caggtggagg tgtcggatat ttcactgaaa gccacaacac ggagaaactt ggcttcacag
                                                                       120
                                                                       180
gacgagagga aggcatttcc gcctatgcgt ggccttgctc attgctgccg tctgagacta
accaagteet aaaagatagt tgeaaagagg tteetttete teaaggattt ggetettatt
                                                                       240
                                                                       300
ccttaacagc tctttttccc cctttttcgg gggtattatt ttttcaggag gggagtagcg
gcttgaccag ttgccagatg acgattcccg ctgtgacact tacttgagcg aatgcttcgt
                                                                       360
gccgaactgg ggtatctcta agcagaggtc acgaggtcga tggcttcctg tcgtactcct
                                                                       420
tttacttcat tgccaaagat agggcgtagc gtgtgccttt tgagggggag aaattttcca
                                                                       480
                                                                       540
aggatagget cetteegeet gttetatege acagatacta tateetttge ttteaattet
                                                                       600
ctattgcatc cactaccgaa gagaaatact cccatttcac actgtcctgg ctcctaaagc
tgtcttgtgt atgtcgggat gaggtggccg agctgtgttc cgcacaagca tagcccttct
                                                                       660
                                                                       720
aaccgaaaag catcggccgt tctaaaactg acccgacatt gttcatacta cgtatatcat
                                                                       780
ccagtatgat cctgaaggta gcttggggct ttcgtgatat tcttctgttt tgagtcgctg
                                                                       840
tattcgatag tcttttttt gcgcatgtct gttgtctggt cggattgagt gatggtgcac
attccattat caaatgcaac gaatttctaa atataggatg aaaccttgaa tggcgttctg
                                                                       900
aagttcagtt tttttcgagt gcagatccca ttataagtgc aacataattg taaatttagc
                                                                       960
aagaagcact cgaacggcgt ctgaatccga gtttctttct tggctgtagt tcagtttgtt
                                                                      1020
ctgtataatg aaatctgttt ggtcgttata tcgatgaaag aagaaccttt agggatgttt
                                                                      1080
gtctaatcag ggcatttttg ctcctcacag agcaaaaccc tcttgttaca cgagaccgaa
                                                                      1140
                                                                      1200
aagcagetea agtaaaaget geettggatg cattagtaga gegattetet atetetgaca
                                                                      1260
aaagtcgtcg aacgatattt agtgtagata acgggaaaca gttgtgtgtt tgccgaaaat
                                                                      1320
acgtatcttt gcaggcaatt gaggggaatc ctctccgttg ctatgaggat tgtctcatgg
tgtatggtag cacaacaggt tttggttctg tttgtcaagg ttcgaatcct tggagacaac
                                                                      1380
aacagagaaa gggttgtatc ggatagtgaa acttccggat tcaacccttt ctt
                                                                      1433
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 642 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...642
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131

-castteact	пассаясяяя	cctttttcat	tatagtgata	cgtattcttt	gggattctgc	60
geacticget	gaccaacaga	agtgggtcag	tctaccctta	catcataate	atattccaag	120
cccgaaagca	aaagaaattt	agigggicag	cccgccccg	ttccctcaca	atcatctttc	180
cgtgagatag	gtgtattcgg	atccattcca	gcatgaatat	Licetteacg	Secure	240
cctcgtcatc	ataggttact	tgaatcgggt	gtcgagtgca	ggctctccgc	Caccgaacga	
gatataagat	ccacatgcga	tattcgcccg	ttggcatcgt	agtaaatgga	geeerggate	300
ttattacccc	attogritti	atgtcacgag	cgatatagcg	gttttctcat	cgaagataaa	360
LLCLLacce	acceptoct	ttgtggagac	agractotas	gaagccactc	ggcattgtcc	420
gtgagtatct	gcagactggt	Ligiggagac	55c5cc5caa	gacaatatot	tctttcgaaa	480
ttctgcgcac	gattttgagt	cggagagagt	aaactcctcc	ggcaacaccc		540
aaggtttgta	gaagaattgt	ccttggtttg	gcccacggct	gcaaagaaag	Caccgaagaa	
atcaaagaaa	taatggttgt	ttttttcatt	tcaataatga	nttatntgat	tgtatgactt	600
aagacggatt	coacaatcga	cccaatctct	cttgggtatt	tt	•	642
aagacggacc	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~		000			

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 838 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...838
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132

```
tcacgaccga agaatgccaa aaccaaatta aaaaccagaa gaagattata tcgtagttcc
                                                                  60
agttaaagaa ggcgagaaca tcgaaagagc actgaaacct tcaaaagaaa gtttgaaaaa
                                                                  120
                                                                  180
accggagcag tacgcgaatt gcgtgctgtc aggcttttga aaagccctcg gtggccaagc
                                                                  240
gcaagaagat gcaaaagcca tctacgtgaa gcagcttcag gttgccgaag aataaagaag
                                                                  300
aataatattg ccgcagtctc tttgcggctc aagaggggtg caatgatcga gaccatctca
                                                                  360
420
aagttcacgc gtcagaacga accgtttgtg acatgcacaa gatttgaatc gctatgccgc
tttcttcagt gaacacacgg ggaagtattc gagccaagcg aacgcgacaa ggatgtcgcg
                                                                  480
cgcgcttggc cttctcttta atggaagccg gacaaaaaag ctcttccgtt cagegcagat
                                                                  540
                                                                  6D0
gagcgcgttg aaaagctttt acaaatacat ggtcaaaatc gggcttatgg gcaaagtcct
gtccgaatgc tgaggggacc gaagaaagag aggccgcacc tgttttcgtc ccgaacaatg
                                                                  660
aaatggaaaa agtgctgaat aagccctccg tgaagatgat ttcgaggccg tacgggacag
                                                                  720
                                                                  780
actgattctg gagacctgta tgaagtgggt ttgcggcgtt ccgaaatagc cactctcaag
                                                                  838
acaggeggta gaagacaagg ceggetgeat taegtateat eggeaaagga atagageg
```

- (2) INFORMATION FOR SEQ ID NO:1133
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...756
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133

gtagacccga ccaat	tcccga tctgcatgta	ggagatctgg	cacccgacgc	tgtcagctac	60
ggccgtttat tgtgt	tggttt ggagaagctg	ttccgatgta	gagccggcca	tcgaagaggt	120
aacacaggca gacat	ttctcg ttgtcatggc	acctctctca	acgtttatcc	ggctgccgga	180
ctgttgaatt atgct	tctcgc aactgcccca	tctatctgat	cgatccaaag	cctgtgcgca	240
gcaccccgg caaga	acatto ggtatatoca	tgctcctgcc	acggaaggcg	taagatgttg	300
cggcaagaac tccgt	tgatat agatcgctaa	aaaaacacta	acccaagaac	ctgccatcgt	360
ggtggttctt ggggt	ttaatt gtatttgtto	gttttcggaa	ggctaatgaa	ccggtttgtt	420
ttcggaggca aaccg	gaacat tagaatgacg	atctcactct	ccgtgaaaac	acgaatagcc	480
	actcct gaactgacat				540
ccatgatttt tcaaa	aagcca gttgggtcaa	aatcgtaaac	ggccagattg	tccgttgtgc	600
gtgtgcccgt acaga	agccaa gtccacaccg	gtcatcgcac	gctgtcgagc	ttgtgcggct	660
ggtgatcgag cagga	atagag gccttatggt	atcnacatgt	ggcataagct	tgtgcagcgg	720
agcacggaat acatt	tgtgct atcgtcccgt	cctatc			756

- (2) INFORMATION FOR SEQ ID NO:1134
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1206 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1206
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134

agaagtcgtt	tggctttgcg	atacccttta	aagaangcgt	ctgcaatgtc	agccatcggt	60
					atncaaaata	120
					caaaggtctc	180
aaatggcggt	ttagcgttgg	aaaaacgtgg	ctcgggaatt	tettcgtttt	ggcgcgggaa	240

```
gtaaaatttt acgcgccaca acggaaaaat tctcgctcgt gaatctcaga aaaccgaacc
                                                                       300
gcattccggc caattccgga accaaattcg tgaggaatct gctacaacgt ctgttcgacg
                                                                       360
tatgcttaag gcccatcgag gtcaagccct catgaaagtc agaaacaact caatcggatg
                                                                       420
atcagtaaga cgcgctgctt gtagaacgta ccttcggtag tattcgacga tggttctgtg
                                                                       480
gcggacgatg cgctaccgag ggttagccaa gacacatacc cggaatatcc ttgaagctag
                                                                       540
gcctacaatc tcaagcgtat gccggggctt cttgtgcttc aaggcgcaaa taggcgtaaa
                                                                       600
acgccggcac ctcgagggca attgccctcg aggtgcggaa aggggactaa tccccaagct
                                                                       660
gcaaaacaga cgagaatggt caaaaaacac cgggaacaag cgagcagaaa gaacagcctc
                                                                       720
tttgtgcaat ggtctatctt gggattgata gatgaggata ttccccttat cgtccttgtg
                                                                       780
ctcctattat ttttagttac aggacaaatg tagtgctttg tgccggcttt ggtggtctca
                                                                       840
gaatttgaga aattcaagag cagattccaa tctcaaatgc aacttttatg aataaccgga
                                                                       900
aataatacag ctcaatccag atcggccata ttatcttcca ggtagaatcg ggaaaaatca
                                                                       960
gataggattc tgctcctgac ttcggagttc ttcccgggcc tttttcattt cctcgcggta
                                                                      1020
ttgtttgcgg ctttttccat ctctcggcgg agcttttccc gctccttgcg ccattcttat
                                                                      1080
tttgcttttt ctgagccttc atatactctt ggtagtattt ctcctttgct tgcgatattt
                                                                      1140
tegeatagee teegagttgt caggetteaa aacatteaet eettgeggaa ataaegegaa
                                                                      1200
                                                                      1206
cggccg
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1142 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1142
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135

```
ttccaatgtt cttcgtcccg catcatcatt gtcgagatag cattctatct gcgataaacg
                                                                        60
cccaacacta tcttgcgttg tgggtcggga ctatgaagga ctttccgata gagactgaat
                                                                       120
acatgactaa cggttcatac aacgacttaa aatatattga acgctgtttt gaatgtgtaa
                                                                       180
atgcctcaaa cctgatcgac agaaatgtcg ttcgacaaat gaattacctt tgttgggtag
                                                                       240
ttatagagaa aaaggcaatg aatccgccca aaagactgct tgtcattcac cgcgccttgc
                                                                       300
tccttaccgt atcgaactgc tcaatactct gtcggcagct ttcatacaca tatctacttc
                                                                       360
gaatttgcat cacctataga acagcgattc gagcaggcga actagccaag cgtgttcact
                                                                       420
ttcaaagcag tgtacttcct ccgccccaaa aatcccggga ttgaaaaact ttcgtcccta
                                                                       480
tgccgcctca tggttcgcag tcttcgtccc gatgtcgttc tctgtagcga attcaatctc
                                                                       540
tgacactgac ceteactget geetetegee tgtteagtee gaaaaceage tgtatgtett
                                                                       600
atgcgatgac aatgaacaaa tggcagaagc agagctgact acggtcgtgg cctcaaacat
                                                                       660
cggatgctct cctatgtgga aggcgtattc tatgtgatag ccgtgcctgt gatctctatg
                                                                       720
cctctcgctt cgctagctgg atagggagcg attcgtttac ctccccatcg tacaggacga
                                                                       780
aaagtgotgo gooccotota tgaacaggto ttoggtatag googggacot gogcatgoto
                                                                       840
tcattcctgc tggtgctcgg atgatactgt atgtaggacg ctgtcagagg aaaaaaacct
                                                                       900
gccggcactg atcgataacc tttccactct accgatgatg ttcatctcgt tattgtcggc
                                                                       960
gacggcccga tgcagtcagc ctaatgaatc aagtgcaagc tacaggccat ccggaacgaa
                                                                      1020
tcatatttga gggaaaaagg aaggagcaga gctttatgcc tactatacgc aggccgatgc
                                                                      1080
ctcgtattac cgagcatgcg cgaatgtttc gttcggtcgt aaacgaactc tcatagcagg
                                                                      1140
                                                                      1142
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2284 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...2284
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136

```
cgaaaaattt tacgctcggc attttcaggg acatgaaaca agttttttcg cgccacttcg
                                                                        60
                                                                       120
cattttcatc tcgaccacta tccgcagtcc ggcgaacctc cgactactga ttttgtttcg
                                                                       180
tttatatata atagagagag actacagcgg ggacgatgca ggagtccggt atgcatacct
                                                                       240
tacagtagtc cgaacggggc ttgccgtaga tcagctatgt acaagccaaa gtcaaaaaca
aaggacataa gaaaaaacta ctcgtcaaga tgaaaacaac gaccttttcc gtagaggcat
                                                                       300
gatgtgtggc ggttgtgctg caagtgtaga gaaagcagct ctcgtgtaca aggcgtacaa
                                                                       360
                                                                       420
acggcattcg cttctctgga ttcccatagt ctacagtgga ttatgctccg gagacaacct
caccggagge aataatgaag gtgtacgeet egeeggatte gagtgtaage tetgacaage
                                                                       480
ccaatcetta aaccegatag teccegtgat atgaaggage aaaaaegttt ttecegtagg
                                                                       540
                                                                       600
ggaatgcggt gtgccggctg tgcgcatagc gtagagcagg ctgcctccag gtagaaggca
ttagcgatgc gaacgtccaa ctcgccgaga atatacttct gtatcggtgg acgaaaggtt
                                                                       660
aacttcggca gaggatctgc gcaaagtatc cgcagcatag gattcgacct gatagtggag
                                                                       720
gattcggagg cagagaactt cgccggcgcg atgccatgga agcagcagaa ctgagacgga
                                                                       780
tgaatgcgat acgatcatag cttggtcgtc cgccatcctg ctgatgcttc tgagctaatg
                                                                       840
                                                                       900
ccgcatttcc agatgatgcc ctacctgatg atgctcatag cctgcccgga tacacatggg
caggaaggac tttccaccga tcggcactca acaactgcgc cacggcgtat tttcaatgga
                                                                       960
                                                                      1020
tacgctggta tcgttgagca cactatctcc tttttttata gcctgatagt cctgctgttt
ttccgcgaag gccggccggg atgaagctcc acctctactt cgatgcttcg gccatgatat
                                                                      1080
cgcatttgtc ctactgggca aactcatgga aaagcgtgcc ggccgaacac ggggcaagcc
                                                                      1140
attcgtgaac tgatgcgact acagccggcg gaggcatggt cgtgcgcaac ggacgcgaga
                                                                      1200
ccgtgatgcc cattgctgcg ctcgtgcagg cgacttcgtt cgcgtacgtc cgggcgagca
                                                                      1260
gatacccgtg gacgtatcgt gaccgaaggc agcagctccg tacaagagag catgatcagt
                                                                      1320
ggcagccctt accgcgagag aaagaagtcg gctctatggt tttctccggc acatcaacgg
                                                                      1380
ctccggtgtc ctcaccgtac agtctactca cgtaggcagc gcacggtact cgggcgcatc
                                                                      1440
                                                                      1500
atccgcacag tccgcgaggc acaggccagc aagcgcctat ccaacgtctg gctgaccgga
tcgccggcat attcgtacca tagtcatcgg gctatccatc cttacctata ttatatggca
                                                                      1560
actgacggag cagccgatgc ttcggtctac ggactcctct gtgccatatc ggtgctgtga
                                                                      1620
ttgcctgccc gtgcgcactc ggtctggcta cgcctacggc tctggtgtag ggatcggacg
                                                                      1680
                                                                      1740
ctcggcacga aatggtatcc tcgtacgcaa tgccgagcac tggagcgttt cgctaccatc
                                                                      1800
gatgccgtgg tcttggataa gacagcacgc tcaccatagg caagccggaa gtgaccggta
tcgattggtt tgttcggata ccgatgtacc gaaagtacgc cggctgctct actccgccga
                                                                      1860
gatcttagca cgcatccact tgcagctgcc atttgccgag cctttgccga aacggcagga
                                                                       1920
cggaggagct gtcggaagtc cagaatttcc ccggtcgtgg atcgaatttt ccttcgaagg
                                                                       1980
agagatctac agagtgggca accagacctt gtcgaggagc ttggcgcaca gataccgacg
                                                                       2040
gatataaccg ctctgtcgag gatgcagcca tcctctattt ctcacgtgcc cgaaagatta
                                                                       2100
                                                                       2160
ttgggacttt ctgtgtgacc cgacgaactg caaccttcag gcagcagaag tgctcgacag
                                                                       2220
cttcatcgac atggcattcg caccatttat gctgaccggg cgancgcccg aaacaagcgg
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1184 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1184
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137

```
ccgcctccac accgacctgc acgaatgcct cggacatggc agcggacagt gctcccggt
                                                                        60
gtaccaggcg atgcacttgg agaacacgcc tccacgctga ggagacgcgt gccgacctct
                                                                       120
togocotota tittotggoo gatoccaaat gatogaatta ggtotittga cogatocoga
                                                                       180
tgcttacaaa gccaacatta caaatacatg ctcaacggtc tgatgaccca actcgtgcgt
                                                                       240
atcaacgagg agaggagata gaggaggcgc atatgcgcaa ccgtgcactc atagtcgcta
                                                                       300
cgtcttggag catgccgagc ggccgggggc aatgtcgctg gtcgcgaaga gggcaagacg
                                                                       360
gcactcgtga tcaaggacta tgaagcagtg cggcgatcat tgccggtttg ctgaccgagg
                                                                       420
tgcaacgcat caagagcgag gcgactatac cgccggcaaa gcgttggtag agcgttatgc
                                                                       480
cgtccacgtg atccgctctt gcacgaggaa gtgctgacgc gctatgccaa gctggatatg
                                                                      540
ctccgtataa gggatttgtc aatcctcggt tgagacccgt atataattgg agggcaggct
                                                                       600
tacggatgca acgatagaat acacggaagg ctatgccaac aaatgcttcg ctacagtgca
                                                                       660
gaatataget teetgeetae agacageege ttttgeagga ggeaegaaga ttgegetege
                                                                       720
acctccgacg ggcgaggacg gtgtactatc ggccagtatg cgtgagaaag gactccacta
                                                                       780
eggeteaact ttggagteae tegegaacat etgeteegae tggetegeae ggegaegett
                                                                       840
ccgctccact ggccgactat ctgtggagac gcgatgtaag gggacgaaga tactcgccac
                                                                       900
gatgattttt ccggccgaag aactgactca tagcaggcaa cgagattgct ccgagaggcc
                                                                       960
gacaacgigg aacticgcga caacigacag ccaatcigci ggagcgaatg cccgaagcga
                                                                      1020
tccggagcac ggccgatgga tcgagagcaa agagactact cctgacatga tgacgggata
                                                                      1080
ttgacgcttg cagccagatt ggttacacgc cggcatcttt ccggaagcgt gccggcagag
                                                                     1140
aactettaae actggeeatt etteattett etteegtgag gage
                                                                      1184
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 549 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138

	atttcagtc	gtcagcgtta	ttggggggaa	cctttcccct	ctactacaag	60
gcgcgatgct	atticage	gastasaast	coactoccct	ccgattgccg	gaggtagata	120
gagggtatgc	Ctcacgcgct	ggatgaagat	cettagaaga	actaccaact	ggcatacagc	180
aattcctccc	cacagaaagc	ggtgaacgcc	cccggaaga	eccatages.	ggcatacagc	240
cgaaggttat	ccatacaatt	gagcacaatg	cccggatttg	ctggtagtag	tgcttactat	300
ctccctatat	ggatccacaa	aacgatactg	cactegteag	Cicgaicgge	gaacaacacc	360
agastascat	cgatctatac	atcegtggta	cggagcacgc	cacggacacc	igatitatag	
oogettttgg	aacaaatttc	tcttcgacct	tgtatcgtat	gcgaagccga	accerege	420
actactag	atcagogaat	gtccaaggac	gcttcaactt	cgtctatcga	atcaagaatn	480
aagciggiga	atcagggaat	gactgctcga	gcaatatgag	gtgactccac	ttcatgtagt	540
	gicagotacg	gac cgc cog-	8	0 0		549
gtcaatatc						

- (2) INFORMATION FOR SEQ ID NO:1139
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1117 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1117
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139

				i i		
2222222	gattttcaca	atacattgag	agcaacctct	togataagột	tcgggaggtc	60
ggcaacggag	stactccatt	taractarta	tacgatetet	gcatccgtac	gggttcaaca	120
aaagaaacac		caceccettt	ggacaatcct	cccggagctt	cttttttctc	180
gggatcagat	acgggaggtg	gccacgcccc	ggacaacccc	tacttccctt	atogocaaag	240
ttcttcgcat	cgtctctacg	tgagagggat	teerstate	tacttccctt	ctacagatag	300
atggagtgcc	ggaactgttc	ggccttaaaa	teggagatte	tttcctcgat	tetacaactt	360
nangcaactg	agttggcagc	gcggtactcc	tgccgatttg	gactggaggg	CCCBCBCCC	420
ccgaatacca	agctattett	gcctttggca	ttgtagaatc	ittataggag	84645-9999	480
++caccatcc	gcaacgaggg	gatcatattc	atccttacgg	galgaaagge	r B c a a B a a B B	,
tasaccatt	ctttatcgat	cetcacetec	cacgaagccg	gagggaagag	gettggetet	540
thankenger	acagaagtgg	tatopatcat	gggctatgcg	gctgatcgcg	attcgccatc	600
ttgccaagga	acagaagegg	anastatoto	ctcttcttt	cgggctatag	agcttgctcg	660
gatgagctgt	cggatacgga	agaacacccg	ccttcacatc	catcaggata	aaataagcac	720
atggcttttt	ctcttgcccg	ggagccccc	teesttees	cattcataca	aaataagcac	780
ggtaaaggcg	gagtaggtat	aggaatactg	tccattgaga	cgccacaca	aggatttgag	840
ttcgatatgc	gagcgggatt	ggtgaaatag	gggtgtaatt	Cggaaacgac	accgcatcta	900
tataggrate	popagccaat	cgtcctttct	ctatcaaaag	ggaaggcgcc	CCCCGGCGGC	960
actoggacto	agtttccgct	cggtagcgac	ccttctatgc	tcataccigc	Cagcagcaac	
trangratte	tctcgtgggt	gtctttttct	tttccttggc	tüttttctct	ttactctttc	1020
		O				



gattgccggg gctgttggca gggcttcgtc cttgggtgaa atgctgcgta cccattcgcc atcagctctt ccgtccgaag ttcctgtctg ctgaggc

## (2) INFORMATION FOR SEQ ID NO:1140

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 643 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...643
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140

aggtttcctt	gtaattggct	tgccacatca	agagcagaag	acatcttgtt	ccggaagcat	60
tctccttggg	tgtacgcatg	aagcgttcgg	tgtaaaccaa	tcgtagaaac	gccagtctgc	120
		ccgctttaat				180
		cacccccata				240
		ctgctatctg				300
taggtacact	tgcgccattc	ttcgccgcga	gcaccggtgc	caccccatcc	acacatgcca	360
		aggtagtgtt				420
-		atgtaccatc				480
tcaataggct	cacgatccag	gcattcagtt	caagacccga	ttgagttttg	atagtggtaa	540
ctccttcggg	ttgtaacgat	aggctttcag	ccgttcacgg	agagcaactt	atcctccagt	600
gtacgcagct	ctttggcacc	tttgcttctg	aataccgaac	cac		643

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 637 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...637
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141 *

ggttgccgag	cagaatttgg	gacagtttgc	actctatctg	cgaggcgaat	tcccggattc	60
	agttcaaccg					120
	aatgatggag					180
	actatagagc					240
	accctccaga					300
	gtatcggatg					360
acaccattca	cggtcgtggt	gcagccatcg	cgccggcgtg	aagacagcca	atccggagct	420
ttccgtatgg	ctcgcatccg	ggatggtgac	agcttggcta	tcggcggcaa	ccacttcatt	480
catgccgtgc	caggaatatc	gatatcaatg	cagttctctt	caataaccgt	atctatggtt	540
gaccaaaggc	caatactctc	ctacctcagc	tcgcggattc	gtatccaaag	ttctccctac	600
ggtacggtag	aagatccgtt	tatccccgca	gaactgg			637

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1169 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1169
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142

```
tgccgtcaag caatggggca taaaagaaat aacaggagat atcatcgtca tgcatcagct
                                                                       60
tttgacattg agggagtcaa tgacagttgg ctcgatgaga caaaggcaac tatttcggtg
                                                                       120
                                                                       180
ccggcgtcta tggatttaac atcaatgtaa tagaatagat gtcatccttg ctacaggcaa
agcaggetee gaagetatat eetgagaata gageeteete ateeggaggt teggtgggaa
                                                                       240
                                                                       300
aacagatcga ggtaatccac cgaggaaagg atactgccgg atgctatggc gaaggttgga
tottaagoga accottacgg gagtoottoo gacaaatato gttootaccg cotcaagacg
                                                                       360
gatttgcccg atcctgctct atacggagct gctgggccaa aggcttattg tctgctgccg
                                                                       420
                                                                       480
gcactctgtg ccaagggaag tccgtgcctc atatcaagcc gtaccgatca ctcaagaatt
                                                                       540
attaatctac aatcccttcc attggattca ttggtgcggg tgatgaattt ccgtagtcta
                                                                       600
atcattttgc agaggctttt gtcaaacagt tggctcccct tgcatcgaga atcatcgggg
                                                                       660
taatacaaca gagcgtggtc tgtccgtcat ccgaaacatt ggacttccca aacaggattg
                                                                       720
cagcataccg acatttctct ttcggaggat ccggtctttc ccgtaaaaat cgctttagcc
                                                                       780
cgaatgccct cagccaatac tgatcgatat gatcagtcgc ggcgatcttg ttaccacttc
                                                                       840
gttctgaata gcctgcctct cgcaggaaga gagggtacgg tgaagaactt cataaagacg
aagcaataga ggcatacctc aagagtggta gtatgaaagg tgtttagggt atgccggcta
                                                                       900
tgtgcgattc caaggagaat ggtacagcgt ttattgatgg gtaatgattt ttcttctcc
                                                                       960
                                                                      1020
gcaccggttc gtcgtgcttt tcggattttc ttctctcttt cttctcttcc gctatctcta
                                                                      1080
ctaagcaagc ctgctaaagg aaaagtaaac agcagcttat ttcgtctcat tcctcttact
                                                                      1140
gatctcgtgc caattttatg tagggatgat tgccgacaac aagcataata tagctctcta
                                                                      1169
taggtattca ttcgcgttta agtcgcacc
```

#### (2) INFORMATION FOR SEQ ID NO:1143

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1042 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1042
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143

atcgtcaatg	gccgggtgaa	atggccgatg	ccgactatgg	ctacgtaggc	cgggtccggg	60
acgaatcgat	ctgtataacc	agaagatatg	tgttcgtctg	gtattcctca	ggagcaggcc	120
gtacaacagc	ttatcgaact	catcaaaaaa	acggagactg	gaaagagcgt	tagtttttcg	180
gaaggactat	ttttctagtt	gatcactttc	ctctcagaga	cccaagcaat	gaaaatcaaa	240
attataatcg	ctcgcatcat	cccttgccga	catatgcgac	ttcggcatct	gccgtatgga	300
tctgcgtgca	tccatcgaag	agcctatcac	gttgttgcca	ctcaacgtcg	tctcattcca	360
acaggcctct	tcatcgaact	cccggtaggc	tagaagcaca	gatccgcccc	cgaagcggac	420
tggctctccg	acacggtatt	agctggtcaa	tagcccaggg	actatcgatg	ccgattatcg	480
cggtgagata	ggattattat	gatcaatctc	tcgaatactc	cttttaccat	agcagatggg	540
aacggatttg	ccagcttgtt	atcgccagac	atgaacaggc	cgaatggggc	ttacagacga	600
attggccgat	acggaacgag	gtgcaggcgg	atttggtata	cgggcaaaga	ataattttca	660
atctcccttc	aactaccaca	gatgcgatcc	attctatcat	tctcctgctg	tttcttttag	720
ttatttctcc	tgtagcggaa	gtatatccat	tacagacagt	acagcatcta	agttcgaccg	780
atattctatg	aaggtgtccg	gcagcgagaa	caggagaatt	atgctgcagc	tttgacatct	840
ttcgctattg	ccatcggttg	aatcccaacg	atgcggctct	ggatcggagt	tgggaaaact	90 <b>0</b>
ggatatttgc	cattgggcgt	caggaggaag	gaccccggta	tttggaacaa	agcctatcgg	960
ctctatccga	ccaccaagga	ctatggcaat	atattaaggt	gctgggtatg	aacgccaggg	1020
acgagctgag	atgctgcagg	ct				1042

- (2) INFORMATION FOR SEQ ID NO:1144
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 304 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...304
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144

togttogtto	aagggtcttc	ccaaaaataa	acagttgatc	aagtatctgg	cgaacccggc	60
atcaagagct	ccatoctoaa	gaccgaagaa	gcatacatgc	tgaaaacatg	aggaatatgc	120
attagagee	agacgaattg	tatttcacat	agatgaaaag	cgtaatagcg	tanagcttac	180
attiggicat	agacgaatte	gacatacaat	acadatoacc	cgaaattett	cgtcttgcct	240
cgagaaaggt	attgattttt	gacgcccgc	acagacgacc	contactte	agacttacag	300
gatatgcagc	tgagttatcc	gctttggaca	atatggaatt	cgacgcacaa	aaacttgcga	304
agcc						304

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1024 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1024
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145

```
60
gacaaggaca cgaagcgctt ctggttgttg ccaagagggc cgaagccaat cgggacttgt
                                                                       120
gcaagcaatt ctattataag acgacggcat cgttcctacg tgcactggta tggggacgtt
tcgactaccc gatcgggaac cattaccgca atataggacg cgacctgaaa gaccgcctgc
                                                                       180
                                                                       240
aaatggcggt attccccccg atggagatat tggcaaaccg gccgtaacgc attatcaggt
cttggagaac tggcatacgt cagctggata gaatgccgtc tggagacagg gcgtcccatc
                                                                       300
agatcagggc acacatgaag cacataggcc atacgttgtt tgcgacgagc gttatggcgg
                                                                       360
                                                                       420
cgatcaaatc ctgagaggaa acaatacggc cattaccgcc gattcgtgca gaactgtttg
                                                                       480
gctatctgtc cacgacaggc ttgcatgcca agacattagg ctttcgccat cctgtcacgg
gagtggagat cagttcgact ccgatatacc tgccgatctt accactttgc ttgagcgttg
                                                                       540
                                                                       600
cgtacgttta tcgcctgcat atctgcagga caggactata tctgaaccat tcggctgatc
ctcatacaaa tagtacaata ctttccccta catattaata aacagaacga tgaaaaaacc
                                                                       660
                                                                       720
aattgtggct gtcattgcag gcggttttcg ggcgaacatt cggtttcgct caaaagtgct
                                                                       780
gccggcattc tgtccggctg ggaagcgagc ctttctccac ctttcttgtt ctgatcgaac
                                                                       840
gtgacgctgg tcggtaagag tatcggagca gagagaggtt ccactggata agacgatttc
agotttgato togatggoga acgaataogg tttgactatg ctatatoaco atacatggaa
                                                                       900
ctccgggaga gaacggtctg cttcaggggt actcgacatg atcggcatcc catacaatac
                                                                       960
                                                                      1020
gggtgacncg ctcgtcgaat cctgactttc aacaaatatg tgtgcaatcg ttttctctcc
                                                                      1024
ggct
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 670 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...670
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146

```
agctccgatc cgattagtgt cagaagccat acaccgcctg ctttccatca agccataacg
                                                                        60
gaagtgaatt atgcacacga tcccaaggcc gaatttttag tccagcgata gatcccgaga
                                                                       120
aaataacggt gggcttcatt ctcgatctat agatcgttat gggagcgaac acttcaaggt
                                                                       180
agacaataag gtccgatcgc tcccgaatgg caagcgatag aggattcccg tcagagcctg
                                                                       240
cacatccccc tgcggacacg ctactaaaga atttgtagga gcttattctc tgagactcag
                                                                       300
agtattctga ttactcagag tactcggatt gctcggactc gaaagagctg agatccggcc
                                                                       360
gtagtcggct tgtatttgtt gacgaagagc ttcaaactat cgaacttcat atcctctctg
                                                                       420
ataaaggata caaactccac tgtatctgag atccgtagat agttttatca aattcgaaga
                                                                       480
gattgacttc atcgttcgct ggtcaccgtt gttcaacgtc ggcctgcgac ctatatacac
                                                                       540
atgccattgt atcgttcgcc acttacaatg gctctgacgg catagaccca tcgcagggga
                                                                       600
                                                                       660
tcaacttgtg actgtcgctt acagtcagat tggccgtggg aatcccaatt cgggcccaat
                                                                       670
cttaaaccat
```

- (2) INFORMATION FOR SEQ ID NO:1147
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1136 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1136
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147

ncngttgcat	gcatttcgac	tctttaggat	cccnggcccc	tctgcaaaaa	ctggcgcggc	60
		tatcatcccc				120
		ggcaaacgac				180
		atgccagttg				240
		gaaggcgaac				300
		tcggcgaaac				360
		tgtgaagatc				420
		acgcctacat				480
gatccgatcg	atctttcatt	actccctcac	ggggctgtac	cgaaggaact	atccgggtaa	540
gccccgtgtt	cttttccgga	tattatcgac	taaccaattc	ccctccaaat	catcagatag	600
ccgcacgtca	gctctcttcg	gactgtctat	ttcgagctcc	tgactgcgat	attcgcccgg	660
		tgaaatcttg				720

toatagooga toto	ccggacc gtcttatccg	tatagcgcag	caaggacttg	gcctgctgga	780
tgataagetg ttga	atgactt tggaggcaga	ctgtcccatg	acggtcttta	tcgcagtgcc	840
aaatgtttgg agct	tgaggca cagcctgtct	gcatagaact	tgccgtatgc	tgctctttgt	900
gatgctcgga gacg	gaggagc agaaagtcgc	gcaaatagtc	tccgacctgg	tgtgcttgca	960
ptccttctcg acct	togtogg aatcatatog	tcnagaaaga	gaaagagaga	gctgatcnga	1020
tagatgacat ttct	ttcctga tgacgccccc	cgttttgcag	ggcgttgcgg	atgagatcaa	1080
cgttgccgtc agaa	aaatctt tctccatgcg	ttccggacgg	aacggttgtt	gctgtg	1136

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1311 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1311
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148

```
attacacggg caagggtatc cagtcggcct attggaagat ttcgcgcgac tgaagtttgg
                                                                        60
                                                                       120
caageteeeg tttecattea tttggagtee aaeggagget etecacaage tttaettteg
gacacgatgo totaaatogg tgocaccaca cotacaacaa cocctoottt acacgtggat
                                                                       180
ttacgatcac gcccattaca agcatctggg tgcgcacgac ttccacacct atcagatcac
                                                                       240
cggcattggt acatgcacct ttctggacgg tctgcttacc ttcaacggct tcctgatctt
                                                                       300
                                                                       360
tggggtttcc cccaagagaa cccaatcggg ggccctgtgc tcaagaaggg gataagttcg
                                                                       420
tattcctgtc cgaaccgcag ttctggatca actcaatcgc atcaaaggca tcgacaagga
tttcaatctc agcataggga cgagatggaa atcagcagga acttcgctcg catggacaaa
                                                                       480
ttctcctgca ccctactctt gcggtcaaat ggactttcaa ctgaacgaaa ctcttcagta
                                                                       540
                                                                       600
aaaatgaaaa cttggcaatc cattctcgga ttcaatcccg agaagcaccc gtccgaacgg
                                                                       660
agtttattgc aggggtgacc actttcctga ccatgagtac atcttggcgg tcaaccctga
tattcttgct gcagcaggga tggacaagga gccgtattca cggccacggc actttcttcg
                                                                       720
                                                                       780
gccgtggcta cgctgtgatt gcatttttgg ccaagctgcc cttcgctcaa gctccgagca
tgggatcaac gctttcttcg ccttcactct ggttcaaggc atgggctact cttgcagact
                                                                       840
                                                                       900
gcactggctg ccgtctttgt ggaggggatc gtcttcatcc tgtgacggca ttcaatatcc
                                                                       960
gtgagaagat cgtcgattgc attccttaca actgcgctat gctatctcgg ccggtatcgg
                                                                      1020
catgtttatc gctttcatcg actgaagaac gccggtatta tcgtatccca tccggctaca
                                                                      1080
ttggtcgctt cgggcctttc actccgatat tcttgctggc catcctcggt atcatcctag
cgcggcactg gtcgtgcgca aggtgcgagg ggctttgttc tacagtacgc catttgtacg
                                                                      1140
atcgtcggca ttccgctggg agtgacagcc attcccaagg atttgcccct atctcctctc
                                                                      1200
cgcagagcct aagtcccact ttcctcaaat ggatttcgcc cctctccttt cgttcgatat
                                                                      1260
                                                                      1311
ggctatgacg atatcgctct cgtcttcatg gatattttca atacgatcgg c
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1141 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1141
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149

cagttgcata	cgaatttcat	cgcccttgag	tcccataccg	atgaaccttt	ttcgcgggtt	60
			cttcgtggct			120
agttgtgtcc	ttcgcgggaa	acgggaacat	agtgctcgtg	cagatactcg	aaccaacgga	180
			ttccagttcg			240
aagcacatgg	cctcgtgctt	gggcaaattg	aagcggagga	tccgtgccat	gcgttttcca	300
acaacttctt	cagatcgtcg	taggtaatgg	ggcgaataaa	acgtgggcat	aaggttccag	360
cctcgcctct	acatgcatga	gagcatcctg	ttgctctcgg	cctcttcgaa	'ctcacgatct	420
ttatagatac	gctcttctat	gaaatccgct	cgagcgatgc	tgccaaatac	tgttcccgct	480
			cagcagctcc			540
cgcagcaaat	cagtcactcc	caagaatacc	ggcttgtcgt	ccatgatgcg	caagcattag	600
			catagaggca			660
tacacccgca	gccagatgaa	tacgtaatcg	gcttcggcag	ccgtcatatc	atctattcgt	720
ttgatcttga	tcttgccttt	tcattggctt	tcagaatgga	ttcgatcagg	gaagacgtcg	780
tcttccacag	ggcagttcgg	taatgctgag	agtacgattg	tccagtitgc	gaacttagcc	840
			tcattgtacc			900
cggtagggaa	atcgggataa	agatcgaaag	atctcctctc	agatgtgcga	tacatgccat	960
gagcagttca	ccgagattgt	cggcaagacc	ttggaattca	aacctadagc	aattccttcc	1020
			cgggcaacgc			1080
			atcattgaaa			1140
g				ļ	,	1141
						5

- (2) INFORMATION FOR SEQ ID NO:1150
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 469 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...469
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150

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- (2) INFORMATION FOR SEQ ID NO:725
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 362 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...362
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:725

catatatata cagagtee	g ttcatcgccg	tgcgtattat	cagcgatatg	ccggcgaagg	60
tcgggataac tttgcgga	t atatggactt	ctggcgcagg	cttctccggc	taccttttct	120
attotogaaa gagtatto	ga tocaatoaga	aataagacaa	tcccgatatg	gagatggaaa	180
aaattcccag ttttcatt	ac atratattro	cctcaaacga	pocatatate	totocogcaa	240
ggacttatag ggggagag	t setteeset	ttcgatattc	gaatgaaaga	accesteses	300
ggacttatag ggggagag	gi ggilacgaci	tttgatattt	stateactec	anacttatet	360
aaccggtgct tggggcac	cc gaacttgcat	acgatcgage	acceggeege	aaacccaccc	362
gc					302

- (2) INFORMATION FOR SEQ ID NO:726
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 393 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...393
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:726

agcagaacgg cggcaggag	a gccgagccgc	cttttcgccg	gctctctcgt	gcactgggag	60
ccgggggcgg catggaagc					120
agggatttcg ctccggcta					180
catgagcgag aggcgaatt					240

ctgtttattt	tcatctgaaa	gccggatatt	cgcgcagtcg	ctccaacgaa	ttgcccactt	300
					atcttaacgc	360
ttttttcgc	ccgatatgcg	tctgagcaag	ttt			393

- (2) INFORMATION FOR SEQ ID NO:727
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 468 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...468
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:727

ggccgttatc	agtatcgggg	ggaacctcct	gcggattccg	ctggctctgt	gcttatcggt	60
atgggcttcg						120
tggccatcgt						180
accetetteg						240
tgacttggag						300
ttcgagcaaa	acgagacttg	ccttcgtgct	tatatccctg	gctcaccgat	atagcatccg	360
acattcctgc	gctattggag	cagttttcca	ctccggggct	tctgtggcaa	atactcatcc	420
gagatccaac	cggatatcaa	cggaacgaac	agtgggaaaa	gaacttct		468

- (2) INFORMATION FOR SEQ ID NO:728
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 263 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...263
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:728

agatacttca	tcacagatgg	atttgcttat	ttgctcactc	tataattcaa	cccaacctgt	120
ttttcattgg	gtttgtcgct	caaaaaggaa	tagatcccct	cgtaaaatag	ttggcgtgta	180
ctgaatgaaa	aacataagag	accattgcac	aataaccctt	ccatctcctc	atatngatca	240
aaacaacaca	tgcattgatt	cgg				263

- (2) INFORMATION FOR SEQ ID NO:729
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 491 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...491
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:729

gatggatttt	tcttcctata	caatcctttg	ccttaatcgg	ctcgatgcag	gataccggct	60
		gcataaggga				120
gaagcagaaa	aacgcctata	accgactact	aaccactacg	acgatgtcct	caccggacgg	180
aaatggtggt	cttggcctat	atgcactgtc	tctggaaaac	ggacgacaat	atcatcgcag	240
gctcgtgctg	gacatgattc	ccggcaactt	cgagggcaga	atactcgacg	tcccgtagga	300
acagccattt	tcacctatga	caaatacagg	cggatgcccc	aagcgagatt	gtcgggctgg	360
actattcgca	ggaaatgctc	gacatagcag	cgtgcgcttc	agtgcagagc	aaataaccaa	420
		agtcggcagc				480
gctcttcgat	а					491

- (2) INFORMATION FOR SEQ ID NO:730
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 599 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...599
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:730 •

+	ccaaccaact	catcggcttg	taratagara	acgctaacga	tccgaccaga	60
tagaggticc	CCggCCaacc	taccegoode	cececeace	teatteatet	tetetaagag	120
ccgaagctcg	tatggagcgt	tggatcgctg	ccatgggctg	laallaalgi	t testagag	
ccggagatcg	agatcagagg	gaaactgtta	gcgcgaaata	aaagcgtatt	tgtcatcaaa	180
gcttactcct	cttctcgcct	tcggctctct	cgttaccact	cttttcctct	tccccttctt	240
tccgtattta	ttcgactcct	gacgatggac	acgcaaacac	tcaatagcga	tctggcgtat	300
tcatgcacca	tatatacgag	tttgaaaaag	gtgtgcgaag	catgtactcg	ccacactggc	360
taacgacgac	atcccatate	cggaagaacg	gcgcgaagcc	ggcagatccc	ctatttcgcc	420
carcetacte	cgaatacgga	ggtaccaatc	tctttttcgg	ctgcaaggag	tgtatgggag	480
cageceacte	tttcataaat	ggacgcttct	ctgaacaagc	ctgacttccg	gaggaagaat	540
getateegee	LLLCGLGUGL	gatacgatat	++0000000	tacascats	ttaatracr	599
catcatcggg	gctatgctcg	gatacgatat	LLECABACAB	cgcgaacgca	5566566	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 664 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...664
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:731

tcccccagct tccaatgta	c gaggttccag	cccttcgggc	agaacgatcg	ttgtttgttc	60
tcttgagcac gtctgataa	c gtcttgaatg	agatccatga	taatacctta	tagttattat	120
agttattgta atgatgato	t tgaaaagaag	gcgagcagaa	ataacgcctt	gtttgcagtc	180
gcaaagatag ttaaaacac	g ggcaataaga	gagatacatt	caaaatactt	tggaaatgga	240
agtatgcttt ggcagggct	g tacttccatt	ctccccattg	cattaatatc	ctttttgctg	300
ttctatctag tacgtgacg	a aagaggatga	cgcaacccct	ctacgacttc	agatagactt	360
cggctgcacc gattctcag	c tccatcctga	taggacaggt	attctattgg	catcattcgt	420
gagccatatg gtaatagco	t tttgggattc	ttgaatgttt	cggattcgtt	tatgagcatg	480
gatacccgat agtatgata	g ttgataccct	ttttcgtttt	ttgtacttca	gaactttcga	540
ttgaaagaaa cagtcgato	c cctttttccc	tgcaaatatt	cttaccggat	gcgctctttt	600
gtactctttg accagtct	g togagogaag	atagagttgg	ctcctatcat	atccagagat	660
attt		5 5 55			664

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1446 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1446
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:732

```
ccgtcactga tgatgctgat ctgctctatc tgtccagcag gttgtttgca gattgtcttc
                                                                       120
ccgtacttcc ttacgagcac atggttgcga ctgataccat gaaagctcct ggctcggtaa
ctaccaaatc gaatatetet eccetettig caattgiett tittgeiget caegeaggat
                                                                       180
ttcgctctct ttcttttcgg gaaattgtct gcacttgaga ccactgtctg ccgcatagcc
                                                                       240
tctcgagagt ctgtttggcc gtttccgaag agagaaagcc cagccgtaga agatgtcctt
                                                                       300
ggcgcttttc cgagcctcgg aggtcggtaa tgatgcgatg tgatggcata gacagtggcg
                                                                       360
gcaacttcgt caatagcctc tatgtccacc tttcgagcag tttgcggtag tactgctcca
                                                                       420
                                                                       480
tgccatggat tgtctccgag aagctgagaa gttttcggtg tcgcgatgga gcgcgagtgt
gatcttgcgt tgagtccctc tttcttgtcc cggctcatgc tccttgaacc atctgcacaa
                                                                       540
                                                                       600
acgtaatacc gaggaaactg aaagagcttt ttatgctcga taccacaagt ccctattcag
cttcagccct ttgcggtatt tcaaatgttc gctcaggctt ggagagcatt tagcggatct
                                                                       660
                                                                       720
actttctccg gcaagaagag tagcagtcgt cggcatagcg gataaattcg gttgttatat
                                                                       780 .
gcccggcgat gtagcatccg tgtcttccaa gtagaggttg gaaagcagag gggccagagg
                                                                       840
gcttcctgtg ggatgccgga ggatgcacga gcatattgct gcttccggtc cacactccgg
                                                                       900
acttcatcca gaggctcaac atacgggtaa ggaagggatc ttggttgttc tttggacttt
                                                                       960 🕻
ctgcaataga gaggggacag ggatagaatc gagaagttgt caatatcgca gcgcaccact
gtatggttct catccagaga tccagcagat gctgcactct acgaacggca gccacagctc
                                                                      1020 (
ccttcccctg cgataggcat agctctgtgc aatggataaa gactcggtga tcggataggt
                                                                      1080 1
atgccggcaa ggcttctctg caagtggaga tccactgccg aagggattgt agctgtcggt
                                                                      1140
                                                                      1200
aagagccatc ccccttgggt atgttcacag agtgatgggc tgcggtatat agctgcaaat
                                                                      1260:
acgtagggct tccaacaaat cttgtgctcc gcttctgcca tgggaaggtc acgatccgca
                                                                      1320
gccagcgaag agagcacttg cgatacaagg tatcgttgcc cgagtgctct ctatctgacc
                                                                      1380
attcccacga ttgtatgatt gcctatatgc acccaatgcg ccattgagag cadaggctgc
                                                                      1440
ttacggatcg tagggaacac gatagaagag ctgacccaat agccgacatg tcgtactgct
                                                                      1446
gtttcc
```

- (2) INFORMATION FOR SEQ ID NO:733
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 620 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...620
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:733

tacgggctcc	gtcccgagca	gatagagtat	ttcagctagg	tagcaccttc	gctttcgatg	120
aagctactac	tccatagcgt	aaagctgctt	tcgtaggaag	ttcgccattg	tgacggcgag	180
cgtagtcggc	cagcattcct	ctgccatctt	cttccctttt	tcccatgcag	ctgctgatgg	240
tgtggctcgg	cattgataga	gaagaggttt	cttccggtag	gaagcgtctc	cggatggcga	300
tatagtcgcc	acccggcgaa	ggtgccgtat	aaccgccgga	gaggcgttca	tcatagaggt	360
cagctccagc	tgtgggctgt	ttttgagtgc	ctatagtaga	aaggtatctg	ggcaatagca	420
tectteagtt	cgctgatgct	cctgccatgg	ctttgtcttt	ggaggtaagc	tctcgtactg	480
ecteattcet	atggccggtt	gcttggcttt	cgacttatca	ggcatcatag	cttttgcctt	540
tccgaatgtg	ccgcttgcat	agaatccttg	ccgtgagaag	gcgttgcggc	tctgctccat	600
	cttggcggcc					620

- (2) INFORMATION FOR SEQ ID NO:734
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 354 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...354
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:734

ggcgaagctc ccgacgttcg ccgcaagttc gtcgcggcag gcgtggcact atccttgctg 60 tgagcggttt tcacgtgggt atcgtattgg ctgcctcgt tttctcatgc gtattctgcc gataccgcag cgatggcgtc gggcagatgg ctgcttccgc ttgcaggggg atggatatac gcattcgttt gcggttgggt gctcctgtag tccgagccat gctgatggct accttatata tagtcgtaaa tgctcgggca gaccgtacgg atggattgaa tgtttgggt gcggagcgtc cattacactc gtggatcgat ccctctctt ttttatgacg tgggatttgg tggc 354

- (2) INFORMATION FOR SEQ ID NO:735
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 524 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature

## (B) LOCATION 1...524

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:735

# (2) INFORMATION FOR SEQ ID NO:736

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 395 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...395
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:736

gcttgtaatc	agaatgccaa	ppgatcgggt	cttgccataa	gtacgcctca	attagaataa	60
gttgtaatt	agaaccctac	acpacticity	cttctacgag	cttgttacga	ccacaacatc	120
acaatcggac	tataaaacto	ccaaaaggta	aaagtggtgC	aaacggtcgt	aggtggagaa	180
acaateggae	aggeattttg	gaaatcacgc	teccetteee	ctttaagtat	gtgacgggtt	240
actactcca	aggeatteeg	atnoggagg	aptcaatecc	tcacctgccg	gaacgaagaa	300
cttatttccg	stoscassos	atasaasas	gattaagata	aattcaaggc	cgggtctgac	360
gtcactttga	testages	ataccactca	aataa			395
gtcaggtcaa	tegttegett	atactactcg	aacga			

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 562 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...562
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:737

gggcaataac	taccgttctt	gcatcgtgac	agcagaggct	gcattgaagc	ttatccatac	60
				tatgtacgaa		120
				gcggaccagt		180
catcaacgaa	tttcccacgg	gaaatacctc	aagcaagcca	aaaagatcta	cgacagcgtc	240
agcaacatat	ctcacaagac	gcttgacgaa	tgctcataca	cacccgggga	gtctccatcg	300
cagcaacata	aaggagacgg	cagagggtgg	atcaacaacg	gaacgatcgg	aagaaaaagg	360
ccctgacaca	agttccgact	aataacaaaa	acatcaaaaa	gatatatgga	gcttaagaaa	420
atgaatgtcc	ccatggacac	cttacacgtg	acatggtgcg	tctgagcgaa	gacacggaga	480
acgtgtacga	gacagtgatg	atcatagcca	agcgtgccaa	tcaaatcggg	cagcaaaata	540
aacaggatct	tggaaagaaa	ct				562

- (2) INFORMATION FOR SEQ ID NO:738
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 926 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...926
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:738

```
60
tggcgcgaga atgaaaaaa tctcgcgcca caacgaaaaa aaagtcgcgg tattttgcag
                                                                       120
aaaagcggtt ccgctttttc tccttttcac gctcgtgatt tcaccccctg ctccggctgc
                                                                       180
acacccctct ctcctgcaga atgaatactt tcaaataccc cccccgcaa aaaaacaatc
aggacacaga gtgggggtat atgccactct atgtcccgat tgcgttagga gggaaatgtt
                                                                       240
gcttaggatt cgccaccgtt atcgtctgtg tgtggaagta ttttgaacga gaagaactgt
                                                                       300
gatogtotca googaagoag atttattoga tttgaacato agtocacott gogatoggto
                                                                       360
                                                                       420
gggattgccg tcaggatata gtcgtaaaaa ggttttcggc ctcgttgcca aagataagcc
                                                                       480
cctgaccacc ggagggataa agttgttcgt cttgattcgg aaagtagtag gaagcaaagc
                                                                       540
cggattgaaa cggccgggat attcatgacg atgttcagtg ctttatcctg cgtcttatga
                                                                       600
cctgacaaga gactgcgttc gaagtggctg tgtattctgt gaatgcattc ctgcaccctt
                                                                       660
ttgtgtgcgg actgcaaatg gattggtaac ggnagggttc ctcactacca cacgcaccag
acgtttgagg tcaggattat cttgtgtccc acaatgatgt ctgacgtaca tgagcctgaa
                                                                       720
                                                                       780
ccgggtgttg cagccatgac aacgaaatcg taccgttgtt gttagtagca ccggttactg
                                                                       840
catcccgcta tatgtgacgg tgatcagatt gttctgctgt gttacgttgc caaattcgga
                                                                       900
taataagccg ctttgattgt gcccgttgtc tgcccatcgg taaggccaag taagtatgat
                                                                       926
ccacttcgat cttacctttc cgggga
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2787 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...2\overline{787}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:739

tgaacttaca	gttcttaccg	ggcactgtcc	tgcaacatgg	caacattaca	cctgccaaag	60
aaaaatcctt	caaagccgtt	tgccactgcc	cgagggtagc	tgtacggcca	agcgaatatc	120
cgtatgttcc	tcggctgaga	gaaagcttaa	tctccctgtc	cgatcgtaca	ggcatagccg	180
ctgggaaact	tttgtggata	gaattcggtc	tatataggaa	ttgtttccga	ccaaaggccg	240
gcgcaagcca	ccgctgcgag	agtagaaatc	gtacagccat	gtttcggcag	gaataggaaa	300
ctacagatat	cgccacggtc	atatatggct	gaaagagctt	ccgcatcatc	gtgcgcataa	360
tgcctttgcc	acgatgatcg	gggtgtgtgc	atctccggaa	atataaccgg	ctgagaaaga	420
agtgccaaaa	attcgcagtt	gtaaggaagc	atttgcagat	gtgctacagc	ctctcctgtc	480
tcgctatact	tagcaaggta	taatcctcac	ggaaaacttt	gtggaaataa	agctcaatga	540
		agatgcgcca				600
gtcatgatcg	cgtcgcagta	tggctgtttg	tttgggcaaa	gaatggcagg	gcgataagat	660
agtttggcct	ggcgcagtcc	cggcagccca	aatcctcctc	gcgattgatg	tagcggaatg	720
		attctctatt				780
		cccaaaagtg				840
		cgtagtactc				900
aaaagcacgc	tctaccatct	ctacctccag	cctcttccgt	cctgatcacc	tcggctatcc	960
		aagcattctt				1020
		caaatttatt				1080
		ttcacgttcg				1140
		caatgttcct				1200
		cttcggcact				1260
		cccacaggaa				1320
gttgaaacgg	atgatcagac	agccctccac	aatagcccaa	gacgtgccat	agcgaaactc	1380
		agccaggtcg				1440
		gcaggttcta				1500
ttttgtcacc	ccctgttcaa	tagaagggag	acgttaattt	atcggtgaaa	cacctttaac	1560
accgaaaagt	ttcatccttt	tccctatttc	aattcggcaa	atgtgtcacc	tgcggagaat	1620
ctcctgtctc	gaaccctcgt	ttgaaccaat	acatcctctg	agaggagtgc	catgtgcgaa	1680
agcatcaggt	accacatagc	cctgcgattg	tttccaacag	gaagatgggc	tataccacag	1740
ggcagatggt	ggtactccgt	agagataacg	ggctatcccg	tacggctctt	cgagctacgc	1800
tgtagagctc	agcaggtacg	ctctacagcg	tagcgagccg	agccgtagag	ttccgctccg	1860
		ctgagccgta				1920
		gctcggtacg				1980
		agtatattcg				2040
		cctttttatg				2100
		aataatcatc				2160
		catgactgca				2220
		cgacgaccgt				2280
agttaccgtg	atcgtctttc	ctaaactgtc	agcgtgtaag	gcttctgagc	cgttacgtct	2340
gccaacgaag	tgtattcaac	gtagcagttt	cgatagctga	ttctccgttc	gggtaąacaa	2400

ctttacaccg	tacgtgtaaa	aaccggtagc	caagtccgga	tctcggtaag	agtctccgtt	2460
acgcctgatg	ctatctgtgt	attattacga	tagatcgtaa	ggtgtaagac	ggagcgttcc	2520
ctgaagtgat	tacaacatca	tcaaggttat	ccagaagaag	tccgtacagc	cgaagtgacg	2580
озаросласа	tacttagacc	cgcaggcaac	tgtaccgtct	tttgatacca	ggtgccctga	2640
gcacgatacc	acgaatggct	tcaggtgccg	taacaactgt	cttggccgtc	agcactcttc	2700
Caacaaaaca	ttggcgaagt	tggaagcgtc	gttacccgta	gaagtgcgta	cacggcatag	2760
	cataattggc					2787

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 525 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...525
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:740

tgaaacgggc tgctacgatg gctatcgcgg atttggcgcg agagactgtc ccgacgaagt	60
actgcgagcc tatggcaata ctcagttgca cttcgggagg actactttat tcccaagccg	120
gtggatcctc gtctgatcgt tcgcgtacta ctgccgtagc acgtgcggca gtcgagagcg	180
gagtggctga gcatccattg cggattgggc tgcttatgag gccgaattgt tgggacgggt	240
gggacgatga gccaccttac gcgtcgtctt catgaatctg ccaagctcaa tcctatcgcg	300
tgatctatgc agcctgcgag aatccttcgg tgctgaaagc tgcgtatcgg cacgtgcaca	360
tggaatagcc cgaccgatca tgttggggga tggaagcaaa ttcgggattt tgccgcagag	420
ttggatttat ctttggaggg ttcgaaatcg ttaattaccc gcttccgatg aaagaaaagg	480
cttcgccgtc ttcattatgc ccgtgtcttt gccgaacaga actgg	525

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 453 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature

#### (B) LOCATION 1...453

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:741

						60
cgacagaaaa	acacacgtat	gcccagcagg	acaaaagcca	gtccgaccac	agaagagaag	00
		tattgctata				120
		taactcaagt				180
		ccacgaaatc				240
		gtgaaatttg				300
coacetagec	aatctcgtaa	tagagaaacc	CEECaacacc	cggtacgaaa	cacctcgaaa	360
Ceneerneer				anagantaca	ccastasnaa	420
cggtcatcct	tcagagccat	atgggatatg	ggatgccgaa	gaagaacgcg	ccgacaangg	
ttcatgactt	tcgaggaacc	gccttattcc	cgg			453

# (2) INFORMATION FOR SEQ ID NO:742

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 721 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...721
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:742

```
60
tttttcgaat tctgcctcat cgctgttttt attacaccgc aaaagccgtt atggatggaa
                                                                       120
gtcgtaatta agaatacggg tagtcaagta tcttggtggt tgcacggatg gtacggaagc
tatactgcat ggcgaaaggc aatctgctct gaaaggcatc cgctccacca atcccgtaac
                                                                       180
                                                                       240
cgtaggcgat cgcgtgagat tgtccccgct tctcaggacg gacagccggc ctacatcaaa
cgaatcatcc ccgacgcaat tatatcatca ggcgagccag caacctctcg aaaggtccca
                                                                       300
tatactggga gccaatttgg atgctgccgt gctggtctgt acctcaacga tccggtgact
                                                                       360
                                                                       420
accaccgtct ttatcgatcg tttcctcgct acgcagaagc ctatcgcgta ccggttattc
                                                                       480
ttgtattcaa caaaatagac tctatacgca agaagatcgc ttgcaattgg accggctgtc
                                                                       540
ggctgtctac ccgccatagg ttacccctgc tgccacgtgt cggcgattac gggcgaaggc
                                                                       600
tcccggatct caaatcccta ctcgatggca agctgacact ccttgccgcc attcgggggt
                                                                       660
tggcaaaagc tctttgatca atgccctgat tcctcatccg atttgcgcac aggggctata
tcccaagccc atcataccgg catgcaacga ccacattttc ccaaatgatc gacttccccg
                                                                       720
                                                                       721
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 502 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...502
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:743

gccggccgtt gagaaaagga	ctgtcgcggc	tcttcgtttc	gccccgatcg	cctgcttctc	60
gttgctgcgg gagctttctc					120
acaagctgtc ttcatccgac	acttttcggt	catcgggaat	ccggagccac	gcgagggcaa	180
actgcgaatg caggtaaact	gacaggaggc	tcctccccat	cttatatcct	gtacatccga	240
cacgagggga atacgagccg	gtcgctcgcg	gcgatatgct	caagcttagg	aaatctatgc	300
ccgatcggtc gaagaatggg	agcagaaagc	tccggcaatg	gggggtatat	ggcgggcaaa	360
ggactgtccg gcagtctgca	tgccaagacc	gggatgtaga	aatcttgtcg	acagccaaag	420
ggccgttctc cctcaggcaa	aaggctttgg	atctgtcgga	tcgcttggct	gccacattgt	480
acgaactctc ccttcgctac	tg				502

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 349 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...349
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:744

ggatggagtg	gagcgtaagc	tgacggccga	ggatctgatg	atatgcgatc	gaacggcgat	60
cccatgtgtg	tggcgggcgt	tttcggtggt	cttcactcgg	tgtaacggaa	aagacaacag	120
atatattcct	cgagagtgcc	aatttcaccc	gacgatggta	cgccgtacgg	ctcgccgatt	180
gggtctcaat	acggacgttc	tttccgcttt	gagcgcggat	tggatccgga	gcgcacggat	240
tgggcttgcg	tcgtgctgct	tcgcttatat	tagagattgc	aggaggccat	ctcgtgggat	300
gacagatgtt	tattccaatc	ctctgaaacc	gcacctaatc	agttgtctt		349

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1062 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1062
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:745

ccttggacgg	tcccctcaat	atttgtctca	gaaatggatt	ccttctcgtt	tttctctgtc	60
agtgctaaga	caaagataga	catacgaaac	cataatgcga	taatatctat	gctaatacat	120
		gcattagaaa				180
ggatattgag	atgaaaggct	tttgagcaaa	gggcttcttt	tcggtggagg	aagttttgtt	240
ttcaaaaagg	aaagatcaat	agtgatatat	ataccgatgt	cttactgctt	ccatacccca	300
tataaatgga	aattctattt	atccttattt	tcatgaacac	ataaaaaaga	catggaaaaa	360
ggattcaacg	cctacgtagg	tggaatgtat	ccgtattgaa	taatatatat	ctgcgaggtg	420
agttttccat	gtcgatgaat	gaatgaactt	aagatggctt	atcctacgag	tataaacgag	480
gaaacagccg	tttaagagta	ttcaggcctt	acattagtct	gatgaaaaac	aagggggtat	540
ccggtttaac	ataggctctt	atttttcctc	ctatagacaa	aaaacatccc	ggaactattg	600
agagagaaat	ctcttttta	tattgagcca	catgcttaat	cgaattagta	atgagtaacc	660
agcatcggtt	aatgctgtct	gtctctaagc	tgtttctcct	tcaaccatcg	attacttttc	720
tcagcagatt	ttggcaaagg	atacaataac	ctccaattac	cctcaaaatt	atcgaaccct	780
tttgaaaaag	gtttaaggga	aacttatcct	atgcctattt	cagcttgttt	aacggctttc	840
gatgtatggc	aatttaagtt	atatcaagga	tagagatacg	caattaccgt	cacaacctca	900
aagggactat	tgatcagtaa	tttttatcaa	gtggaggatg	gagcaataca	ttaagaacaa	960
acgcctattt	gagtaaggga	tcggcaccct	ttcattggac	ataaaatatc	aggtaaatat	1020
acgctcagca	acacaacctg	atgcgtgtag	ataaagaaga	cg		1062

- (2) INFORMATION FOR SEQ ID NO:746
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 667 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...667
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:746

gccggcaatc	tggccaatct	caaggatata	gagtccaagc	cgaactatct	ttcgtaaagg	60
	caatgccaat					120
cattcatctg	gcggccgaaa	gtcatgtgat	cggtctataa	aagatccttt	agcttttgcc	180

cgcaccaacg	taatgggacg	ctgacgctcc	tgcaaacggc	caaagaggct	tggcatgggg	240
			gaccgatgag			300
			tacgacccac			360
			atacgatact			420
			caattcccgg			480
			ccgtctatgg			540
			catcgatctg			600
			gaatggagaa			660
tgatccg						667

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 649 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...649
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:747

gaagaccgtt	gcctgtcgtc	gactctacag	gatccccaac	aagctgacac	gcttcccagt	60
				gccagactga		120
tgaaatgttc	gaagctgtcg	cgataatctc	tgccgtgccg	tatatatcca	tatgatcggg	180
				ggaatgaacg		240
tctgctcgac	gactactaaa	tcacttttgt	ccgatagcaa	cagattcgat	tgatattgtt	300
ggaaattcct	cccagaaacg	cattgcagtc	cacatggctc	tgttgagcaa	atgtgccagc	360
aaagtagagg	tcgtagtctt	gccatgtgtt	ccgcgacaca	gagtgcacgt	tccatcagag	420
ttatctcgcc	gagaacttct	gtcgcttcac	cacgcgataa	ccattggatc	tgaagtaggt	480
caattccgag	ggtcggccgg	cacagcaggg	gtgtaaacga	tcaacgaatc	ggtgggagaa	540
					tcttgatcaa	600
ttgatcggta	atgggactcg	gagtcagatc	atacccaaca	cattaaatc		649

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2241 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

# (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2241

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:748

```
gatcattgca ggccttatca tttatatacg atggaaatat cggtggatct ttcntttgcc
                                                                        60
accgtcttgt ccacggtctt catgattata aacatagcaa accggatatc cacaacaaga
                                                                       120
cattgatgcc ggctctcgaa agtccgtctt cgtaccccac gtaatctcct acatctttgc
                                                                       180
atatgccatg ctggggcggc actgctcgta ggcggctact tcctcttttg caagcgcaaa
                                                                       240
cacaagaggt gaatgcaaaa gtcatgatgc atacgactga caatctggtc tacagggatt
                                                                       300
tgcttttttg atgacgggac tgctattagg cgctatttgg gccaacttgc atggggcacc
                                                                       360
tattggaatt gggatccgaa agaaacatgg gcgcaataac cgtattcagc tacttgctct
                                                                       420
                                                                       480
acatccatca ccggctccat ctcctcgagc ttttgcccat tctttggtat tgctaatcgt
                                                                       540
cagtttcctt tcctgcaaat ctgctggtat ggggtcaact accttccatc cgctaaagat
ccagcattca tacctacaca cgttgaattg cttgcctgca tagattgtaa agatcatggt
                                                                       600
attgcatttg catatgccga tatagcagaa cctcggcgaa tctcaagcca tagatacaat
                                                                       660
                                                                       720
tccggtctat cttctattca agaggaggaa aaacagcttt tctcggagaa atctcccttg
                                                                       780
cttttttggc ttataattgt ttctttgaag tcctaaaatg agacctcttt ccaattcgag
actttctttt ggggattcgt cacactactt agtaatatcc ttttcaacaa tgaaaaaacg
                                                                       840
ctcgtaatag tcgttcaccc cgatttgacc aaatccgtta tcacaaggct tgggccaaag
                                                                       900
ccatcgaagg tgcagccact atccaccatc ttacgaacag tatccgaacg gacaaatcga
                                                                       960
tctagcacat gaacaagccc gctggaggct catgaccgca tcgtcttcca attccccctc
                                                                      1020
tattggtatc agctccctat ctgctgaaga agtggatgga cgaggtcttt actgagggtg
                                                                      1080
ggcctatggt gccggtggag acaagatgga gggtaaagaa atctgtgagc agtctcctgc
                                                                      1140
                                                                      1200
ggatcaccca aatcagcttt tgccgaagga gcacagaatg ccacacgctg cgaagctact
tgaatgtatt cgacgggata gctgcttcct gcgcgctcga ttcaccggct accatgcctg
                                                                      1260
                                                                      1320
ctacgattcc tacatcctcg cctgccggaa atgctgccgg ccaactgcga agcctatctc
cgcttatcaa aggagaatga atacagaggt aatagccatc attccggctc gattgcttcc
                                                                      1380
agccgattcc cgggcaagcc actggccgat atgcttggca atctatgatc caacgggtac
                                                                      1440
                                                                      1500
atgagcgaat agtcggtgtc gtcccccggg cgtcgtagcc accgatgacg aacgtatccg
                                                                      1560
tcaggccgtg gaggacttcg aggagaggtg gtgatgacgt ccccagagtg cagtagtggt
acagaacgtg tcgggaggca ttcgacaaag taggtcgggg agaaaagatc gtcctgatct
                                                                      1620
gcaaggcgat gaacctttta tccaaaagga acagatcgat ctgctgtttc ggccttcgac
                                                                      1680
aaaccagaaa ccgatatagc tacgttagca gaagtttctc gtctgacgta agcttcgagc
                                                                      1740
gtttgaacaa tccaaacagc ccgagatcgt attggatcat ggaggctatg ccctttattt
                                                                       1800
cagccgctcc gtttcccata tctcaggggg gtacagcctg actcttggtg ccgtcggcat
                                                                       1860
                                                                       1920
actactacaa gcatatcggg atctatgcct ttcgcccgac cgtcctccgc agataacctc
                                                                       1980
actgccacaa agtacggcag agcaagccga aagtctcgaa agcttcgctg gctggaatac
ggctatcgga ttcgagtgct gcaaacacac agagtacgat aggaatcgat acgccggagg
                                                                       2040
                                                                       2100
atatggagaa ggccatagct atctccgttc gcagggaatg gaatgacaca tctgcgacat
tatatgtata gaagtatata ggatgagatg attgacgatc tgactcgaga aaggatctcg
                                                                       2160
atgcggccaa tatcgtagag gtcgtaagcg acttatgttt cgctcgtaag cgtggagtga
                                                                       2220
                                                                       2241
actacctcgg cttgggtcct t
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 822 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...822
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:749

cgtgccggtc	tgctgactac	agaccatggc	cccatagaga	ctcccatctc	atgccggtag	60
	gagcgtgaag					120
	ggcaatactt					180
gccggaggct	tgcacagttc	aatagctggg	agcggccttt	gctcacggat	agcggaggtt	240
ttcagtgttc	tctttggcgg	agaatcggaa	gatcacagag	gagggtgcga	ctttcgttcc	300
catatagacg	gctccaagca	cctttttca	cccgaaaggg	tcaggacatc	cagcgcgtta	360
	catcatcatg					420
	tcgatgctcc					480
	actctatgga					540
tcccgatctg	cgccgccggt	cggccgagat	ggtagctgcc	gtcgatgcgc	cggaaatgcc	600
atcggaggat	tggccgtggg	agaaccgacg	gaaaagagta	cgagatgatc	gaactgacca	660
acgagatcct	tcccaaagat	cgtccggcta	cctcatgggg	gtaggtactc	cgatcaatat	720
attggaagcg	atagacgtgg	tgtggacatg	ttcgactgca	tcatgcctac	gcgcaacggc	780
cgtatgggca	gctctttacc	tgcacggacc	atcaatatcc	ga		822

- (2) INFORMATION FOR SEQ ID NO:750
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 454 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...454
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:750

gggatctcac cacagg	ggtt ggtggagact	gtacggaagc	ccagatcgga	tagcaatcgg	60
gtaccgattc gcggat					120
gttgtggatg attttg					180
ttggcatcga tggggt					240
catcgcgatc ttcacc					300
atgaaggatt cngaat	cggg atgcttgatg	gatacggaca	gcaaagtgca	ccgcgacggc	360
cgtcttgagc tactto	gcgc gtactgttgg	agagcgttcc	atgaaaggaa	ccagaccggt	420
ggatgtgagg gcggag					454

- (2) INFORMATION FOR SEQ ID NO:751
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1205 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1205
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:751

	++00000000	tagssatttt	accatcaaga	aagaatttag	tteeateect	60
gctttaaata	Ligiagicga	tggaageett	testacacat	ccaatatcca	atoroosass	120
ttgaaattaa	agatacagat	gttcttgctt	tcgtacacat	ccaacgccca	acceptacada	180
ccattctatt	atcaatgccg	ggcaagaagc	cttgataaag	Cagageetac	agctacagaa	240
caaattgttg	ctacccctct	gtcaaagcat	atgttcagaa	tggcaaaatt	gttgtagagg	
aagagattcc	aagatggaag	tattcaatgc	aactggtcaa	cttgtcaaaa,	atgatecett	300
gtccccggtg	tctatgttgt	ccgtataacg	gcaaacggtg	taagtatttc	cttaaagtct	360
teettcctte	atttatagag	ctaagattta	aagaaaactg	cgccttctta	atgttttata	420
agaaggcgca	gttttcgttt	tctcattcca	ttctccgggt	ggtcgtcgaa	ggggactgcc	480
totcatcttt	aaacgaggaa	tatcagctcc	cctcacacaa	cacgatgtcc	acaaatccag	540
ttcatagcct	atttgagacc	tttgaaaaaa	gagaaggttt	cttatatcat	aaaggcacta	600
aaaatcagtc	gattgacaat	gaaatctcca	agaaaatccg	tgcgacagtc	tcacttatat	660
agatecagee	aatootetoa	tatatcaggo	tgttgtggat	ggaggatagt	acacatagtt	720
agacgeggee	aacaacattc	atactaaact	aaaaacaaaa	gcattatgac	tcctatcctg	780
tigcacciga	aacaacgttc	acactcaatc	cctatcacaa	toocoaattc	aaataatcac	840
aacacgtttt	CCCCgagccc	adactcaatg	agtogttttc	tacccaataa	ctttaccttt	900
caacgaagac	ttgaaaggca	agtggtttt	ggtcgttttc	nganttoaag	caacttogag	960
gtatgcccga	cggaattgga	agacctggcc	ataaatatga	agaatttaag	caacceggag	1020
tagaggttta	ctcttgcagt	gcgataccca	cttcgtacac	aaggcttggg	ccgacgette	1020
tcctgctata	agaaggtaca	gtatcccatg	ttggccgatc	ccttcggtgc	actcactccg	-
atctggtatc	ctgatcgatg	atgttcatat	ggcttaccgt	ggctcttcgt	gattaacccc	1140
gaaggcatta	tcaaaatcgt	agagctgaac	gacacacgta	tgccgtgatg	cagaagagat:	1200
cctcc				i	i.	1205

- (2) INFORMATION FOR SEQ ID NO:752
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1482 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
    - (ix) FEATURE:
      - (A) NAME/KEY: misc_feature
      - (B) LOCATION 1...1482

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:752

agtccgggtt	ctttnaagat	actgtatctg	tatgcgnatn	nncagtccta	attgcgaaat	60
acacgggatt	ctcctgttcg	gtaatgacga	gcatgaacgg	cctcgatcag	ctgagatact	120
tctactccat	aggctccgat	gttttggcag	ccgatgctcc	cacttggccc	ggaatgagag	180
		agttattctc				240
cataccgacc	ctacacgcaa	aagaatgctg	tcctgatcct	tgtgcagttc	ggtgtaccct	300
		ataccatgaa				360
		aatcttgaaa				420
gcgtcgcatg	tgtagtcaat	caccaatctg	tccgggctgc	aataccgaat	gtattgcgct	480
		tgatgtccat				540
		tccttgacgg				600
		cacgtagcat				660
		ttctttagag				720
		ccaatcgaga				780
ttctgacgga	tttgtacatt	ggtagccggt	ttagaaacta	tcggacgagt	ttcatatcct	840
		tcacgttctt				900
		cgaatgcaac				960
		gtttgagtta				1020
		gggatcgact				1080
gtggacgttt	gtatatgcct	ttttcctatc	actattttat	tggataatag	ttggccgaat	1140
cacattgtct	ttatctattt	cgggagctat	tacattctgt	cctcaaagat	tatatcggat	1200
		caatgtttt				1260
acacactaaa	aacatcgatc	atggatgtta	ttctctcgat	tctacccatc	gttctcctca	1320
tcgtttgatg	cttgggctta	ggatggcggg	tgacaagagt	gctgttctgg	cattgtttgt	1380
					gattttaccc	1440
ggacaggtgt	ccggatgggc	ttttgtggga	ggtgccctca	ag		1482

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 465 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...465
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:753

```
60
gcaggatgca aaaaggaacg tcagtgcggc gaaaaaaatg agctttctgt tgtcatctgt
                                                                       120
ttttgtctta tgatggactt aacctcgcaa agatagcctt ttctatatat aatgtagttg
                                                                       180
ccgtgtacag attccagtta taaatgcaca ctaagtcaga tctagtaaga agcgttcgaa
                                                                       240
ggggtgggct atattcgggc tgaggcattc aaaacagcgt tctatatggg gctgtgtcaa
                                                                       300
aatccaaaat ggattttcca acaaaaagac acaaatgcca ccttaatcat atcggaaaac
                                                                       360
cgctatcaag taggatgatt ttgtcctttt ggtagcggtt tcttatacaa attatacaaa
tgatagtatc ctttactcta aacggaattt tgcacactct catctatctt ctgtgatcag
                                                                       420
aagataggca aggaatcggc tgatcggtcg gtaatggtga gggga
                                                                       465
                                                                       :
```

- (2) INFORMATION FOR SEQ ID NO:754
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 563 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION  $1...5\overline{63}$
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:754

ggcagtggca	ctttctccat	atttgtcgaa	cgcgccctgc	gggagacctt	cattacaaga	60
			ttcccggtag			120
taaggaactg	gcagaaaaca	gacctgttat	tatgccggtg	cagacggatc	gatgggacat	180
gctttcgttt	gcgatgatac	gaaccagacg	gaacgttcca	cttcaactgg	ggatggggtg	240
gcatggtaac	ggtaatttct	atctcaatct	actcaatccg	ggttcgcttg	gcacggcgca	300
ggcgatggag	gctactctac	tgaccaagag	gttgtcatag	gcaagagccc	ggccagcaat	360
gaagtccccg	gtatcggtac	cggatccgac	cacacgcttc	tatggattgg	caacacaata	420
tgtctgatga	aagcactttg	actgagtgta	aaaatcaaga	acctactcca	catatgcagg	480
gggatgtgaa	attggcttat	cgcctgacgc	ttcccaatgg	aacggaaacg	actaacccac	540
cgtcaccgtc	cctatcgttg	gga				563

- (2) INFORMATION FOR SEQ ID NO:755
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 515 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...515
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:755

tgcccagtgg	acctatattc	acgggaatcc	cctgcctcag	ggattgggtc	gggcgctttg	60
tttacgaata	atacggatac	gcctctttat	acggaagggg	ttatttgaga	tatgccgcag	120
ggaagagatc	ttcccgttgc	gatgtcgggc	cttgttccgg	gaaagatatg	gaaacggagg	180

cttatgaaaa	ttctgttgaa	gacaggtatt	tcggtttgcg	ggagatagcc	gccggcgcct	240
tgggaatgat	gttccgtgga	aatccgcatt	gcgtgcattc	gtatcggaat	ggtggattca	300
cgggatttta	tagaggtgcg	tacttccggc	tctacgggta	tgccaagctt	atccatctgc	360
ctaaaaaagc	gatggcggct	tcggcacggc	tgccaatgct	tttttcgaca	tatcccggga	420
ttccgtactg	atgctctctc	tccgctttct	tatatagccg	gtaaaatgat	ggtggtgagg	480
gcattcgaag	aggggccgtc	tgttgccgga	acctc			515

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1905 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1905
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:756

```
ccgcgttgan aaaaaggcga acggcatccc ccttgaacta ttgcacaggt gacataaagc
                                                                        60
                                                                       120
gcggtaccat taccttagtg gttccaggcc gtgggcaatc tttccaagaa attgnccgaa
ctcgaagtcg gcgactatat cacggattgg taggtccgct gggacagagt acgcatatcg
                                                                       180
aaaaggtcgg cacagtgttt gtgccggagn cggtgtgggt gtggctcctt tgctcccgat
                                                                       240
cgtggggctt tccacaaagc aggcaaccgt gtaattgtcg tattggctgc cagactaaag
                                                                       300
                                                                       360
atctggttat ccttgaagaa caaatgcgag ccaatagcga tgagtgatca tcatgacaga
cgatgggtct tatgggacga aaggcctcgt aaggatggag tggaaagcgt tatcaaacgg
                                                                       420
                                                                       480
gaaacggtag acctctgcgt tcgatcgggc cggctgtgat gatgaagttc gtttctctcc
                                                                       540
tgaccaaacg tacgagatac cgaccatagc ttctctcaat acaattatgg tggatggcac
ggtatgtgtg gggcttgtcg tataagcgtg ggaggacaga cgaaattctc tgtgtcgatg
                                                                       600
gccccgaatt cgatgcacac caagtggatt tcgatgaatg atcatgcgtt tgggcgcata
                                                                       660
                                                                       720
ccgagagatg gaataacctt attttcgcct tattgacatg actacagaag aacttatccg
actgcgtcgc tctgaccatg gagagaggag ctgcgcaacg cgctcaaaaa taaagaacgc
                                                                       780
atgtgcgtcc acgggctgaa atgcccgaac tcgaccccct ctatcgtagc tccagatcaa
                                                                       840
                                                                       900
tgaagaggtg aatcgcggtt tgtcccgtga ggccgctatg gcgaagcctc tcgttgtctc
                                                                       960
gattgtccgc aaccgagctg tatggaagga ttcctgtgag tatcaatatc ccgaccttta
                                                                      1020
tcaagcagat agaagtaggc atatactggc tgcagcatct actttgcgag agacaagctc
tttgccggcg tgtgcggacg tgtctgtccg caagagaagc aatgcgaaag ccggtgcact
                                                                      1080
                                                                      1140
atacgaaaat gaacaaaccg gctgttgcca tcggtttctt ggaacgcttg ccgcagacta
cgaacgcgaa cagggcgcac tcaaagttcc cgaaatgctc ctcgcaacgg tatcaaagtg
                                                                      1200
gctgtgatcg gaagcggtcc ggccgacttt ctttctccgg agacatggcc aagttgggct
                                                                      1260
                                                                      1320
atgacgtgac cgtatcgaag ccctgcacga aatcggagga gtgctcaagt acggaattcc
                                                                      1380
ggatttcgtc ttccgaatag tatagtcgat tcggagatca atcttctcga aggatgggcg
                                                                      1440
tacgctttga gacgaatacg attgtcggcc gaacgatcgc aacgatgacc tgcatgaagc
aggatttcgc ggtgtattcg taggaagtgg gccggtctgc ccaatttcat gaatatcccg
                                                                      1500
                                                                      1560
ggtgaaaacc ttgtaggagc atgtcttcga atgaatacct gacgcgcgtc aatctgatgc
atgcgagcaa gccgacagcg acacacccgt tttcaagggc aagaatgtag cttgtcacgg
                                                                      1620
gggcggcaat acggccatgg actccgttcg tacggccaaa cgcctcgagc agaacgtgcc
                                                                      1680
                                                                      1740
atgatcgtct atcgacgcag cgaagaggaa atgccgcaag attggaagag gtgaagcacg
ccaaggagga aggaatagag ttccgacact gcacaatcct atcgaatata tcggcaatga
                                                                      1800
acgaggccga gtgctgcgat gcgcctgcaa aagatggagc ttggcgagcc ggatgcaggt
                                                                      18:60
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 843 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...843
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:757

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1068 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature

#### (B) LOCATION 1...1068

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:758

```
gccattctct cggctacgat cattatactc tataccctct atgccacage ggcgaagtca
                                                                        60
tatcgaggaa tggcccgtat ctgtacgtat ctgtctttcc gttgccaccg gacttttcca
                                                                       120
ttatctgaga cacgtgatag tgaaaggtgt cattgcaatc cgaccgatat gctctatcag
                                                                       180
gaccacgggc tccagcttcg gtagttgtgt ggatcattct ttattcgata agcccttatg
                                                                       240
tcgcaaggcc catagccata ttcgatttcg acggtacgct gacccgatgc gatttttgct
                                                                       300
tccctttctg cggcaagccc agccggttat tctcttttgg ctcgactgcc tttctatctg
                                                                       360
                                                                       420
gccatgtgga tgtgctacaa acttcggctg gcccggccga ccggacgaaa gcagccatcc
tttccacagt cttgaaagga aaagggaggt ggaatgccgg gcaatgggac agcgattcgt
                                                                       480
                                                                       540
gcctgctatc aaagcattct tcgtcccgaa gcccttcgct gtttggaatg gcatcgcagg
aaggacatcg gctggtgcta ctgacagcct cgcttctgcc ttgtgtgggc catgggctga
                                                                       600
aaagacgggg tttcataccg tcattgctac ccttccgaga taaaatccgg cattctgacg
                                                                       660
ggtcggttcg aaggcaataa ctgcaaggaa aagagaaaat ccacaggttg gatcgagcct
                                                                       720
tgccgcattg gcgagttcga tctcctatgg ctatggcgat agcccctccg accgccctt
                                                                       780
gcttgcctct gcacacattc ctactataga agattccctg ctctatagcc tgcgccgcgt
                                                                       840
ccgtatcgtt tggagattgt cgattcatcg gtgtcccgat ggtacccatt ttcctacccg
                                                                       900
accataaacc gccatcagag cagaaaaaag cctcttctgg atttccacat aaacgactgc
                                                                       960
aatgcaacgg tttgtgattt tcagttttac acataaattt tcccggcctg gaaaaaaatat
                                                                      1020
tttccaggtg ggaaaacatc ttttccacgg gtggaaaata ttctttc
                                                                      1068
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 912 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...912
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:759

gccagatgat	agatttattt	cagatcgata	caggatcttc	tctgcttctc	cattcgcaga	60
				atatggatat		120
ctgaatcatg	agttgataac	tcacccaaca	gcacgttcta	cggaagggta	aagggcaatt	180
caatggaaga	cgcccagtgt	tcgacggcga	tattcttgtt	atagacaagt	cccttgaagc	240
gcgggtggcg	atatggctgt	ctgctttttg	gatggagaat	ttaccctgaa	aacatccgca	300
tcaaatcgga	agagattcta	ctcgaaccgg	ccaaccccga	ctacctacca	tacatgtatc	360
ggcagacaac	gatttcgtca	tctgggggat	cgaacctatt	gtattcataa	aataagaaga	420
tgatcggcct	atgtatgccc	tttagactgc	aacaacttct	tcgtcagttg	cgaaagggtg	480
ttcgacccct	gctccgaaac	aggccggtcg	ttgtcctctc	caataacgat	ggttgtatct	540
cgctcgcagc	aatgaagcca	aagcattggg	gatagggatg	ggacaacctt	cttcaaggtg	600
caggacttga	ttcgccggca	caatgtggca	ttcttcactc	gaacttcatt	ctctacggcg	660
atatgtcccg	acgaatcatg	tcgctttatc	ggaacttgta	cctcggatgt	cgatctattc	720
gatagacgag	tgtttatgga	tttgagagga	gtgaaagata	tatgtcgtat	gccacatgat	780
agtcatagag	tccgccatgt	acggtatacc	gtgagtatag	gtgtagccga	tacatgaccc	840
tgtccaagtg	gcatacaaat	atgccagagt	atgcggttac	agcgtatgcg	catagactcg	900

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 617 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...617
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:760

tggggaacga	attoaacaco	ссерсравва	gcgaattgaa	gccatcggca	atactccgcc	60
cggggaacga	ttastatatt	tatracrete	caccggttgc	ccgaaatcat	cgaattggcc	120
cgatacacgc	Ligargiair	cattactte	tancatacat	caaccctato	ocoataaagg	180
gtaatatccc	ccgttgcttc	gatggettaa	taagatagat	-1-11-0000	gtgcgatctt	240
aagacagatt	caggctaggc	cgtatttgaa	tggaacaggg	atatttagta	gracece	300
cgtcgctcca	taccggagag	atccactcga	ccgaggatgt	aagccaaaac	ataacgacga	
gcagaccgag	tacgatggag	ctcatacgaa	tgtatttgtt	tttctcttat	tgaagaagag	360
gaagattacc	aagacgagag	cagcaatgct	gaattctgcc	agttgccgaa	agtcccgtcg	420
gacgcccacc	anttacetee	trocatoaoa	taatccccac	tttgatcaga	ctcagaccga	480
ctcatcgccg	Cattgettee		catestasta	tectteagat	aacggaagga	540
tcagcaagac	acgattcccg	aaacgagagg	cgcaacgacc	nonnecents.	aacggaagga	600
ccggcttgac	gatcatctct	accggagctg	ccgctatcgt	acaaccgaca	taagtggcag	617
gcccgccggc	caggccc					017

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 510 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...510
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:761

gcagcatcct	tcgttccttt	ttcctacgga	tgcagcagaa	gttcttcggc	aagtgcaaca	60
aagagtctgc	atccatgcca	cagtctgcat	actgttcggc	acagatccct	gcccgataaa	120
gcgatcgggg	actcccaccc	gtcggatcgt	gggtggtagt	catggtctgc	cataaactcc	180
atgacggccg	atccgaaccg	ccttggatgc	aaccatcttc	gacggagatg	atcgtatcaa	240
acttcttgcg	atgccatgga	gcatntcctc	gtcaagcggt	ttgaggaata	ccattcgtag	300
tgggctgcag	atacaccttt	ctcagccagc	cgttccacca	cttctgtacc	atattgccta	360
tggggcctat	ggagaggaag	gctatagctt	cgcctccgtc	agacagcgtc	ctcgcgctat	420
ttcgaccagt	cgcggagtgt	tcgccagtcg	gtcaagcacc	ctttgccacg	cgggtaacgg	480
		nccttgnatg				510

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1414 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1414
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:762

```
gggaaaagat gcaagggatg ataccccaga tcaggcacgg ttgacatcct gatcaaaaag
                                                                        60
ctcggnaagc gggtcatngc aagccattcc gatgaagcac ccacttcgat catatcgggc
                                                                       120
                                                                       180
aacatcttat gctcacagcc atgtaagtct gtactccttc gatacgaagc agattagagc
cgacaccctc tatatggccc ccatactaag cagcatcttg caaagttgct gcagatatgg
                                                                       240
                                                                       300
ctcacggcag cattataaat agtggtaata ccatcagcaa ggacagctgc cattggatat
tggcagtacc cgtcacagaa gcttcgtcca gcagcatata agtccggaaa gccggcttgc
                                                                       360
                                                                       420
agtcaattca taggcttgca tatcggaatg gtgtcgcacg tggcacntaa tgcctgaata
                                                                       480
cctacaagat gagtatctaa ctgtggcggc cgatcttatc tccccctggt ttcgggaaaa
                                                                       540
tggcgtaacc aagcgactga tcagtggccc aacaagcaag accgaaccgc gcaaggcgca
                                                                       600
ctcttttcga gaaactgctc gcttttgata tagtcgagat tcacattaca gcttggaaaa
                                                                       660
cacaagtatc gcgggtgggt ctttttacct taaccccatg tttcgaagca ggtcgatcag
                                                                       720
gttgttcaca tccaatatat cggggagtta cgcaccacaa cctcctgatc ggtcaatagc
                                                                       780
gtagcagaga tgatcgcaaa gcttcgtttt ttgcaccctg gacgagaatc tcacccttga
                                                                       840
gactttgccc ccttctatta cgtaagatgc catagagata atgtgtttta tattctgtat
                                                                       900
gattatttcc gccggaatac cttgttccgt ttggtgttgt tatgtccttc cgatccgaag
catteggtat egteagatga caacteteet egteagetet atgegeeett eggacagtte
                                                                       960
                                                                      1020
gtacaaatcc ttgaatatct gtagtcatcc accgtatctt tgttccatgt cagatacgaa
cgcttcatcg gttggcgatg agcagctcca gcgcataacg ctcttctccc tgctccatgc
                                                                      1080
                                                                      1140
acaagccttg aggatcattt cctgtatgag atggccgtag tgccgattac gatgtcgttg
gccgagtagc ttacagcttt aggcttccgt tcgagcgctc cggactgatg atctccatcg
                                                                      1200
                                                                      1260
gaataatcga tatccaactt gaatcggaca taatagccag atgatcccaa agaatatgct
                                                                      1320
tggtctcact gtttcccgcc gttcgggaaa catgtttccc atgattgtaa tgatcgtttg
                                                                      1380
tgccagcgat tccgttcgtc acgatcaccg attgtcatgc aataatttac cagttttgga
                                                                      1414
tattcctgcc atattccgga atagccaaag gttc
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 840 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...840
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:763

tacatacaac	getgacente	gatcgtaggc	tcgaaatttt	cgaggncgat	gtgcgaaaag	60
Lacatacggc	accatectet	gcacgccata	aagccgctct	tgtgaagtgc	cacggtcggc	120
cctccacgtc	accaccece	genegeenen	acceptaget	ctatcaattc	actgagcatt	180
tcggaaatga	acctccttgc	Catagogogo	accaacagac	ctgtcagttc	ttcaccattt	240
tcctgccgaa	aggaggcata	cgtttttgca	tcgggtttat	attttgaggt	ccaccgccc	300
gagcttcgtg	tttacttggg	caaatgccgt	gtatcctccc	accggaagca	aagcagcgac	
cateccaace	ccagcgatag	ctgttttctc	ttcttcatat	tatactattg	aatttagaat	360
gaatctctcc	aaatgtaacg	acaatcgagg	agtaggatat	aaattttgaa	taaaaagcag	420
etatagagt C	acacaataac	ottotopaaa	taaaaagaga	cgtacctccg	gaggggagat	480
Clatagagec	tttccttt	tatatetaet	ctotatoaec	aggggagtga	aatcagggat	540
acgtetetge	LLLLEGLLLL	cgcacccgcc	concettest	-0000-0-0	tattogcacc	600
agcaaacgcc	ctgagctacc	atageettgg	Caaccicac	gaagccggga	atacatatat	660
cttcacatag	tcgatgtagt	tgccgtcttt	accgtattaa	cgcactgctc	guggauguu	
tocateatct	ggtgcagcca	cttgtcactt	cttcattcgt	ccaaacgagg	tgcatagcgt	720
tetgegteat	ttcgaacctg	agcaagaaac	accacctgca	ttaacagcct	tacccggagc	780
gaaggratet	tootttectt	acatagtatt	cgctggcttt	cggccgacaa	ccctgttaga	
	2862282		0 00			
840						

- (2) INFORMATION FOR SEQ ID NO:764
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1943 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1943
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:764

```
120
gnagacettt etetttgtge engaacagga categeagat ggegtacatg tgeacgatge
cattgatage aagegeacga tgategtgtg tgtatggete ttttgeegge eetgetette
                                                                       180
ggtatgtata atgtggggta caacattata tggccatcga tgctcccgta gtattttggc
                                                                       240
                                                                       300
eggetttete tteggaette tegeegtaet geecaaacte attgteteet atgegteggt
tiggggatag agtttgccgt agctcagtac cggaaggaag aaatcaggaa ggcttcctcg
                                                                       360
                                                                       420
tatogggtot gottatocog atgatogtgo ogtagataot cogotgtgga tgatogoogt
                                                                       480
ggcgacggct tttgccgtgg ttttgccaag gaggtgttcg gcggtacggg acgcaatata
ttcaacgtgg tctcgtgacg cgtgccttcc tctttttcgc ctatccggcg gctatgagtg
                                                                       540
cgatcaggtt tttgtccgca cggctgatac cttcggcctc ggcgcaggac ggtagcggac
                                                                       600
ggcttctccg gagctacacc tttggggcag atagccaggc cggtgccaag atgcctgaaa
                                                                       660
tacataatgt ggcaggcgac ccctctccct gatggatgct ttcctcggct ttatacccgg
                                                                       720
ctccatcggt gaaactctac tctggctatc ctgatcggag ctggccctgc tgatttggac
                                                                       780
                                                                       840
ggggtcgcga gctggaagat catgttgagc ggtttggtag gagcctcagc aatgctctcg
tattcaatgc catcggcacg acggcggcga tgcagatcac tcgctgatgc acattgtcta
                                                                       900
tggaggcttt gcttttggct tggtatttat gccaccgacc ctgttacttc tgcccgtaca
                                                                       960
gaaaagggga aatggatctt ggtttcttcg tcggtctgat ggctgtattc atccgagtgc
                                                                      1020
tcaatccggt taccctgaag ggatgatgct tgcgatcctg ctcatgaacg tatttgctcg
                                                                      1080
ctgatcgact atttcgtggt ggatagcaac atcaaagcgc gcaaagccgt atgctcaaga
                                                                      1140
aatcctaacc gctaaatatt tcgataaaga catgaaagag ataaaaactc gtacaccatt
                                                                      1200
ctctatgcct cggtgatggt tattgcgtgg cggttttgct ggcttacgtc tctcagtcat
                                                                      1260
                                                                      1320
tgggcgacag gcaggtgaca acgagaagat agacaagatg cagcagatcc tccgctctgt
                                                                      1380
gaagccggaa tagaagataa gggcaaagta atagctcggt acacggacgt gacaagcaag
aactgctcat caatcaggat ggtacggtag ccaagacctt cagggcgagc agttggcaca
                                                                      1440
                                                                      1500
aaatgaagca ttcacgctca atacgcgcaa gctttcaaat cggccgctaa tgatccaagc
atttcgctcc ctctctatac gcagagatag agggtcagaa gaaatacatt gtcccgatga
                                                                      1560
acggtgccgt ctttgggggc cgatctgggg atacattgca ctgaacgaag actgcaaacg
                                                                      1620
atattcggtg cagatttcag tcacgaaggc gaaacgccgg gattggagcc gaaatcactc
                                                                      1680
gctcggagtt ttccggtcag tttatcggca aagaatcttc aaagagggcg aattccgatc
                                                                      1740
tgttgccgta gtcaagaaag gccaaaagcc gaaggaaagg actatgtgga tggcatttcg
                                                                      1800
ggcggtacgc tgagagcgat ggagtgaatg agatgctcat atcctctctc cgtccttatg
                                                                      1860
cttataccta atgaacaacg taaaaaaata agggctatgt cactttggaa taaaagaata
                                                                      1920
                                                                      1943
aggaaattct tctcgggccg cta
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 978 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...978
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:765

```
taaaagatta ggtacttttc aagaaaacca tcaagtactt tcacaaaaaa ttaggtactt 60
tttattggat tatcaggtac ttttgaaaat agatttatat atttgtagat gtatttaaga 120
aaacgccttt cagaggattt ctccgacttg ggaaggttta tcaagtggag actaaaacgt 180
atgtaataat ggcaagaaac cattgcaatt tgtggtcgta gagcgaaaac tgaatgtggg 240
taaaacgcag gtaaagtaat gcagatagca agaccgacgg ggagacatcg tgtaactttc 300
```

```
gctccttttg cgaacgtgta tccaagtcca ccacattcaa ccgcaagaag tcgaggctgt
                                                                       360
attgaactat gctacagaga ttgccaaaga catgtatcga acggcgacat cgtggagttt
                                                                       420
ggagacettg geacactaat gettettea aaagtaagge ggtagaacag ggggtaaagt
                                                                       480
tcaatgctaa gttcacatcg aaaagcctgt tgtcttgttc caaccttcca aaaagtactt
                                                                       540
acteteaceg atgtaageta tgaacagaca actgccagge caaagaaaga acaaaacetg
                                                                       600
ctccaaagcc tgataccgga agtgggggga atagcgggag ggcatataag aattagataa
                                                                       660
gcccacactt aacctttcag aagttttaaa accagaatag agagtttgct ttgccttgga
                                                                       720
gcaaactctt tcttttagac ttttctgaat cttgattagc cccttttgtt catcatcttt
                                                                       780
gaggggcttt tgatggtgtc ggtctcaacg tcttttagtg catcggcaaa aacagtttga
                                                                       840
gggaaagagc catctcgtct tgtttgccga cacagaaatg ctccaaatat tccaaccgaa
                                                                       900
atgatacagg totaaagaga tatgaaagco ttttgtotat cactatacaa actccgtttg
                                                                       960
                                                                       978
aatcatcagc atagtaag
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 800 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...800
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:766

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 464 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...464
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:767

tattctttgc	tcctgagaga	gggctggttt	ctatcctaag	tcgctacaat	tcactatcga	60
ggagaactca	cccgaggagc	aacaagtggc	actagaccag	agctactcgg	caaggtcttt	120
gagaatctcc	tcggagcata	caaccccaga	ctcaggagac	tgctcgcaac	cagagtggct	180
cgttctatac	tcctcggagg	ttgtcaacta	tatggtggat	gagagcctga	tttcttattt	240
aggagtagcg	atctggtgcg	ctctctgttt	agaccagatt	tcgtactgca	ggagacaaca	300
aagtgcaatg	cgaagctatt	gcaagcaaac	tcaaagcagt	caaatactag	accctgcttg	360
tggctcggga	gcattcccaa	tgggattgct	cataggatga	ttgagctact	tgagcgcata	420
	agaaaagcta					464

- (2) INFORMATION FOR SEQ ID NO:768
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1007 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1007
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:768

agcggagatc	cgcgtcctct	tcgatcctgt	cggtcgatca	ggagctttct	caagcggatt	60
cgggttttct	ccaacgcgca	atcttcaccg	ctggaactag	tataagcggc	acggttacga	120
ccctcagtgg	tgccataccg	catgccttgt	cttggcgata	gggccgctac	aggtgagcaa	180
tgctcgcctg	cttttcctat	ttccatgcct	gaagatgagg	gggtggtacg	gttggtggtg	240
aacaaacgga	tgagtccgac	ctgcaagttg	ctgtcgtatc	gctaccttca	tttgatcgct	300
ggacgatcgg	gcattccggc	tgcaagctcg	tgagcccaga	gagtgaatct	ttcgcttgcc	360
gtacctcgca	atatgcctcc	ggggatgaag	gagagcctct	cgttttggag	gtaacctctc	420
ccgaaacagg	aaaaaaagcc	gtgattccgt	catggtctcc	ttgccgctgg	tggacaattt	480
ccctgccctc	ctgcagccca	aacaggcgtt	atggaactca	gcacctattt	ggacatgggc	540
agttggatgg	agagacgaca	aaggctgcga	tagagattcg	caacgtcgtg	ccggccctct	600
ccgattgcat	agcgtcacca	cacgcaatcc	ggctttgctg	ccgtacccga	ccggacggag	660
ataaagcccg	gcggaagcac	actattcgga	tcgctgtgga	tccgcaggtg	atgaaggctg	720
aggggtggca	gagtaagctg	ccgatatttc	cattatttgc	aacgatccgc	aggctccgct	780
acgtgtatca	aggtcaaagc	cgaactgtag	cttttccccg	tagagctgct	gccagcggta	840
ctgcaagcga	gattgcccgc	agatctgata	aacagaacat	tactatggac	gaactacttc	900

والأراز المستعمر المراجعة فتناز أأراز والمسالية والأراز

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2523 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...2523
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:769

	anganactta	acattcacaa	tagtcgagag	cagetetgaa	'aagtgcgaca	60
gcaaaatcga	aaggaactig	acgcccgcga	tacctucauc	cacaaatata	caaggaatga	120
ggacggaatc	aggaagatgg	agacgacaga	tacctgcagc	catcttcttc	agtatogact	180
cgaaagggat	tccaaggcga	ciddiddigi	ccactgctcg	atacctatat	#Ct ratacca	240
accgagcaac	tatccgaccg	gcataaagaa	cgatgccgat	acggeracar	acetacatca	300
aagagccttt	ttcctgaaaa	gaccggaata	ccacgaagtg	cctaagcgac	ttastasset	360
ccatcgcgca	attccgttcc	ttcggggaag	gcaggtacaa	aaacctttct	Licetgetet	420
gcgagcatgc	actcagacag	agcagaaaag	aagggagaga	atgcaceggg	Laacgaatge	3
attaagacgc	aaaactgtaa	accgaaggga	tgcttatttc	ccgatcgctt	catcgacaag	480
ccatttgttg	cgatattcac	cacatgaacc	gtggttgtat	catcttcgaa	atccagatag	540
tgacccaagc	ttccttctcc	acaatactat	ccttgataaa	ggtaaactgt	agtttggttt	600
ggcctctccg	cccaaagcac	catacagatc	gacaagctat	tggtgcgttc	cgtgcaatac	660
ttcttagcct	cttcatattt	ctgtttgcca	tgttctccga	gaagttcttt	acagcatctt	720
tcgggccgga	cgatgacagc	cggccatcaa	ggcagcggca	aacaatgçcg	¢tccgatttt	780
ccatttttca	tattagaatt	tttactttt	aagtatcagt	tgcttagcaa	agaagcgaat	840
atccctatct	cctcattcgt	gcaggtgaca	ataatcgtcc	gaaaaggccg	aaaggagaga	900
caaggccagt	aaaatgtgga	gccggaatca	gagaaacatg	gttccaaaaa	atctgaaaaa	960
tcgaaccaaa	acaaaaactt	tacgttcggg	aattttttc	ttttggcgcg	agttccaaaa	1020
aattcccgac	catgtttta	gggatgtgtt	ttgattgttt	ttcggcgcat	gaaaagaaaa	1080
atgetcagct	tccccttcc	tcttcgctct	ttttcatttc	ccccaagtac	aacagggggc	1140
gcagagtttt	cggatcggac	ggattcgatc	gggaacaaat	ccggccgatt	ctgtttaacc	1200
atatgagacg	aaaacctgtc	gaatgtgcca	atatgcaatc	atgaatgtac	ccttţgaaca	1260
paatcatcaa	cttaaaacag	tcaattatga	agacaaaaag	actttttcta	ctggcgatca	1320
ttgactatgc	agcattcatg	catcaatggg	gcttgacctc	caaaaacgag	taaagggaat	1380
pagcaattcg	cctctgaaga	gcgtttggca	gagcctttca	cgcctttcgg	catcaggcag	1440
catteatatt	cagatcgaat	actccccata	aggcacccct	ccgaatagaa	gccgagtcga	1500
acatcatacc	actaatcaaa	caacggtaaa	gaaaggtgtc	ctgaacatcg	aattcgaaaa	1560
aaaacgttca	tatcgcctaa	tectecaete	cgagttatcg	tcagtgtgcc	ggaaataaat	1620
cagtcacact	gggcggtagt	ggcaatttga	ttttcggttc	cggtttaacc	agcccaccct	1680
gasagtasco	attaacggta	gcggcagtat	aaactcatcg	atacaaaagc	ggaacaactg	1740
gadageadee	trastootso	cogtacette	pcppcapcat	ttttgctcat	aaggatatac	1800
gacacegeag	gaaggatccg	gcaatatcac	tctttccata	gacgaaacca	agacgattca	1860
antaatatna	aaggaagtgg	aggtattaag	ctgacaggaa	aagcttcgaa	ccgatactga	1920
agiaatatga	~~66~~6~66	ttcgactgcc	aaaacctaac	actoaccato	ccgacataaa	1980
gaagereggg	aagcgggacg	geogeetest	ataaccagac	asstractor	caatctatca	2040
aatgagcgga	aguggaggug	catagaasaa	ctanataga	ttcttataaa	caatctatca	2100
ggatccgccg	guillacege	cackkaaakk	ccaaaacagg	ccccacaa	ațaggaçget	

cttcttcttc	agtatgcaac	cgtaagcggt	tccacatctt	aagccaataa	atacttcctt	2160
tttcgtaaac						2220
gactcttctt	ttttagctct	caatgcgatt	gaacgaggag	tgatttccct	ctttcgaacg	2280
taatgtttt	gcgcccattc	gagtagagag	ttcgagaaaa	aacggtttga	gatgtaacat	2340
ttcgggggct	tgccgtctta	ctgatagaac	gactaacaag	aaaccaatca	atcatgtgga	2400
caaaagactc	cttttcctcg	tgctcgcggc	agcaagtatc	agttttgcat	tgcccaaata	2460
atctcatgga	aacgcatcaa	gggtaacggt	aaagttcagc	agaagagcgg	cgtataggtc	2520
aat						2523

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 513 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...513
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:770

gttacgtaga cttgggatta aaatgtgcct gcccctgcag atggatcgat cgaatatctg 60 gcacgaggcc ctcatgagaa ttatgtggat cgtaggcaag tgctttcttc ggactgtatt 120 ccgaccgtgt gagccgtatg gtcgaaccta tgtacgcccc cagagtacgg gcaatagaac cggccttaga gctctgccct gacggatgat tccggcaggg gtatcagggt ggaagcttcg 180 240 ggacagtcga tttctccatt cttccctatg aggacgaaca tcttgcgcgg actctcatca atgggaatta cccatgcctg cgcatcatat cttgcgcttc gacatatgca gcgcggactg 300 360 ggcaatggaa gttgcgggcc cggtactgct ccacatacct ttgcccctca tcgggcactt 420 480 attecttega acttegtttt eteetetetg aatgtgteeg eagetaette gaatgegaag 513 agaacgggac ttaattctct ttcggtgaag ccc

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 808 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...808

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:771

		+	anttoatano	actacceaca	60
cattcatgcc	tgagatetet	tgagcagtcg	gattegegae	gergeeacg	
cgttagaaat	gctctaaaaa	caatactttc	atcatgatag	ccattatttg	120
tttccgtatc	tataatttct	gatcaacatt	tagcgttacc	aggtagaaac	180
cccccccc		ant at ant an	oottoggata	antatttaaa	240
gttggagtat	tgaactgtat	gcigiaataa	CCCCCggaca	gatgtttggg	7.11
tatcagccga	ggctccattt	attccatata	tttttattac	agaaaggaag	300
atagtagatt	attettacaa	cagctttcgc	cggttgggcg	aaatagagat	360
****	++00+++0++	acttctaata	02002000	agtacctgtt	420
ttatcaagge	Ligatiligit	gettetaatg	gaggcaggag	agcacccgcc	
gagttgacaa	caataatttt	ttacattttg	atggctttcg	agcgatttcc	480
gaaagtatgt	tcaaatctat	accagtccct	ctgagtgagt	ctaactgcaa	540
totcaccaao	gtcaatgact	gcaaaaacac	tetcctease	gagatttcac	600
cgccaccaag	Becautgees				660
attttcgtac	caatcgatgg	cagactgtag	ttttcacaca	caatategea	000
aggaaatcag	ctgtcgggaa	caagttctgg	gaagagatga	tggttggatt	720
taatetteaa	accttcataa	trantaceta	acattttctc	tatootgaac	780
		ccggcccg	40400000	cassa c Bana	
agcagctatt	gcaaaagt				808
	cgttagaaat tttccgtatc gttggagtat tatcagccga atagtagatt ttatcaaggc gagttgacaa gaaagtatgt tgtcaccaag atttcgtac aggaaatcag taatcttcaa	cgttagaaat gctctaaaaa tttccgtatc tataatttct gttggagtat tgaactgtat tatcagccga ggctccattt atagtagatt attgttacaa ttatcaaggc ttgatttgtt gagttgacaa caataatttt gaaagtatgt tcaaatctat tgtcaccaag gtcaatgact atttcgtac caatcgatgg aggaaatcag ctgtcgggaa	cgttagaaat gctctaaaaa caatacttc tttccgtatc tataatttct gatcaacatt gttggagtat tgaactgtat gctgtaataa tatcagccga ggctccattt attccatata atagtagatt attgttacaa cagctttcgc ttatcaaggc ttgatttgtt gcttctaatg gagttgacaa caataatttt ttacattttg gaaagtatgt tcaaatctat accagtccct tgtcaccaag gtcaatgact gcaaaaacac attttcgtac caatcgatgg cagactgtag aggaaatcag ctgtcggaa caagttctgg taatcttcaa gccttcgtaa tcgntgcctg	cgttagaaat gctctaaaaa caatactttc atcatgatag tttccgtatc tataatttct gatcaacatt tagcgttacc gttggagtat tgaactgtat gctgtaataa ccttcggata tatcagccga ggctccattt attccatata tttttattac atagtagatt attgttacaa cagctttcgc cggttgggcg ttatcaaggc ttgatttgtt gcttctaatg gaggcaggag gagttgacaa caataatttt tacaattttg atggctttcg gaaagtatgt tcaaatctat accagtccct ctgagtgagt tgtcaccaag gtcaatgact gcaaaaacac tgtcctgaag attttcgtac caatcgatgg cagactgtag ttttcacaca aggaaatcag ctgtcgggaa caagttctgg gaagagatga taatcttcaa gccttcgtaa tcgntgcctg acattttctc	cattcatgcc tgagatctct tgagcagtcg gattcgtgac gctgcccacg cgttagaaat gctctaaaaa caatactttc atcatgatag ccattatttg tttccgtatc tataatttct gatcaacatt tagcgttacc aggtagaaac gttggagtat tgaactgtat gctgtaataa ccttcggata gatgttggg tatcagcga ggctccatt attccatata ttttattac agaaaggaag atagtagatt attgtacaa cagcttcgc cggttgggcg aaatagagat ttatcaaggc ttgatttgtt gcttctaatg gaggcaggag agtacctgtt gagttgacaa caataattt ttacattttg atggctttcg agcgattcc gaaagtatgt tcaaaatctat accagtccct ctgagtgagt ctaactgcaa tgtcaccaag gtcaatgact gcaaaaacac tgtcctgaag gagatttcac atttcgtac caatcgatg cagactgtag ttttcacaca caatatcgca aggaaatcag ctgtcgggaa caagttctgg gaagagatga tggttggatt taatcttcaa gccttcgtaa tcgntgcctg acatttctc tatcctgaac agcagctatt gcaaaagt

# (2) INFORMATION FOR SEQ ID NO:772

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 643 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...643
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:772

gtttctg tccgagggt	c ggcatggga	aatggactac	tggagcgcaa	60
				120
				180
ctacaca aggtcgtca	a acgcctcttg	gacaagctac	tggattatat	240
				300
				360
				420
				480
				540
				600
				643
	tattcgc cggcagagc accccaa gatcaaaaa ctacaca aggtcgtca gcccctc cgtctcggg ttgccgt gcaggtatc actttct ttttcttgg catcgcg cgtggagct gaaggca tggactctc ctccgga actggtcgg	tattcgc cggcagagct gttgccggta accccaa gatcaaaaac cggcctcggc ctacaca aggtcgtcaa acgcctcttg gcccctc cgtctcggga cggtctttca ttgccgt gcaggtatcg gctgggtagg actttct ttttcttggg aggctattgg catcgcg cgtggagctt gccggaactg gaaggca tggactctcg tctctgtg ctccgga actggtcggt aaagctgggc	tattcgc cggcagagct gttgccggta ctcgtacggn accccaa gatcaaaaac cggcctcggc tccacaaata ctacaca aggtcgtcaa acgcctcttg gacaagctac gcccct cgtctcgga cggtctttca gcgactctgc ttgccgt gcaggtatcg gctgggtagg gcgagcggca actttct ttttcttggg aggctattgg tggatatcga catcgcg cgtggagctt gccggaactg tatcgagagt gaaggca tggactctcg tctctgtgtg agctatctga	gtttctg tccgagggtc ggcatgggga aatggactac tggagcgcaa tattcgc cggcagagct gttgccggta ctcgtacggn tatctccgtg accccaa gatcaaaaac cggcctcggc tccacaaata gcttactatg ctacaca aggtcgtcaa acgcctcttg gacaagctac tggattatat gcccctc cgtctcggga cggtctttca gcgactctgc tcctttgccg ttgccgt gcaggtatcg gctgggtagg gcgagcggca tgctcattt actttct ttttcttggg aggctattgg tggatatcga tctgcctcc catcgcg cgtggagctt gccggaactg tatcgagagt tgtcccacgg gaaggca tggactctcg tctctgtgt agctatctga cgatagagct ctccgga actggtcggt aaagctggc aaccgtttta cggatgcgaccttgctgc cctccga actggtcggt aaagctggc aaccgtttta cggatgcgaccttgctgc ccttgctgn ccttggaacc gatatgccat nca

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 495 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...495
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:773

aaaagagact aaaaa	ttttc aaacgcaato	gccctgacca	tctgtccgaa	tgggatccat	60
ggtattatat cgtct	tooto otcattggta	ttgttggcgc	tactgtgtac	cgacgcggta	120
gccggatgga ttatt					180
cgccacagcg tggca	ccaaa gtgcatacac	gggtagcgaa	gcgatggttg	gaggagcaca	240
agtgcgttgc cggtca					300
ttccactagt ggaaas					360
tatctttcca ctggt	ggaaa accggcgtgt	acaaatagtc	gcctgacaca	caataagaag	420
aataaacaaa agcgc	ctgct tttgtgcaaa	gggcccatta	attcgaactt	gttaataacc	480
gaacgtagca tcggt					495

- (2) INFORMATION FOR SEQ ID NO:774
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 457 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...457
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:774

cgctctatga tcccgaaga	aa ttttacaatc	agacgatgat	ccatagtcgc	ggatggaaga	60
gctgttcggt gtaaaacco	cc gagtgctgcg	caatacaggt	tgatcttctc	cgacaacatt	120
gccacccaag tggcagaaa	at gggttttaag	ggatgctcac	ggaaggagcc	aaacacatac	180
toggatggaa gagtocaad	ct atctgtacaa	agccggatcc	gctccggagt	tgtccctctt	240
gctcccaatc cgaggctga	ag cgatgccatc	agtgccatgt	tcacccgcta	cgatggaacg	300
aatatcccct gacggcaga	ac aagatgatcc	gttggatcga	agaactcccg	aagaggagca	360
gatattcaat ctcttcat	ga actacgaagt	ctgggatcgc	tccatccgag	gagtcgggta	420
ttttcgattt ctttcgtgc	ca ccccttcttt	ggcgaaa			457

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1393 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1393
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:775

```
cgttttctat accggggata atggcacaca agccacgacg tttggcctcc gtacctcctc
                                                                        60
cggattagtc gcctgcatca ggctctcggg atgcgagaca cttgggagcg aatagcttcc
                                                                       120
agettacetg tggcatagte egtggeeget teagagaage ategtetege teacettgeg
                                                                       180
                                                                       240
gcagatatgc taccatacac acgcatcgac aagcccctct cgcatcttcg gagcatcgac
                                                                       300
cagtgatttc ctcttttcgt aaaatcaaat tccggacaga agtgcatggg cgtgccacat
                                                                       360
gcgaatccag cacaattacg gagcggtgta ccgctttggc ttggcaaaga gagaagcctc
                                                                       420
ggcgaccaaa tgctcgaaca attgctgctg acggtgtcac cggcataggc catttgctcc
                                                                       480
ggatgccatt gtaccgacag gtaggtttct ccggataggc ttccatagcc tcgataacgc
                                                                       540
catcggaaga agggctgtca cgcggaaagg tttcggcact ctgctgactg cctgatgatc
                                                                       600
aggetattga cacceageag etegecateg ettaggecaa gtattegtee aagaeggaat
                                                                       660
cgccctgtaa acggacttgg tgtgccgcaa acgatatggg attttcggat taagccctac
                                                                       720
cggattttcc gactgggcat atatatctga tacattcctc cgccgaaagc tgtcgcaagg
                                                                       780
agttgatgcc cccggaaata ccgaggatcg gcacattgcg gcgagtggct tctgccacca
                                                                       840
atagagttcg ccccgatctc gctcgggatt gacttcgccc agtgtgggaa tgggtcttct
                                                                       900
cccaaatagg acgggagtaa atcgtcccca ccggaaagaa tcgcccatcg atgaacgtgg
cataatgacg tatgacctct atatccgtag taaagggata agtaagggta aacctcccgc
                                                                       960
                                                                      1020
acgtattaca gactoggtat ggototggoa atacacgago cogaggtatt ataattogot
                                                                      1080
gtcaaaccat aacaggtcga gagggagact ctcctccctc aaaagcttgc ggcgcacctc
                                                                      1140
aagctcttca tagagctgtc ggagcgccgc aggataatac tgatagtctt aggactaagc
                                                                      1200
atctattctt gcataagtag cattttcttc tataaatccc tgcgcggacc tacctcgtct
                                                                      1260
cccatgagca tggagaatat ggcattgcct cagcagcatt ctcgatcgtc accttacgaa
                                                                      1320
gcgtcctttt ctccgatcca tcgtcgtctt ccaaagctgc tcctcgttca tcttaccaag
                                                                      1380
gccttgtacg cttgtacatg cacacgggtt tcattaccat cggcataacg gtgacaaacg
                                                                      1393
cttgacgctt gtt
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 443 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...443
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:776

	actettttg	gcaccggcta	cggtctgatc	gaatttggat	ttctgagccg	agcttccgtt	60
•	geeeeettet	ttttttcga	gcgaaagaag	taatcgcttg	tgcttcagcc	ttgaaaacgg	120
	gegggeteet	2000303000	atoraroaot	aaagattott	ttgttcatgc	ttgattatag	180
	gcaggargca	ggcgacagcc	ttcttctatc	gtagcaccac	agaggcaagc	cggctcggct	240
	ggtttgattt	atgattattt	accastacts	tccgaagctg	taagcctcgc	acaccecect	300
	cccgttatgc	caagagateg	gccggcgcca	atantagata	tagatogata	acaccgcgct	360
	gacatatata	taagggaata	ccatgcaagt	atgatggata	cagacagaca	agcetttte	420
				taccccgtga	gcggaagang	ctcgctctgn	443
	ctgatcattt	tccacgcttt	ttt				443

- (2) INFORMATION FOR SEQ ID NO:777
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 970 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...970
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:777

nannagacta	acatctacta	ctatcttcca	aaagccatac	gctccttaag	aagaggactt	60
agaaaggccg	Reference	togggatace	caaagatttg	aaggagcaac	gaacgatgat	120
cittacaaa	gacgagacata	ctatcgctca	aaaatttcaa	agaggtagag	ggcgaaaaga	180
gettettet	Sccaeaeacacac	ccotacoaoa	gcacgacttc	tgctttgcgg	tgcttttgga	240
ccaaggrgcg	atatasasca	coasosotto	aataagagaa	tcgtctacct	cggtgagaac	300
gaccccaggg	tcttatogat	cttatogagg	taagtgaaga	gacttcaaac	tcaacattga	360
gacaaccccc	cttaccacco	atgagaagca	ctcaccgtgg	tacttctatc	cgatgctatg	420
gageteeace	ageteettga	oogotaaaat	ttgcaagcac	ggaggtgaaa	gactttgcct	480
atttactcac	catotaggaa	cacacagatt	ctacaacaag	aagaagaaaa	gagaggaacg	540
geegeeae	aadttaaaac	ggctctaagt	caccaacate	aactataccc	agaggttccg	600
tatttactt	coatactaaa	Peccarage	atcaatttet	gaggacctcg	agaaggtccc	660
caacttccat	accatcoact	acaatctect	atcatcatcg	aaccaacaaa	aacaaaaaa	720
taaccccat	cagaaatgaa	aacagcagct	tatateatcc	attgccttac	caatatgcat	780
ctactacac	agataccacc	tacqaaqtqq	topacaaate	tgtacagcga	gattaaccac	840
gragetacco	tacatctact	cctccagcct	caaggagett	tggacagttc	ttttcgaaac	900
agggatgee	cgagettaac	tattotttt	ggaagatcag	agcagggtta	gaaaaatatg	960
	cgagcccaac	Lucibette	8888-	8966		970
gcatgagaag						

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 946 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...946
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:778

```
60
ggacgattgg aatacaatat ttatagaagt gcctatcagc acatttgctc ggtcaagacg
                                                                       120
gtcaatgacc tcttgcgacc tgagcaccaa ccctgtcaag ctaaaataat caacccataa
taaacaattc cccaaaaatc ttttaaaaaac aatgacaaac gatatcttgc agcgtcttgc
                                                                       180
gtctttgcgc aaagtctgag tcatgagcat atcgatgctt atatcatccc gagttcggat
                                                                       240
                                                                       300
gcccactaag cgaatacaca ccggaacact ggaaaggtcg ccgttggatt tccgtttcac
                                                                       360
cggatcggcc ggcacagtag tggtcacagc aaataaggcc ggatatggac ggacggacgc
tacttcctcc aagcaggcca acagctcgaa ggacttctat cgacctctac aaagaaggca
                                                                       420
tccccggaac tccctccatc gacagtttct tgccgccgag ctgaaagccg ggcaaacagt
                                                                       480
                                                                       540
gggtatagat gacgttgctt tccggcaggt gctgcctctg caaccgaatc ggctttggaa
                                                                       600
tatacggcat caaactaagg actgacaagg atcttttcga tgaagcatgc gagatcgtcc
                                                                       660
agaaatccct cgtggagagc ttttcgttca gcccgtgagt atgcaggaga aagcgtgaaa
                                                                       720
gacaagatcg cacgtgtcaa taaagactgg cgacacaagg tgccaatgcc actattatca
ccatgttgga cgaatggctt ggatattcaa tcttcgtggt agagatgtgg agtgcaaccc
                                                                      - 780
                                                                       840
cgtagagttg cttttggtta tgtatcggct cgagaatctg tcctctttgc tttcctgaga
                                                                       900
agattactaa ggaggttcgc tcagctatgg aagaaggcgg ggcaagaata tgccctacga
agccatatat gaatatatcc cagcactacc tccgaataaa gctgct
                                                                       946
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 525 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...525

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:779

cggctcgcag atgctt	ageg ccaaggeggt	aaagagccgc	agcggaacct	tatacagcag	60
ggaatagaaa tgagca	ttat tggccggatt	gtccatcagg	caaaatccag	ctcatgcccg	120
gtacggatca tccaac	pppa atcggagctt	tgagagggaa	cgtcttctct	cccaacaaat	180
tcagtgtcca tcctcc	taac gaaggggtga	caaataggtg	tcgcgcgtta	tgcttccgcc	240
accacgacca tatagg	caga atgaatgcgg	taggcggact	gctccgtggg	caacctctac	300
tcgaagaatc agttgc	aaac gctgtattgc	taccgtggga	agatcctgcc	cccatgccaa	360
caatccggtg agtagc	agaa gcggcaaaac	aatgcgtatc	gtctattcgt	tttcatcgtc	420
gtcgaattgc aatcgc	tgga tcccaagagt	tcgtctctta	tatcttcatc	ggaagcaatg	480
gcttcgggtg aacctc	ggcg aagctctcgt	ccggatcggt	tgttt		525
8000088608	88-8 0	00 00	<del></del>		

### (2) INFORMATION FOR SEQ ID NO:780

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 527 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...527
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:780

gcttcgctct gcagccacat as	agatcctat	gggcgtattg	tcctgcaatc	gcccgaagtc	60
cccacctta cgagtgtgag to	ttgcgtagc	cgatccttac	ctggcgggta	tcgaagtcta	120
tattggccag agcatccagt to	cgttcagac	tatatctata	ttatcagagc	cgatgccgtg	180
gctctgcacc gtgatagctt g	tcgccatac	caccccgtga	cggtatgaaa	ctccctattg	240
gatacttgca ttcaatacgc to	cgaaacgag	aggcgactgc	atccactcga	gcagatcacc	300
taccaatatg accttatcgg co	caattgttc	gggacgaata	tgcgatgaaa	gaccgaaccg	360
tccgtattga tgatcagctc g	gagggggga	atgttcttt	ggttttcata	agttcattaa	420
tgttttaaga ggtgagacag a	caatcggta	agatgggctt	ctcgaaaagg	tcggccttgg	480
gtctaaaagc tttgcacggn t	tggaactcc	tgnttctgac	ttccttt		527

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1580 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1580
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:781

ottaccacta	aactcttcgt	ggcgagagag	atcgaagtca	gtccgactag	gatgccttcc	60
citgitgita	agccgaacgg	catctcgaac	tcaatatcgt	ggcagcattg	gcatagtgtg	120
acticitiga	atgatcatgg	aaacggtttt	gtcgtctccg	aagccgaggg	cgcggtgcca	180
ccagcingic	aggttttcca	cttctcgaac	cattgcagct	cttcacccgg	tcgtacgaag	240
ctgcatacgg	catttgttcg	aattcococa	tccggaagat	gaactgacgg	gctagatctc	300
aactgatete	gccttgccga	trtograsst	tccggaaggg	atctcattcg	tcccgtcttc	360
gttccggaaa	ggaaattgac	anatatocct	taaccatttc	рорасраара	tataccttca	420
tgcacattca	ggaaattgat	adatatgeet	ancesaceto	aggttgaact	ggcgcacctc	480
tggcaccgtc	ggccgtagag	ceatettegt	accatctcac	agtcgaggat	aatctgacga	540
tgtccagtta	gcgtaccgct	gateggaeag	tegatetege	ttcatatact	gatctcgctt	600
tttcctccag	attgttgtca	ttcagtgcag	tagtaaagtg	angesteate	tasatacete	660
ctgttgatat	tcgatcacac	gggcgttggt	ggcccggacc	tatentetat	tttaaccaaa	720
gccgaagcgt	ttggctgctt	tggcgattct	tttgctattt	ttttatttat	tetatanaca	780
tgatcctcca	cgagtcatcc	gcacgataac	gctttttgga	atccttgttg	terantages	840
gatcttgaac	gcatccacgt	gtcccgaagc	tttccagatc	gaaggatgca	tgagatggta	900
gagtcgatgc	ccaccacatt	atcatgcagc	agggtcatac	ttcccaccag	tagcgtttga	960
tattgttctt	cagttcagaa	ccgtattgtg	ctagtcgtac	acagctgcca	gaccgtcgta	
tatctcggac	gaaggaaaga	gaagccgtat	tctttgcagt	gtgagactat	tttttgaag	1020
agatetteeg	ttgtgccatg	ctatcttgat	gtgtgaatct	tattgtattc	ctacatttac	1080
ctcgcgaaaa	taatcctttt	tcttcaatag	tctcctaaac	gatttgagta	cacatcccac	1140
aaacaaatgc	aacactaaga	taaatttagc	aagaagactc	gaaaggagtt	ctaaagttta	1200
gttttttctg	ggtctatggt	tcagttggtc	gtattgttgt	tcgacctgac	gaaaaaggcc	1260
ttcctatccg	aaaatcatca	cactatcatt	ttctccttga	attcggtttt	cataaagggg	1320
atttctggaa	tgattccaaa	ttcctcctcg	tcgttgaaaa	cttttggcac	ataaaacatt	1380
gatgcatgcg	gacttgattt	gccacaaaaa	agagcaccga	acagaagtcc	cggtgcacct	1440
taataatcaa	tatogaaaac	tccacttact	tttgccaagc	agcatatcga	ggttgcgctg	1500
cacatttaca	tctccttctc	aacggcctta	cggaagaagg	tttcggcacg	agcaaaatct	1560
			30 0 00	30 0	_	1580
cccgcacggc	ataagcagct					•

- (2) INFORMATION FOR SEQ ID NO:782
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 538 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...538
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:782

```
tttcaagcac tcgtatttga aacataatac cgattttctc tcctctaac accttgagga 180 ggtttcccgg cgtatcatat cgaagacgac gatgggtagg ttgttctca tacacatggc 240 cgtggagtca gatccattac tttcagacct cgggcataaa tctcatcgta tgtgtccggt 300 cgaacttcgt agccgaggga tccttctccg gatctgccgt gtaataccat ccacgcgcgt 360 ccccttgagc atggcatcgg ctttctaatc tcatgccgc gaaagccgat gaagcccggt 420 atcccgtagg tgaaagaaaa ggattggcct gtacccgcaa ggagaaaaat gggtcaacat 480 aacccctggt cgagccaatt ctatgggcat gccatttggt tggagaaact ccccttaa 538
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2029 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...2029
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:783

cgggtaccgc	caagtattcg	tggaagtcga	tgttgaaaat	acggcccttt	tgatgtttgg	60
aatactaact	cgcggcgtgc	aaggacagtg	tatggtggta	gtttgactgg	ggtggtcgcc	120
			ccctcaggcc			180
gtgtaatggc	acaaggtgct	tgactgggag	acaaacaagt	cgcacaggta	ggaaactaga	240
gcatatgatc	cggtggttcc	gcatggaagg	gccatcgctc	aaaggattaa	aggtactccg	300
gggataacag	gttgatcact	cccaagagct	catatcgacg	gagggtttgg	cacctcgatg	360
tcggctcgtc	acatcctggg	gctggagaag	gtccaagggt	tgggctgttc	gcccattaaa	420
gtggcacgcg	agctgggttc	aaacgtcgtg	agacagttcg	gtctctatct	gttgtgggcg	480
caggaaattt	cgagggtctg	acactagtac	gagaggaccg	tgttggacag	acccctggtt	540
accggttgta	ccgccaggtg	caccgccggg	tatccacgtc	tggtaaggta	agtgctgaaa	600
gcatctaagc	acgaagccgg	cctcaagata	agatttcata	aatagggtgg	ttaaagacta	660
tgaccttgat	aggctgcagg	tgtatgttgg	taacaattaa	gccgagcagt	actaatagcc	720
cgaaactttt	gtgcacccga	aggatgcggt	ataggttggt	ttgttgccgc	aaagcttgag	780
gaatatttgt	tggcctttcg	atatgtcgat	tgccttttcg	aagtattcag	gtgttataac	840
			agagaagtta			900
ctgcgtcaca	gtgggagagt	aggacgccgc	ctttttaag	aagcgtgaga	gagaggggg	960
gataggatct	ccaccctcct	cccggaaaaa	aaggtgaagg	agagagtctc	gaatccgagg	1020
ctctctcctt	tttattttct	ctctctccaa	aaatcatttt	gcttttctct	ctattccttt	1080
tctccttttc	cttccttcct	ttcctcccc	ttgctgcgcg	ttattctata	acgtgagttc	1140
gatataagtt	tatgcgacta	aatcttaaat	caactcgtga	agaagcccaa	gttcaaagca	1200
atccgaatga	agtttttagc	taaccattta	catccaaaaa	cacgtaggca	agaaaactct	1260
gaagttggct	ctggtctgaa	gcatagaatt	gcatttttag	cactatgggg	aagagctaaa	1320
taatcaaagg	tccgtgaaaa	agtctaatga	caaatctgtg	aaaagcaaat	ggcgattaat	1380
agtttcaatc	aaggcacagt	gggtaatggc	caaaagtgta	ctttgtttt	aagaatcaag	1440
gataagccca	tgatagtctg	tattgccgaa	agcccagtgt	ggggcgtgag	atcgctgctg	1500
tactcggtgc	caccaaagct	ataaaggcta	tatggagggc	aacggttatc	aggtgacatg	1560
gactttcgac	atctctgtgc	cctcaaagaa	cctcacgact	atgcacccga	atggaaggat	1620
ggagtatcag	ttctctaccg	atgataccac	tgcgatttgg	catcaactca	tcgatagcga	1680
			aaggctgtcc			1740
aactgcggtg	atgccggaca	ggaggagagc	tgatccagcg	tigggtattg	cagaaaacgg	1800

```
gctgcacatg tccgtgcggc gactttggat atcttctctt actgaggagt ctatccgtga 1860 agctttgcga ggctgcgcga cagcgaagaa tttcattccc tatatgaggc cgactggctc 1920 gtgccatagg cgactggcta ttgggtatga acgctacgcg ctttataccg cttccgcttc 1980 gggggcaacc cgacaggtac ttttccatcg accgtgtcca gactccgac 2029
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2702 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...2702
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:784

```
tttgcgtcgg tttcgtttgg tttcggccag ttggcggatg gcctgttcgt atgacctccc
                                                                        60
gatttttctg ccagctgaag cacttccatt ttttccggct cttccgttgt atagcagaga
                                                                       120
tacttette ggeegaagae ttegggtgea tagacageeg attgegtgee geecageeeg
                                                                       180
atccagacct ctttgtgagt ctggacggat cgttatccat attgatggac aggatctgcg
                                                                       240
                                                                       300
acttccctta tcggtcagcc cgaggaggtt ctgtatctgg tcgaatttgt tggctacttg
                                                                       360
cgctggtcga gaagaatctt gcaatccgaa ttgttgatga tgcctccttt accaccggcg
                                                                       420
aagagatgat gtcgtccacc tcctgcgtca cccgattgcc tccccgaaat acttgcgcac
                                                                       480
cgttttgtac atatacttca gtagtcggcc atattggccg aggcgatcgc tttccaggct
                                                                       540
tectegacga cagttgtttg egaacgeett tgagtegeet catettattg atgaaageee
catgatgatg atggttacca cggggaaaag ttcccggttt tccttgatgc atcgatttcg
                                                                       600
                                                                       660
aagacgataa accgcttcga caggaggtcg atgttttgtc cgaattgagc aggaagtcga
aacgaccgcc ccggtagtac tggcgggcgt agtcagaaag ttgtcgatat tgaaatcttc
                                                                       720
ccggctgact ttgattcgcg gttttccagt tccggccggt aggtatcgcg catgaattcg
                                                                       780
taaacgtatt gaagctcggc gttatccctc tgtccgaacc gatcaggcgg ataaggccga
                                                                       840
                                                                       900
gacagogotg cogagotogo cogattoggt titogatatt titocototto gottitocag
agcgtcaaaa gcagcgtttt gatactgtct tcttttcgac gtcgaacacc ccgtcatcgg
                                                                       960
                                                                      1020
tataaaaagg attgaacgaa tcggctcctc ttccgtatag gtaaaataga tgccgtcttc
                                                                      1080
acctttcgtt tccggtggat gagcgaacaa agtccctggt aggagttgcc cgtatcgaca
                                                                      1140
gcaacacatg cgttccctgt tcgtaatact gccgtacgag atggttctga aaaacgattt
                                                                      1200
tcccgaaccg gacggtccca ggacaaattt gttgcgttcg tgataatccc gcgtttcatc
                                                                      1260
ggcaagtccg aaatatcgag atggacggtt tgcccgtcag gcggtcggac agtttgatgc
cgaagggtga aagcagctgc ggtagttcgt ctcggccgta aagaagcaga gagccggctc
                                                                      1320
                                                                      1380
gataaggtgt agaatgtttc ttcggaggga aaatcgcccg cattgccggg cagcccgccc
                                                                      1440
aatagagogt agoogtgtoo gtogtattgt gaoggggaog gaotocatoa aggooagogo
                                                                      1500
cgagcctaca tcgtttttga tctgccggag tcttcccggt cgtcgctcca tgccagcaca
ttgaaatgcg cacggatgga gcgagtccct gggagtgcgc aacgttcagg tattcctcga
                                                                      1560
tccactcgga ttgatctgat tggagcgaga gaagcgtgca agtgaaagca tgtttcggcc
                                                                      1620
tgtttctcga agcgcttgag attttcttcg ctgtcgtcga taaagagtac tggttataga
                                                                      1680
                                                                      1740
tatggttaca cgggagcatc agcccgacgg gagcgcaaag ctcagccggc agtcgctgcg
atcggtggag agccgttcgt aacgccgtcc gttgcgacgg cagcaggcag atcgtcccgt
                                                                      1800
atcggacaag gtagcaggca gaggatttga tccccgatcc gcacttcatc ggcgccgagc
                                                                      1860
                                                                      1920
cgaggtette gagegtgeet geegeategt egegtaaega gaggtaaegg tgageaagee
acgcttgtcg tccgtgcctg cgatctcatc cgccgaaaga gtctgaggcg catatagccc
                                                                      1980
```

```
2040
gaatcgttga tgatccgttc gaactgatca cggcctccag aaatttcagg acggcatccc
                                                                      2100
gctcccggac ttccttcgca gaagggttcc gcgacagagc gtcgagaaat cgcttcgttg
                                                                      2160
cgccatggct gtttcgtcgt tttcgtcaga cagaggtaga cggaatggtg caggaaggac
                                                                      2220
gttcgttgaa atgccgttcg taagagcggt cgaggaacga gagatgtcct tttccaactc
                                                                      2280
cggacggtag cttttccgaa taaaccagtc ctgctgtgca ggatgctgta aacgggcaag
                                                                      2340
accttcaccg ccttgtgcca ggcgcatgca tcgccgcgta ttcgggtgag gtcacggtaa
                                                                      2400
agagttcggg cattcaagag agaaagccac ggtgatgtcg gcatctttcg atacgatgca
gcgttctcga tggccagcag cgggaacttc tcttccagtt cgcatttctt cggatatttc
                                                                      2460
                                                                      2520
tcatggcgtc ggttcgtttg tcgttacagc ccggacggaa gaatacggcg gacaggacgg
                                                                      2580
cgagagagca ggtaacgggg atgccggcag cggctccccg tttcatcagc ccgtgttctc
cgtacttgcg gttcatccga acgtttgcca caccacgagg gtggcacccg atacgcccat
                                                                      2640
                                                                      2700
gcccagcaga gatactggtt catgccgcac atgtagcaga tgacgacaag gatcacgtcg
                                                                      2702
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1603 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1603
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:785

```
60
acattttgca ctgcaaagcc cagtttttcc tgagcactca gccagaagga tagtaaccgg
cggagcggag tagcggtatc agcataggat cgtcatacat tttcctcctg cacggctttc
                                                                       120
                                                                       180
tccaatagac atcatcgctg caatcgacct tgagtattag gcttggcact gaccacatcg
                                                                       240
tcgaattgta cagcagaccg gatgcaagca gactatccaa tcggggggta ttctccagag
                                                                       300
gataacatag ctatgcatat aatcaggtcg ggctgactca cccagaacga gcacaccgtg
                                                                       360
tgtggcgctt taggggagac tttggtaacc atatctctct ttgactggag ttaatgcgat
                                                                       420
cgaaaagggc attgatetet ttgcetteca teagetttge gagatgetee ataccaacet
ctcacaaggt gcagctgtcg gtaggagaaa gcatagcctc tatcttcgga gagctgatca
                                                                       480
                                                                       540
agagetttgg atagtgecaa actgetgeat agagtattgg getaagaaac agaageagtg
                                                                       600
aggaaagaga aatttaggtc tgcttgggag tagatgtagt agccgaccag ggttagactc
                                                                       660
acaagccaaa cgatcgcata ccaacctgcg acatgacaat atcgctccaa gagaaagcct
                                                                       720
ctcgccagaa tgcactggcc tcggctatgt agtagcaaga aatgcagtag ctatataggg
                                                                       780
gataaaaaca gtccctagca cctgagcagg tacatctcga ctacgtacat aagcgttgcg
                                                                       840
atcagatcac gggccacata atgcctcgat ataaccgacg gctcgggatg gctcaagtaa
                                                                       900
taaataaacg accaagctcc aaacaatcgg ggcaatcaga attccgcaaa tcgaacctcc
                                                                       960
atattccaag agaccaatac tcggcgatag gttcattgac aataagctgt aaaaaaggcca
                                                                      1020
ggaaaaacag cagatagctg ggctcagcag gcggtggaca taggtgttag aggcattctg
                                                                      1080
ccgaagactc aatccgagtt gcgtaatttt gaaaaaaggt cgatcatagt attttttta
                                                                      1140
ttgctaatga ctttgattta taagtaacat tcgtagacga ggaggctatt ggattgagat
                                                                      1200
tgtataccgt ttagaggatc atagtagaag tatgtatgtc caaaggtgtc ggaatgtgtt
                                                                      1260
ctttgaagat gttcaactga aacgcacaaa gatatgtaaa aatattgctg catagatgaa
                                                                      1320
attaaccaat agactcaggg gacaaccgcc tcaaaatgct cccgtttaag tttgattgta
gtgtgtgttt ttgatatgcg aggggaatag tcttttgaga gagagcaaat actgttgatt
                                                                      1380
cgttcgatct catggaaatg tcgttcctgt catcactcat tecgttcagt cttcgtgact
                                                                      1440
```

atacagtgta	aaaaatttaa	taaggtttgC	ceaeaeeaee	tgtgtcggtt	ttcagcggag		1500
acacagogoa	ggaagcccgg	caabboooga	gagtaaagcc	teacetetee	ttcctttctg	٠.	1560
gacticggga	arggeerggg	Caacggcgca	agentages	000			1603
gccgatgaca	acgatgtgcg	tegggeeega	agaatacgtc	cgc			1003

- (2) INFORMATION FOR SEQ ID NO:786
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 762 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...762
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:786

60 aaatatgaag ttagcatcgc caactttctc ggaagtaagc catagcactc ctgtagatga agtcaaatcc tcgattatct atccactggg aaaaatcttc cggaagcact gctggagtta 120 ttcataaaat tctacaagaa ggtatcttac gaagcctaat tctcccatgc tcaacgagga 180 atattatatt ccggcttggc tttcttgatg aagtcgccaa aggtgtcctt tgcagaacga 240 : atacgctgaa agagcgatac gagctgatgc tgcgcaatcg aatcggcaca aaggcgagga 300 ctttatctac gaacagacca atggcagttt acatcgcctc agcgcagatt tacgctcaac 360 420 accatactog tottttatga geogggatge caacatgtte egagetgatt egecaactge atcaggatga ttggctgcgt atttggtaga atccaaacaa ctaagtattt tattcatata 480 tccggataat ataaaaatgc atgggtggcc ggtttgtccg attttcccga tttcgtggag 540. taggaatcaa tagcgatagc agtatcacag atcgacaact gtatgataca aagcctcacc 600 66Q aacgatctat ctgcttgata atcacggata tgtaatttaa aagatgtaca aataggagtt 720 ataaaagagt atctgaaaga gaaaaagaat actctctgct tacgaagtat ttatgcatta 762 cagggaaaaa ataccgagaa tcttctttgc agctctgcag at

- (2) INFORMATION FOR SEQ ID NO:787
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 402 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature

### (B) LOCATION 1...402

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:787

cggcacaccg	222000000	gccgggtcgt	ccgcgcaaaa	acgccgaggg	gaagctcccg	60
aaagcgaaga	aataacaacc	actectacea	agregaacae	pappaapete	aggccaaacg	120
aaagcgaaga	Cgccgcagcc	geeeeegeeg	apactagaa	929922922	ogaggatoto	180
caagcgtggc	cgccctcgca	aagcggcgaa	gagatagtgg	aagagacccg	Sease tacca	240
cagcagctcg	tggctcggct	gctgcagagg	agacaaacgc	aacggagaag	gagagegeeg	300
ggcggagccg	gcggcgaaaa	cgtccaccgc	atcccctgcc	aaagcccctg	ccaagccctt	
cccgtccgg	cggagaccac	cccgcgcgtg	gcaccgtctc	cccttccacg	acgcccgtga	360
gcgagccggc	caaggacgat	gccaagcccg	agcgcccgct	cc		402

### (2) INFORMATION FOR SEQ ID NO:788

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 639 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...639
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:788

gggccttaat	agtccggcac	caataccgag	aagtgagata	tgcaagģagg	aagaaattag	6Q
agatatectt	gactcctgtc	aagtgatccg	agggcttcca	tatcctttgg	catactgtga	120
gaggaaagtg	aaaagcgcac	ttccgtacaa	tgtttgccga	tctcatagcc	ggccttcgtg	180
aagagttcga	tcttgttaca	cttttgttcc	acttgttggc	tgttgtgtag	'gtcagaccga	240
agtettacge	aaaccgttgt	cccaactcca	tttatctttc	aggtagttgg	catcatgttc	300
aaatagaggt	tacctgccac	cgtgttttct	ccaccggcag	cccgttggtc	agagaagtct	360
gagaggcatt	tagtccggtc	acacctttta	tatccagtcc	tttttgggag	tgtcagatgc	420
agtotttoct	tottetecet	tecaagegte	aacagcaagc	cacccattgc	cagaaaaaca	480
atcagtccgt	tcatctggta	ttttcttctt	tttttaaagt	gaaaacaaga	aagccgcaca	540
gaatcatcga	tecttecace	gcttgaaaaa	aggtgggccc	aataggatcg	aacctatgac	600
		ctctaaacca		20 0	•	639
CCCCECCE	5466546456	00000000	88		•	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 831 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...831
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:789

```
cccctcgcat catacgagtc aagaaaaact ttttacacaa cacctgatga tatgcccacc
                                                                        60
ggggaaaccc acaagtotoc coettettee tegeateggg actgteegat geegaagtet
                                                                       120
tacatagoog agotaccoac ggotogacga actgactoco ogogagogog aatogototg
                                                                       180
gagcaagttt ttcgagagtt caaagatccc atcatcatca tcctgctcgt ggccatggtg
                                                                       240
                                                                       300
ctttctttgc cgtggcttgc tatcactact tcacgggcgg agagggcngt ctcctctttc
                                                                       360
tggagccgac aggggtgctg ctcgctgtcg tattggccac ggggtagcct ttttcttcga
gatgaaatcc gagaaagagt tcgagatcct gatcaggtca atgaagacat attatataag
                                                                       420
                                                                       480
gtatatcgca acggcatgat cgcagggtgc tcaaaaaaaga aatcgtcgta ggcgacctgg
togttotgga acgggagago aaattooggo ogacggooga otoatogaag coatotogoa
                                                                       540
cagatogacg aatocagoot gaogggogaa coogttgtaa acaaaaccot gaooggcagg
                                                                       600
acttcgacgc ggaagccacc tacccctccg attacattgc cgaggcacca ccattctgga
                                                                       660
cggccactgc actttcaggg tggaaaggtg ggcgacgcca cggaatacgg acgggtattc
                                                                       720
                                                                       780
gagggtgccc gaccaacaac agcgtacaga cgcccctgaa cagacagctc gaccatctgg
                                                                       831
ccggctgatc acgaacgtca gctatagcat agcagccttg gtactcatcg g
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 531 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...531
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:790

totoggo aaacogcaaa cagagaagag 60	tattctcggc	ttgatggtac	otoottatca	gaccastsca
acgcaca ggtggtgacc ggtgtgtgca 120	cgtacgcaca	ottaagcggg	tactacatac	ggccgacacg
ttccagt ctggtaacct ttgcgcatct 180	gtgttccagt	Appointete	ataaaaaaaa	ttagccacga
tatogoo cotatgacaa agooggttog 240	cectatcecc	ttatctcgaa	gagatratta	gagtgatgag
ttcagcg agtggagggt tcgtctacaa 300	ccattcagcg	ggctacatcg	gagaccacca	tacquataca
tgaactg aaaactttgg cgaatcaaat 360	taatgaactg	atttectcta	ctacccettc	tatagacaca
agagata actaacaaaa caatataaga 420	aggagagata	cccgaagtgt	atatttgcac	tasagtetet
agagact gaacaagcat ggctttcggt 480	gtaagagact	acctctaacc	gaacatatca	gcaatgaaaa
ggccgtc gccgtgcaaa g 531	attggccgtc	gccgtcgtgt	acegcaaate	ctcatataac
tategee cetatgacaa ageeggtteg 240 tteageg agtggagggt tegtetacaa 300 tgaaetg aaaaetttgg egaateaaat 360 agagata aetaacaaaa caatataaga 420 agagaet gaacaageat ggettteggt 480	cgctatcgcc ccattcagcg taatgaactg aggagagata gtaagagact	ttatctcgaa ggctacatcg atttgctcta cccgaagtgt acctctaacc	gagatcatta ggaatggata ctacccgttc atatttgcac gaacatatca	gagtgatgag tacggataca tgtcatggga taaagtctct gcaatgaaaa

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 570 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...570
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:791

atccccgaca	ttttttgcag	ataggacttt	gaaagtaagg	cctctttcta	atgaaaaacc	60
			atatgatgaa			120
			tcgtagtgat			180
gcgaaaggat	agctccgacg	gtgccgaccg	gctggtgacg	tatctgttgg	tttgcgcttt	240
ggagcggtcg	tactcatcct	attacggtgg	gtattgatcc	ggcggtacaa	gatggcgagc	300
gtcgccggca	cgatatggaa	cagtatgccc	gatacgatga	aaacccgacg	aatagtcacc	360
taacgctaca	gtgaagtatg	acgaacacgg	caagctctat	ccttacatat	tcaatcccat	420
tcttcgaccg	gtcgtgtggg	gggccgcagg	atacgccctt	tcaagggaat	ggagcccgac	480
ccgacgaaaa	atcggagaaa	gctgggagaa	tttcgcatgt	gagcgaccat	taattcggtg	540
	ggccttcttt					570

- (2) INFORMATION FOR SEQ ID NO:792
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 780 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...780
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:792

cagaagaata	aagggtaagg	gtaggtcaaa	aaaggtatta	tagaatagac	tccaaacgtt	60
ttgcacaaaa	ccgacggagt	tcgttcgttt	gtaattgtca	actccccttt	caagctttcc	120
			tgcgatggct			180
ttggttcaac	atgtctatag	actgatgaat	aatgaagggg	tatgatgggg	ctttttaatc	240
atgaaatctg	caagtttctt	gctataaaga	taagaaaact	tgcagattta	tcaaggtttt	300
cgcaaactaa	tcagggcaac	cgcatcaaat	ctttagtagc	tittgagata	gtctatattc	3 <del>6</del> 0

					gatacaatgg gagctcgaca tccccaatgc	420 480 540
agtatcctcc ctcgaatata cctatctatg	taaaggttac ttgtccgatt cgagtctctc	atccaaatgc aactgacaat cctctaaact	cctcgggtgg actaatccac	taaactgcga gctccacttg ctctgaagct	tccccaatgc tataatactg aattaaactt agtaatgtgg gatgacacct	600 660 720
780						

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1069 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1069
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:793

```
togggoagta tittoagagt gattigtigo tiagigaagg aagatattog aagggoogat
                                                                        60
acgacgagga aaatatgaag agtacggtag tgccctttgt aacggcatca tgctggcggt
                                                                       120
agctgcgggg ttagccgaga gcaggggttg aggcggattt atatcgccaa tcacttcggc
                                                                     - 180
gaccatgcca tatacccgat tgtcgtgcct catttattcg tccgatgacc gaagctgttc
                                                                       240
ggtgcgtacc acgaacggcg tgctcataga agcaccttat actgatatta ctaaacagat
                                                                       300
attgcacgga taggagcttc attgggtata gactatgccg agattggagt tgctacaagg
                                                                       360
ggggggtgtt tcattgtggc gtttgtggta ccgtgtagag cgcagggagg ctttgcacga
                                                                       420
tgccggcatt ccggatgcca cgagtacgaa ggttgagtat acttcattcg gcacgaagtt
                                                                       480
                                                                       540
atcaggogog tgaagaaaat agggotgota toogatacgo atggotatat ogacgaaaat
accggataca tttcgccgat tgcgatgaga tttggcatgc cggtgacacg gctctgtaac
                                                                       600
                                                                       660
ggtagcggac tatttgtcgg gtttggctcc gctgcgtctg tctatggcaa tatagacggg
                                                                       720
caagacattc gtctgcagta tcccgagttc tgcgcttttg tgtggaagag gtgaaagtgt
ttatgacgca tatcggggat accccggtcg gtacgaacct cgtatatatc gaatgctcgt
                                                                       780
gcagacccac ctcgtctttt tgtctgtggg catagtcata ttctcaaagc tattaccgat
                                                                       840
aagaagttgg atatgctgca tctgaatccc ggagctgcag gtagtatggn tttcatgctg
                                                                       900
                                                                       960
ttcgtactct gatgcgcttc gtgaatcgat ggccgagata tacnggattt acaggtgata
gaattggccc gatcgataga tattaaagat gaaacatttc attcttcaaa gcttgcattt
                                                                      1020
                                                                       1069
tetteteeg etggtangeg gatggatate etettegtgg tegtggtgg
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 604 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...604
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:794

```
ataggggaat gtttggcccg acgtatatca gcaggtgggc aatctgctcg agtcgtacgc
                                                                       60
caatcgaacg acagagccat ccctcaagcc atcggccgtg cctcacctac ttcggcgaat
                                                                       120
actggggcaa tcggctcttg gctgcagcgg tgctctgcac gagctgcggt acagtgaggt
                                                                      180
                                                                       240
gtataggact tgggaaaaga ggagaggct gaagactgac cctcaagtac tgccctatgg
catattaaca atagaatcat ggtagccagt atagataaag aagccgttgc cggctggagg
                                                                       300
cagagatatt ccccggcacg atccacctga tcgacaaacc ccagccatcc ccgaagccat
                                                                      360
aaggetgeta teggeeagte geaegategg etegaeaegg agaeeegeee ttetttegte
                                                                       420
cgtggcgccc gtccgtccgt actctgatgc agatgtccac agaaacggac tgcttcctct
                                                                       480
tccgactcaa atgatagata taccggagga actgcaacag ctactggaga atcccggcaa
                                                                       540
ctcaaggtag gactgagcct gagcgatgac atgacggtga tcagacgggc aaaccgatcg
                                                                      600
aacc
                                                                       604
```

- (2) INFORMATION FOR SEQ ID NO:795
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1162 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...1162
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:795

cgagacttcc atto	cccccg atttatatgg	ataagaagaa	cgccattgtt	attccgatga	60
tacagtctac atto	caaagcc nggacaaaat	actccgagga	cgtcttttca	ctgcaactca	120
agatatgggt gagt	acacca tattcaacat	tccggcgact	tactatgtga	gtgaagagga	180
ggacaaatcc gccg	gacccat accgattcgt	caaggggatc	ggacagcaaa	gcctgccgct	240
tctccttcat gccg	gagacca toggtttcto	caaccaccaa	agagcaaaaa	tgaatacctg	300
tacatactga ttac	actttt actctccggc	tttttttccg	gtgtgagatt	gctttccttt	360
cttcggacaa actg	cgtctt gagttggaca	ggatagaggc	gatctcacag	gcagagcgtt	420
aaacttgctg tatc	gacatc cgaccaactg	gtgactactc	tccttgtggg	taataatatc	480
gttttggtag ctat	ggtctg ctgatggcgg	gattgctggc	cgcacctttg	gcgcaatggt	540
tgataacgat gcta	itgatog togttotoca	atctgtctta	tccactatat	catactgttt	600
	acccaa agccattttc				660
tcgccctccc tatc	gtagcg atctatatct	gctttatcct	ctgtctaaac	tcttcaccgg	720

		Lataataa2C	aagaattatg	tecctacaac	agtagggttg	780
tttatctcgc	tctttattcg	telggeggae	aagatatato	CGGAGAAAAC	paaagaacga	840
gggccgtaga	tctcgatcat	tatttggcag	aaaacacgcc	thteesetat	gaaagaacga	900
		+cotccadaa	LECELLERAL		~~~66~6	960
	L	tasaataata	<b>VALEURARUU</b>	gcaaacggac	4006	1020
_		CCGGTTTTTC	Cadeallall	acctacagac		
		++coaocoaa	atettte	ggcaagactg	Bearmer	1080
tgacgtagtg	galalaccea	ccceasaac	atotatocca	ataaactatg	cgactactca	1140
tcaatactac	tgtattcgta	CCCggaaagc	ucgeusges.		J	1162
tgcagcgcaa	gaaaagcatt	gc				

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4479 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...4479
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:796

```
cagcagatcg gactgaagac caatctgctt tattggggta cgacgactcc aatgcaggat
                                                                        60
tggagtttcg catgggaaag aagtggacac tcgatgttcg ggaggttaca acccttttac
                                                                       120
attcagccac catcgcaaac tcaagcatgg ctcgtggctc cggagcttcg ctattggacg
                                                                       180
tgcgaagett teteegecae ttetteggge tteaeggeat eggaggtgag tacaatgtaa
                                                                       240
atgattcgac atccccatcg gccggctcaa aaagctcaac aactaccgat acgaggatac
                                                                       300
gccatcggtg caggtctgac ctatggctat cagtggctgc tggcaaaaga tggaacttgg
                                                                       360
aggcatcgat cagcggagga ttcgtccact tcattatgac aaattcgaat gtgccaagtg
                                                                       420
                                                                       480
cggcaaaaag atcgcggaag gaagaacgac tacttcggtg tgacgaaagc cacactttcg
ctcatataca cattaagtaa taccttattt atacagacaa gctatatgaa acagagtcgt
                                                                       540
atatcatcct gtcgtttctc ttcggaatgt ctacgcttgc cgtgacagcc agacccatct
                                                                       600
cgggggcatt aaggtgagcg agaagcacgt ggtcaagaaa cgggacatac cgccaacgta
                                                                       660
aagatggacc ttgatcttga cggccaaccg gatatgaaca gcaatctgct gatggtggtt
                                                                       720
accccatta ttogtocaat acatogaacg atcaagtogo totocgocog ttoctoctga
                                                                       780
tgggaacaga cgttatcgca tcatcgaccg tcgtatcgct ctcgataagc acccatctac
                                                                       840
                                                                       900
aatcagcccg acaccaagcc ttctgcgatg gtaaagcgtc gcacggcaag gaacagagca
                                                                       960
tggactattc tgccgctact ccatataggc ctggatgcgc cactcatcaa tgattctatt
ggctgagaac tcgggctgtg cgactgccca ctcggatcag aagaaaccac acttacggac
                                                                      1020
gacgetttgt gecactgtat gaageggaet ateaataega gateattgta eeegagggga
                                                                      1080
                                                                      1140
gctgctgaaa aaacgcgaag agactctctc cgctcactta gcctatcggt agggaaatat
gtggtcttgc ctcagttcga cggcaatccg gccgagtggc acgtatcgac agcaaactga
                                                                      1200
aagaaatcgg aaacgatagc gatatatttt cgaaaagctc tccatggtag gctatgcttc
                                                                      1260
gccggaaggt ggcgagaata caacgcgaag ctctccaagg atagggcgca ttcatttgca
                                                                       1320
agcatctcgt taacaagtac cccatcctaa aaagtcgatt cgaatacgat tgaaagggca
                                                                       1380
ggattgggca ggtctgcgtg cggctgtaac caagagcggg cctcgcaaaa ggatgccata
                                                                       1440
ctggagatca tcgaccaaaa gccggtcggt agcgtacagc cgcactgcga gctatcgatg
                                                                       1500
gcgggtctct ctatgccact tgctctcgga ctattacccc ccgcttcgcc gaagcgagct
                                                                       1560
tacattccta tcgtggtcaa aggatttgag ttggacaaag cacgtgaaat tatcaagcac
                                                                       1620
accepteteg tetgagtetg geagaggttt acgeegtage geagagtate eggaagggag
                                                                       1680
ccacgaacgc tacgaaacgt ggacgatagc agagaaactt teccgaaagc gatagagccg
                                                                       17.40
```

```
1800
acagccaatg cggctataat agacttcgtg ccggcaggta tccgcaggct ctggctcgac
tegaageacg caaagegaac ecaaactatg gatgetgttg ggettggeat atgeetacag
                                                                      1860
cgaaaatggg ctgaagccga gagctatctt actcgcgctg cgcagcaagg cggcccggag
                                                                      1920
cacaacacaa totgaacgaa otgogacgot atatgoaaga aatototaaa tggaaaaaga
                                                                      1980
ttcttagaaa acaatattca cttttaaaaa aaaacgagat gaaaaaaaca aagtttttct
                                                                      2040
tgttgggact tgctgctctg ctatgacagc ttgtaacaaa gacaacgagg cagaacccgt
                                                                      2100
tgtagaacta acgctactgt tagtttcata attaagagcg gtgagagccg cgctgtggcg
                                                                      2160
atgacettae agatgetaag atcacaaage teacegeeat ggtettgeag gteaagttea
                                                                      2220
agaaggtatt aagacagtgg aagaggacgg cggatcctta aagtagaagg aattccgtgt
                                                                      2280
aaatctggag ccaaccgtgt cctgtcgttg tagccaatca caattatgag cttaccggta
                                                                      2340
aaagtttgaa tgggttgagg ccttgacgac ttcttgacag ctgaaaacca aaatgccaaa
                                                                      2400
acttgatcat gacaggtaag tcagcagctt ttacaatcaa accgggctcc accactatgg
                                                                      2460
ctatcctggt gggactgcat ccgacaacct tgtttctgcg gaactcctct tgccgttact
                                                                      2520
cgcgtgcatg ccggtatctc attcgcagag tagaggtaaa tatggctaca cagtatcaaa
                                                                      2580
actactattc ttttaaacag ctgacgctaa aatcgcagcc cttgtcgcaa agaaagattc
                                                                      2640
taagatttcg gcaattcttt ggtctcaaac actaatgcat atttgtatgg agtccaacgc
                                                                      2700
ctgccggtct ttacactccg gatgctgcag gagaaacata cgaatggagg cgtctttgaa
                                                                      2760
tacgaattat gctgtaggtg ccggcttcta tgtctggaaa gtaaatatga tgcaagcaac
                                                                      2820
gagettegte egacgateet tttatetatg gaaagetget egataaggae ggeaaceete
                                                                      2880
tcacggaacc accttgacgg atgctataaa tgccggattc tgcgacggag atggcacgac
                                                                      2940
tactatccgg tattggtgaa ctatgatggc aatggctaca tctattcagt gctattaccc
                                                                      3000
aaggacaaaa caaaatcgtt cgcaacaacc actacaagtt tcgctgaaca tcaccggccc
                                                                      3060
cggtacgaat actcctgaaa atcctcaccg gtacaagcca acctgaatgt tacttgccaa
                                                                      3120
gttacacctt gggttgtgtt aatcaggctg ctacttggta atcgacccgt caaacgacta
                                                                      3180
aaaaatttca tagtttgtct atatcggaat acagggagcg gggttcgctc cactcctgta
                                                                      3240
ttcattctct ccaaatcaaa tagggaaatc ccaatcacca atcaagaatt attgttatga
                                                                      3300
acgacgctaa gaaatatatc gtatcggtgc tgtcttactc gtggccggaa tgtttggcgg
                                                                      3360
atgtatcaaa gaggactatt cgattgtccc cgtccgtttc gcctgaccgt cagggcttgg
                                                                      3420
gatgccgata gcaagatatt accgaaaccg gagccgtgca gcgcgtcgtt attttcgttt
                                                                      3480
cgacgaaacc ggccgccgca tcgaccgact gatgatggac gccgcacagt ggctgcacgc
                                                                      3540
aaaccgatac cattggaata cgacggcccc actacgggtc tttcgtggca tgggccaacc
                                                                      3600
ccgacgatca catgctggaa gaaacaccaa tgtgcaaaac gtcaaagact tattcttcag
                                                                      3660
gctttcctct accgaggtat agcccaatcg cccggagacc tttttccgg tgtactgacc
                                                                      3720
tgccaataga gtacggctct atcgaacagg gtacagacca aactgtcgat atcaccgccg
                                                                      3780
tacggcacag gtacatatca tcatacgcgg ctatcaagag tgctggaagc taatggccc
                                                                      3840
agacaactgc cagactatgc cgacatcctt tgggagaaac tcccgacact tataccggcc
                                                                      3900
tggccgagct catcggcaat ccgtccaata ccgtcccgac ggacagatac aaaacgggga
                                                                      3960
tttcatttcc ccatcttcag agtttatccc acacttgata ctactcctct gcatctcaac
                                                                      4020
tctatgcata cggacaagaa ttgctgaata tcagcacagg ttcggatgag taccattcat
                                                                      4080
accogtoata ggcaaaatgo toaatatota catagactgo gtggagcaaa cotcaatgta
                                                                      4140
ctcgtatccg tcaccccttg ggacgagtgc aacaatatgc agaatactaa tccgacagct
                                                                      4200
attatgaaaa tgaatatttc catcatcctt cgggactact tccacgcctt ctcctgttat
                                                                      4260
tgctttaacg atggggcggt agcatgtacc aaggaagata atcccgatca gccacctcgg
                                                                      4320
acgaagtggc aacagtaaag atgtcgcttg acgatgtcga atgcgaggcg gagacctcta
                                                                      4380
cagtggagaa aatctgatca agaaagtgcg atattcgtct ttcgtgaagg gctaaacggc
                                                                      4440
ctttgggttc tcgacaagca aaactatttg cttcggggc
                                                                      4479
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1772 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1772
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:797

caagtacatt	tttcatcccc	aaatggctna	cttcagcagc	aatgtgatct	caactacagc	60
cocatonogo	tecetcegaa	cgaatggatc	atcgggatga	gtncaacgag	gacttcgatc	120
gggtgaaaac	gctgctgctg	cgtctgacga	tgaggaaccg	cgtattatca	aagacccccc	180
ccccaccete	gtcttgagga	attggccgac	agctctgtga	gggtgatggc	acgtgcgtgg	240
tgcgcacgga	cgacctgtgg	aatgtttact	gggatataaa	cgaacgaatc	tatacgaatt	300
caatogtcag	ggtatagcat	tcccgttccc	gcagcttacg	ataacggatc	cgccgccggg	360
саррарсраа	gagggaaaag	tacggaagct	catcgccgga	gaacgtctcc	accaatacct	420
ccctgtaaga	gttgaagatc	tggatttgga	cacgaatccg	agataacatc	cctgctcgtc	480
tatgacgggc	ggttccaagc	cttggtgtcg	tcgaagattc	gcatgatggt	ctccatggaa	540
togtattgac	tattttggcc	ggaggagaaa	ccatgaagcg	gctgacctga	atctctcata	600
cagctccggc	cggaacatga	tattgcggat	attgtccgca	ataccagccc	catcagcagg	660
ttgttctcgt	ccaggacggg	gaagacttgc	gatggctgat	accgaacacg	tgtacgacat	720
ctcccagagt	catatgggtc	tcaccggttc	gaaatccttt	tctatcaccg	catccaacgt	780
catagogtoa	gcacggcctt	gtctttctga	tgcgtcagca	gctttccttt	ctggccaaac	840
ggagcgaata	gatgctgtgc	ggcatgaaaa	ggcggatagt	gggtacgaac	tegtacteae	900
gagcatgagc	ggaaggaaaa	gattgtatcc	gcggtcagct	cggcgatcag	gaaaatacct	960
gtcagcggcg	cgtgcatgac	gcggccatca	ctccggccat	gccgaggaga	gcaaagtttt	1020
tctgtggcaa	tagacctcga	tgaagggaaa	gaagttcagc	gcataggcaa	agatgaatcg	1080
ctcagtgccc	ccatgaacag	actgggcgcg	aaaagtccgc	cgcagccccg	cccgaattgg	1140
tegctacgga	agcgaacacc	ttcgtgatga	tgataatccg	aggaaaacga	acagcaccca	1200
ataggaattg	gaatacggct	cgaacggctg	ccatccatca	aagagctgta	ctggccgccg	1260
agcagggcgt	tgatgtatcg	tagccctcac	cgtatagcgg	agggaaaagg	aagatcagac	1320
cgcgaggata	aaggccgata	tgaggtagcg	ttggcgatag	tgtggaaagt	tctgagtttg	1380
ctctcgaaga	cgaacatgac	cttggagaag	tagaaagata	cagtccgcag	aatacaccca	1440
gtagcagagc	ataggggatg	cgatccatcg	aaaaggatcg	ttgagcgtaa	agctgaacat	1500
ggctccctgc	cccgtgatat	ataggatacg	gcggcggcac	tgaccgagct	gatcagcagc	1560
ggcagcacga	cgacatggtc	agatccagca	ggaggacttc	gatgacnaat	accaacccgt	1620
gatcggagcc	ttgaagatcc	ccgaaatggc	acctgcggcc	ccacaccnac	gaggagcatc	1680
ancgtcttct	gctccatgcg	ganancenge	ncnagttgga	gccgatggca	ncccccgtna	1740
gtacgatagg	gggattcggt	tccgccgatc	cg			1772

- (2) INFORMATION FOR SEQ ID NO:798
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 595 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...595

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:798

cgcgtaagca	attttctgga	agaggtgact	gcgatgccgt	tcgggcataa	gctatcttca	60
cgcatggggg						120
cttcgagcac	caaacaccct	atgggggatc	gttatgctgg	tcgtttctga	taaaaaataa	180
tgaggcggaa						240
atgaaccatc						300
ccgcaaactc						360
ggcaaccgct	cttatgaagt	agtttacaaa	ttacgctaca	ggctgtgaga	aagctctttg	420
aactcggttg						480
cattcagcaa	gcgatctgcc	caatatggag	gatcccaccc	gtcgtgtcct	cggtatcatc	540
gcctacggtt	gaagccgtag	atgagatcac	aagactaagc	acgtaggttt	ttggc	595

#### (2) INFORMATION FOR SEQ ID NO:799

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1156 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...1156
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:799

```
ggcgattatt tccttcgcga caatttgtca cttggtatct ccgttgcacc ctgcgagtgg
                                                                        60
gatggagaaa caattggacg gccaacgtta agttgtcgtt tgtcttcttt agaatctttg
                                                                       120
tagaggacgt tttttcgcaa ttgcagtttt tcagtacacg tcgcttttct caaccgttga
                                                                       180
                                                                       240
gaaaatcttc gtcttgacga gggcgacgcc gtagatggct gagaggcgat ctcgcaggat
                                                                       300
ggcggatcgt tgccgcgaag gctgacggta agcctgcaat tctcgacaaa atccgcgagc
                                                                       360
ggatggaggc tccggcatct ttcaccagtc gcatcacttc tccagcaaag gatattcgaa
                                                                       420
ggcgatagtc agttcttcat acaggatete ttetteeggt eggetgette gagggetteg
                                                                       480
cgagccgctt cgcgataagc acgataagac cgctcgtgcc cagcttgaca cctccgaagt
                                                                       540
agcgcactac gcgacgaata cctgcgtaag ccccaatgag gtgatctgcc cgaggatggt
ttgccggcag tccccgatgg ctctccgtcg tcattggatc gtgtgcgtcg cctttggctc
                                                                       600
                                                                       660
ccagcttgta tgcccagcat acatggcgtg catcgaatag cggcgacgca gatcggccac
                                                                       720
aagcgacagg gcctcctctt ccgacttaca ggataggcga aagccaggaa gcggctgcgt
                                                                       780
ttctccgtgt actgtcttcc gagggagcac tgatcgtgag gtaggaatct tcggccatgg
ttcaaggaga gcctcatctg taccttcctc ccgggcggca aacttttcgg acagacggag
                                                                       840
aggagcgtac tcatttgttt gatactggcg agcgtctctt cgtcacttcc tttttctgca
                                                                       900
agcgcagggt cagcagaccg tatatggcag taggcaagtc tctatctctc ccgtattgct
                                                                       960
                                                                      1020
ccctgcactc ttggctctaa ctgtacgatg gcagggagca cctgatagta gagtccttga
taaatcatcc tttggggtcc gccatcagtc cgtgagtgta tctcttccat ttgcatgagg
                                                                      1080
                                                                      1140
ctatgcggac gatattgata tgcccctgct cgcgaacgcc cttcggtaag catcatcttc
                                                                      1156
accagetteg geatae
```

#### (2) INFORMATION FOR SEQ ID NO:800

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1076
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:800

attetettet	tetetette	gaatggccag	ggaaagtcag	ncgaaaaagg	aagggacttc	60
actottottot	ttattttcca	gctgcgtatc	gnagggcact	cgcgtcctgc	attcagagct	120
CCEEEACCCE	atacaccact	tcttgtcttt	ocooctoaaa	atagettega	taccgcctgc	180
tgaggttcat	accuactact	aatgaaggga	gaagroortc	cgagcatcac	gaagttggat	240
cagatagtcg	aaaggacccc	hanagaga	tactatccac	atcoatcaga	acgtatgagg	300
gcacgacatt	gcctacctca	tcacgggcga	reteteres	tantonggat	attoatoaac	360
aagagattcg	atcttggaga	taactgacgt	agicicggga	cagccgggac	cacaatactt	420
ggaaccgtat	tggtcactac	ataaccgtca	ggttcaaata	aggaagatag	cacacacac	480
ccatcggctc	cacggagagg	aaagatccgc	tcccccgata	gggattaggt	cagagcaaac	540
gggtgcatcc	acaggcgcag	aaaagactgt	acatcaccac	ctcgctggct	catgccatgg	600
tttcggcctg	cttcaaatac	aaattgttgg	tcagagcagc	cgaaccgaag	ctgctgcaat	
ggacaaaatg	ccttggcctc	cgacaccggc	caaaatatat	ctgttttcat	ttcttattt	660
cctcctactt	caateettat	tccttgcctt	tgcacgtttg	gcagctttgg	cgtcgcgagc	720
atecttttgg	atgcaacgcg	acggggaatg	atgacggata	caccttcata	geegaceec	780
tecegatgat	gctgcatagt	tcgtcatgat	tcttgggtac	cggcaacagc	tcctgatgtg	840
atcagaagtc	tactccgata	cceceacaga	tggcctctac	ttgccgtatg	cagacgaatg	900
atcagagaco	tcatogagat	ppattcattg	tcgagataat	caccgtaatg	tgctattctc	960
ctgaccccgg	tcaagaagac	cottattcco	aatgagtgaa	agtagagtcg	ccgattacag	1020
attgatggta	LLEAGARGE	atnggcagcc	cttnggcatc	otoatagate	caccat	1076
acacagccga	acaageegge	aciiggeagee	cccnggcacc	6-666		

- (2) INFORMATION FOR SEQ ID NO:801
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1015 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1015
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:801 5

```
60
aactggaaaa tgaacaaaac cctccaagag gggcttgcat tggcaaaggg ttggacgcag
                                                                       120
ctttgaaagg gcgtacgatc aactgtgacg tgattatcga accccattca tccatttggc
                                                                       180
aagtattgcg gcagccatcg ataccaccgt atcggagttg cagctgaaaa ctgtgccgat
aaggagtcgg gtgcattacc ggagaggtct ctgctgctat ggtagccagt accggtgctc
                                                                       240
                                                                       300
ggtattgatt ataggacata gcgaacgccg tgcttactat catgaaacat ccccatcctg
atggagaagg tgaagttggc tttgtccaat ggcttgaccc ccatttctgt gttggcgaag
                                                                       360
tcttggaaga gcgcgaagca ggcaagcact tcaggtagtc gctcgtcagg tggaagaagc
                                                                       420
cctgtttact ttggatcaga cgactttgcc aaattgatcc ttgcttacga gcctgtgtgg
                                                                       480
gccatcggta gggtaagacg gctacggcag accaagctca agagatgcat gcacatattg
                                                                       540
                                                                       600
taagagtata googotaaat atggaaaaga ggttgogaac ggttgttoat tototatgga
ggcagttgca atgcagccaa tgccaaagaa ctctttaccg tgcggatgta gatggtgggc
                                                                       660
ttatcggagg ggcttctctc tcggtaacaa attcttgcct atcatcgaag cattctgaga
                                                                       720
ttgcttattg tttcaaccct ttcgggcgag ttttatttca aaaggagaaa cgaacgagat
                                                                       780
gaaacgattt totttttagt otootattgo tttogttggt ttgccattcg tcacggaagc
                                                                       840
                                                                       900
traggtttre arateggete atageaaage eregatrage atttegaage tetragtgeg
gagcacgaag gagaaggcat catcaccatc ttcagcctgc atccgtaaag ctgccgtggg
                                                                       960
                                                                      1015
caagtatccg gacgttggcc nttgatcgan ggcgagagca tatccgttga tccaa
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 577 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...577
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:802

gatccggctg	actatcgccc	gctattatac	gccttcggga	cgtagcatca	gaaaccttat	60
				tcgcttcaaa		120
				tacaagactc		180
gcgcaccgtt	tatggtgggg	aggcattatg	ccggatcttt	tcatcccaac	ggatacggcc	240
ttgttaacaa	gctgcatcgc	gagctgctga	acaagggtat	ctttaatcgg	gctgactcaa	300
atatgtggat	gcacatcgtc	agaagctgcg	ccaacgcttc	cccacagaca	gtcatacgcc	360
acgtttacat	tcccgaagaa	ctgactgaaa	gctgaaagca	tttgccgaag	ctgagaaaat	420
cacatggagc	accgaacttt	ngctcaagcc	gaagagctta	tcaagtgtca	gctccatgcc	480
tatatcgcac	tgatattctg	gggagaacga	cttcttctat	ttcttcaatc	gcatggatag	540
gatatataaa	gcactcgatc	tctcatgatc	cgacgaa			577

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 850 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...850 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:803 cgaagccgtc gtgatgcagg cacagctgga aatggaagcc aagcgtttgc caaggcgaag 60 totatoctcg aaaaatttat tgccaagagt actcctcaca gtattggttg gcacgaggtt 120 tcatcctctt gtccgatatt tataagaaga aggggatacg tttacggcaa ggcagtattt 180 ggaaagcttg gaaaagacta tcctaatcat gaggatgaca ttcacgaaca gatagcccaa 240 cggctgaata atcttctgta cgattcatca ctctgagttg gaaataatga acagatcatg 300 aaatatcaat tatatacggc cgtcataatg gctctctctg tatatccgtt tgcggtcaaa 360 ccccacgaaa tacagaaacc aaacgccccg accgctgcgc agggagctta ctatcgttaa 420 tgaccagact gtggagatgg acatgcggat ccgcttccgg ctgcatacaa ggccatcgaa 480 . cctcgattaa acctttccgt ccggaatata acaagcgtac attcggattt gtccctgaat 540 600 ttcctcttca ggcaggaaca atcttccgaa tatcctgccg acggaaggca tatgaagcac cgggggtacc tgaatatcgg tatcggccat acgctaacca gcgaatggat gccggctatc 660 < gtctgataga tgcagagcag gagagatgaa tcttttcctc tcctatcgtg ggatgaaatt 720 ggctttcaat accgggactt cgacggcgac agaaaggata gacgaaatga tggcaggaat 780 1 ggacacgagc agcgcaggcc ttcctttgtg cttgctaccg gcttggatta ttcaaccatt 840 850. atttcaatac (2) INFORMATION FOR SEQ ID NO:804 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 680 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...680 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:804 60 aggatococo gocatgoggo gatottatoo toggotocta tgggcatoac tttgcatgtg tgactgggta cataaggaac gcaaggaaat tattgacagg ggctgcaaaa aaggctgtgc 120 tecteatacg agategeact gtegecetet tgaaagagae aategeceaa etggaegaat 180 acttctctca caagaggaga ctttcgacat ccccctgctt atggcaggaa cggagtttca 240 gcaaaggtat ggggcgagct gctgaatatc ccctacggca ccacgatctc atacccactc .300 ttgcacgacg aataggaaac cccaaagccg tgagggccgt agccgtgcca acggagccaa 360

tcccatatcc	atcctcgtgc	cgtgccatcg	ggaattggaa	gcgacaatac	gctgacaggt	420
tacggtgggg	gattggacaa	aaggaattcc	tgctttcgtc	atgaaatgag	tctgccggtc	480
taaagccttg	aagcctctcg	aaggctattt	atatttgagt	atatttgcaa	gcataaaaca	540
gttatataaa	aacaaagtag	aatatggatt	tcatctttct	tcaaggccga	ccacaagccg	600
gaggcctgtt	cggaggctca	agccagatga	ttctggtctc	gtgctcatgg	tagtaatctt	660
	atgatcaggc					680

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1089 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1089
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:805

gcaaagtoto caattoggoa toattoatag cotoggoaag ggcatagogt;tottggtact 60: ctcaaaagct ttccagccgc tccagtcttg tttggccttg ctctggctac gatctgacgc 120 atcatagaac gggccgaatt gcctcccaag ggctgaagct gtcaaaatcc atcgccaata 180 taaagtaggc atagaaacga cggaggcaac cagattactt tgcagatccg tetcattata 240 ttcgagggat cgaactggtt gtattcgaag ttcagttcct gatctcgcca aatagctgag 300 gagaaaaata ggaggaattg taaatagggc gacgagaagt aacaagagtt cggccttgta 36Q ttgactttcg tctttcactt cggtaaggtt gaggaaaaag gtgcagtcga tacgctctgc 420 aaaactgaat gtggccgttg tcatcgagtc aggttgagga gatctgagag ctgacgctcc 480 aatgtettga tgteteegea ttggeattae tgeegagaeg ttegetaittg atagttaeet 540 ggcattcaac tcctgactta cagcagagcc gtatagaaaa acaggcagtc cacaggcccc 600 accacaatet cetteteate ceaateegat tatatageea caatatette ggecaceteg 660 accttgcttt tgagcggata gtccgaggtc ggccttcact gtcgaatatg gtgatcttat 72D 780 tegtacetae tecaateegg etecegeate ggaaagegaa tteagtaeta tegcateeaa 840 gtgctggctt tcatcttgcg catagcctct tgctcccac tgtccgtctc caagcaaaac 900 ccaccaaccg ctgtcctgca cgtttgagtg ctccgagcgt agcgctatat ccggattagc 960 agtcaagcga agatcgaagt cgcccttggt cctcgtttca tctttttctc tgcctgctct gccggacgat agtcagccac gctgcggaca agacggttat gtcggccttt tcaaaaggtt 1020 teegacaggt tegageatet etaeggeact tteeacateg ataeggteta teeettegea 1080 1089 gttgtctgc

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 569 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...569
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:806

agateceett geat	aacagt tgtttgcttc	gtgcctatct	gtgaatggag	cgcgcaacgg	60
anataccara cttt	ccatac agagaggaaa	gggtagaaca	gcaaaaagca	gggtgaaaaa	120
tagtogtttc atct	ttttgt cttatttttg	tggaaattat	gattgataag	cccttcttt	180
cocttoatop taaa	tgatag tcgtcccata	aagggggga	taagggatga	ctaaataatc	240
tttgcatcac ggtc	tccata tctttccaaa	ctaaaggcaa	tggaatttta	ttgcctttct	300
treattett getg	ttttta gtgttatgat	. tatagcttcc	tgcaaggaaa	cacattttt	360
octtttcaca aggc	tgataa gtcttgattt	tttgttttag	aaatttattt	cttcttggat	420
tttactcatt agca	ttttat gtactctgtg	ataccacttt	atateggtet	gaatetetge	480
ctgtgtggat ccag	aaaggt ctgattttct	. atataatcgt	cccttaaaaa	acccgaatta	540
gccgagatgc catg	ggaata atggatatc				569

- (2) INFORMATION FOR SEQ ID NO:807
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 528 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...528
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:807

cggcgatctc	gccggtttgt	gtcaggtcga	gcctgcctgt	ggcaacggta	tacgcgtatt	60
ctccgtaacg	cecttcataa	agagcaggat	ggccaaaaca	gtcctatctc	tatggcaacg	120
gtcaagtcga	ggatgacggt	aagcaagaag	taaccagcat	gacgaggcta	rcgcrgcgag	180
ggccgcgacc	gatattgcca	ccgaacgcca	tccgctcata	ttgtaggata	ctatgatcag	240
tactcggcca	aacaagccat	cgggatgtat	gccgtcagag	gcccgaggaa	cagcggatca	300
gcagtaacac	gaaggcgtgt	atgatccctg	caatgggaga	gcgccgccgt	tgttgatgtt	360 420
ggtcatcgta	cgcgctatgg	ctccggtgac	ggaataccac	cgaagaacgg	aaccactata	420
ttggccgcac	cctgagcgat	agctcggtat	tgctgttgtg	ctttttcccc	tatcacacca	528
tcgggctacg	ttggctgaca	agcagagatt	cgatagcttc	caacaggg		320

- (2) INFORMATION FOR SEQ ID NO:808
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...653
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:808

tccgtgtcga tgcgatc	cat tcgaattttg	gccggagtaa	cctctccgat	atcttcttca	60
tggcagccat atagttg	ttg atcttggtgc	cacctccatg	agaataatgc	cggcgccgat	120
atcttcaagg aggcctg	aga ggcgtagatg	ttgaggtagt	tggctgtgat	ttcgtccatg	180
cgagccttgg ccaggca	ttg acttcggagg	agcggaactc	tctttcggaa	aatttgtcgg	240
caaagtcatg cggaatg	atc cgttggactt	attgtcgttg	atcatcgaca	cgtgttgagc	300
ttcatgttct ccgcctc	ctg ttctgtcagt	cgcaggctgg	tcaatcgcgt	gtgacgttat	360
aacctcccat cggaagt	acg cgaagcatgg	ccacagcctg	tttttataga	tagataccga	420
tgtacagccg gcaccta	tat tacgtagcaa	catcccaatg	tcaagctcgt	cgtccgaaga	480
gcaatacctg gcttcgc	aaa gcggtgtgac	gaggatgcct	gtcaagcgca	atcccagact	540
tcttctatgg cgatgcg	gat attctgcttt	accgaacggc	gagcagtgtc	aattggaagc	600
cgggcttcaa gcttcat	gac aaaatacttc	cttggccgta	tcttcctgtt	tcc	653

- (2) INFORMATION FOR SEQ ID NO:809
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 626 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...626
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:809

						60
cggtatgggg	caaggtgccc	aaacgtcagg	gtacaggtta	cgctttcgaa	atactgccgg	00
agcacgaccg	aaacaggacg	tcggctttaa	cggacttaga	cggcagagga	aaaagacttc	120
cctacatata	cagagtacat	atcccgctgg.	cctcgatcgt	atcgccggat	gttttgaacc	180
aatggagtac	agatccttca	gtccgatcaa	cgatccggga	ggggataact	tccaccacta	240
tagagggcag	attacgatga	ggcacggaag	tctattctcg	atcgttataa	gcagataacg	300
				cggtacaacg		360

ttccagtacc gattctcgca gttcaaagtc	cgtgtggagc caaagaggta cccgtgcggg	gagttgcgca aattcgagag	acootaaaaa	ggaaacgata	agagaagtat ctatattgtc acctggtata cttcaagacc	420 480 540 600 626
attcgattca	tgcgtggtct	acctga				020

- (2) INFORMATION FOR SEQ ID NO:810
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 595 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...595
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:810

			2820000000	coatcooctt	cgatatgcaa	60
cgtcccttag	caggctgagg	Cacteeggla	aaaccggcac	cgatcggctt	accontanta	120
genagestet	gaageetetg	ccagcccctt	ggcatgitga	gcaaaccgaa	accegemen.	180
+000+0000	cccttatccc	gtatttcgca	tcaactccgc	CCCCBCCCC	6-666-	
	estagogoot	catagacttc	actgccgata	agccccaaac	ggtgggcagc	240
acatetgeee	gatggcgcct		2002000	attecctec	acgtcgccgg	300
catcgtacgc	ctattcccag	CARLLEAGL	aggacgagge	attgccctgc	acttaggtat	360
catttgtgac	cagatgctcc	ggatgcacta	tgcctgtaac	ggcagcccgc	acttaggtat	420
aggategtet	atcetatece	ctcccatcgt	aaggcaccac	LCCCECCIAL	CBCCCBCCB-	
gggaccgccc	anatagtagg	caagacctct	acgggaatcc	cttcggaggg	gaacatggtc	480
cctccacgga	gaacageneg	caagactccc	tacetacac	attopagaga	gcattggcac	540
agattgagta	caacagcggt	egecericea	tggcatacac	accopant co	gcattggcac	595
agctatgcga	ccgaaggtat	aaggatcgga	caaaccgcgg	gaagaaatcg	gggca	

- (2) INFORMATION FOR SEQ ID NO:811
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1492 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1492

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:811

```
tgaaagatto aaaagtgact accgggtoot tttgooggoo agtgaagaaa totatgtoga
                                                                        60
agaagaagcg tttccccttc ttgcgcggta ccgatgcgcg gcatcccgaa tgtccgacac
                                                                       120
ccatattgaa gaacggcgaa cgtgaagaaa ncgaagatgt agtcgtatac gataccagtg
                                                                       180
gcccctatac cgatactcct atgaggtgaa tctgcaccga ggcgtaccga agatacgcga
                                                                       240
gcagtgatag aggatcgggg cgatacggtg cggctcgaag ggctcagctc cgaaacggac
                                                                       300
ggataaggca gtcggacgct tcgctcgaaa agctgcgtta cgacatgtgt gcacgcgtcc
                                                                       360
ccgtgccgcc aaggacggct gtgccacgca gcctactacg cccgtcaggg gatcgtgacg
                                                                       420
ccggagatgg agttcgtggc ctccgcgaaa atcagttgat cgatcaggtc aggacgcgct
                                                                       480
atcgcgctga gagggtgagc cgctcggagc tgttattccg cgcaagatca cgcccgaatt
                                                                       540
gtacgcgacg agattgccgc cggacgggct atcettccgg ccaatateat catccggaaa
                                                                       600
gtgagccgat gatcatcggg cgcaatttcc tcgtcaaatc aatgcgaaca taggcaattc
                                                                       660
gcccatcagc agtaccatcg aggaagggtg gaaaaggccg tctgggccat acgctggggt
                                                                       720
gccgatacgg tcatgatctc tccacggggg atcatatcca tgagacgcgc gagtggatca
                                                                       780
tecgaatteg eeegtgeeca teggeactgt geeetetae eagaegetgg agaggtgeag
                                                                       840
ggcgatgtga cgaagctcaa ctgggagata ttccgcgata cgtcatcgag caggccgagc
                                                                       900
agggtgtgga ctacttcacc atccacgccg gctgcgttgg caccacgtgc ctctgacctt
                                                                       960
gcgccgcctc acggggatcg ctcccgcggt ggttccatca tcgccaactg gtgcaccacc
                                                                      1020
cacaagcgca aagtttcatc tacgagcatt tcgaagagat ctgccaaatc ctcgcacgta
                                                                      1080
cgacgtagcc atateteteg gegatggett gegeceggge tgeateeega egecaacgat
                                                                      1140
gctgcgcaga tagctgagct gaagacgctg ggcgaattac cgagatcgct tggaagtata
                                                                      1200
acgtgcaaac cattatcgaa ggaccggaca cgtgcccatg cacaagatcc gcgagaatat
                                                                      1260
ggagattcaa ctcgagcctg ccatggcgca cccttctaca ctctcggccc gttggtcagc
                                                                      1320
gactggcgtc cggctacgac catatcacat cggctatcgg cgcggcacag atggatggtt
                                                                      1380
cggcacagcc atgctctgct atgtgacgca aaaggagcat tgggtctgcc caaccgcgaa
                                                                      1440
gatgtacgtg aaggtgtagt aacctataga tggctgctca tgccggcggg ga
                                                                      1492
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 556 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...556
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:812

```
ggatcagtac cgatgaagaa gagataagtc gacttgagca agaagtcttg ccttttataa
                                                                        60
agagattgag gcccaagcat cgttgctgac cgaagaacca ttcgggcagc ctccgctttg
                                                                       120
gaaacttctt tgtgcgaatc cttacgcagc tcaatatgcc tcatgtccgt tttgtcgttg
                                                                       180
atattegete gacagataeg geceteaegg ageagaeaag gtegttittt tgttttegge
                                                                       240
gaatagcaga tggagccgga gccggtatcg gagattgcct caggaggaga gattctcgcc
                                                                       300
tgatgttgtg tctgaaagct ctcattgcag acaagcgttc tttccggcca tcgttttcga
                                                                       360
tgagatagat accggcgtat cgggtgaagt ggtgaccgta tgggagagat tatggctcat
                                                                       420
atgggacaag gtatgcaagt gtcnccatca cgcatctgcc caaatagcag cccgagggga
                                                                       480
acggcactac ttgtctataa agatgaaaca ggcgaacggg cacgcacctt cattcgtgat
                                                                       540
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 311 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...311
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:813

aagactgcca ctacaatcaa	tcaagaggcc gacttggcta aagcgaagat caagtctata	ttggtgataa tgacattaac	gaagagaatc aatttaggcc aggctttggt	ttttactcgg gaaatacaga	aagcaagcga gtcctcaggc caaaaacaat gagcttgcaa tggggtctta	60 120 180 240 300 311
--------------------------	------------------------------------------------------	--------------------------	----------------------------------------	--------------------------	--------------------------------------------------------------------	---------------------------------------

- (2) INFORMATION FOR SEQ ID NO:814
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 566 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...566
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:814

		accettacan	tacttctacc	gtattcttgg	aagcggattg	60
ggcaaccact	gccttcggat	agegeegeag	Lacticegee	Beares to age	treattatet	120
ataaagcgga	agtgagccaa	agccactttc	ttgccggctt	gcgcatacgc	tccattgtct	
	accataggta	CCGCCCCACC	gatgatcaaa	agctcggcal	CECCCCACC	
Cacagagge	+00222020	aatatottee	gcaatagctt	gaaccttggc	ttcacgcgta	240
gccgtgtact	LCCaaacagg	1	tantantan	a#contraca	tagtcttctc	300
gcgacatctt	ggcgtgattc	tccggattgg	LECTERTE	accegecaca	tagtcttctc	

caaaccgccc aaacggtgct	agaageette	ctatecaaaa	atacccaata	acassataa	360
caaaccgccc aaacggcgcc	ggaagccccc	CCECCEBEE	acacccaaca	gcgaacgcg6	
gtctcttcat ttctgaagta	aggtctccat	ttgcttcgcc	cttatactga	tccacgtagg	420
gaggacggat atcgggatat					480
gatgaaagca ccgttagcag	gatacceete	tcatatgctc	aaagctatct	tacatgcccg	540
aaagcagaag tcgaagcagt			J	0 0	566

- (2) INFORMATION FOR SEQ ID NO:815
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 458 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...458
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:815

ggagaagcct ccc	ccgatgg agttcgagac	aatggttact	tctactacag	atggcgatag	60
	agtactt atgacccttt				120
	aatagcc ccgaactgtg				180
	tttgtct gtcttcgaac				240
tgcccagctg atc	cgcgagg tagtgctcag	gctgatgctg	atcgtcgttt	atctctctat	300
gcctttcgat ggg	tcaagtc tggaagtttt	. catcgccata	tttttgcagc	ctatgccgca	360
tgtatgctct tgc	tgttggc ttatatccgg	cgatcggcaa	ggtcaatctt	cgtcacaatc	420
ggggctttct gac	accggag cgaagcgcaa	ttttctcc		•	458

- (2) INFORMATION FOR SEQ ID NO:816
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1297 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1297
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:816

```
ggcatccgtc ggacgaagaa gccaagtccg tggtcaagaa tacatggttc atctcggtgg
                                                                        60
taatagttgc gagcaaatcg tattttgtct caagcgtatg ccgagccgtg taagaagcat
                                                                       120
gtggacaaca acttcaaatc cgctgccaag gtctgtgtat ccgaatttct tgctgcacgc
                                                                       180
gaaaaactca ttctcttatc aaagaggcca agctgatcgt gtccaacgaa acggatgaga
                                                                       240
tcttgatccg atgacttacc gcggcaagga catcaagaaa gagctaaagc agctcgcaag
                                                                       300
acacagetta geogeattea geagggggeg ageagtetga agattetete gtetatetga
                                                                       360
atctcttgca ggagtcgcag cagttggtga attattggac gatctgatcc acgccacgga
                                                                       420
gaagetgtte gacecegtag ceggategge aeggaegaag aatttteaa etgaeggeeg
                                                                       480
atagetetgt ttttecteae tgtgeatece eetgataaag ggtetteega atacattaaa
                                                                       540
ggatgtaata acggaggatc agggataaat aattgataaa agcttgtgaa gagaaaaaaa
                                                                       600
atgeettact ttgcaacceg attatgaceg etttatgtge tacaagcagt cetaacgaac
                                                                       660
tggaacgata ataaactaat aacgaatagc aatgtcaaag atttgtcaga ttaccggcaa
                                                                       720
aaaggcaatg gttggaacaa cgtttctcac tccaagagaa ggacaaaacg agtattcgat
                                                                       780
gtcacttgtt cagaaagaag ttctattggg tagaacagga ttgctgggtt gtttgaggat
                                                                       840
ateggetgee gggetgege teateaacaa aateggtete gagetgeeat caagegegeg
                                                                       900
gccgagaagg gcttcttaaa cgcataatca aggagaattc tgtcatggca aagaaagtaa
                                                                       960
aaggcaatcg ggtgcaggtt tccttgaatg caccgagcat aaggagagtg gtatgccggg
                                                                      1020
tatttctcgt acatcaccac caagaataga aaaaatacga ctcagcgtct ggaactcaga
                                                                      1080
agtacaaccc catcctgaga cgtatgaccc ttcataagga aatcaaaaat aaagaggaga
                                                                      1140
tcagacaatg gcaaaaaaat cggttgcaac atttaaaaag gtgatggccg tacctactcc
                                                                      1200
aaggtaatca agatggtcaa gtctctaaga cgggtgccta taccttccag gaagaaatgg
                                                                      1260
                                                                      1297
tcccgaacga agcttaaaag acttctttaa gtaaggt
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 532 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION  $1...5\overline{32}$
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:817

	-++-acctcc	ataacaaaa	ctccgttggt	gtctttcacg	tattcagacc	60
gtccatttgc	attggccccg	graacaaaag		anconactta	gagetggaag	120
ccactcctgt	gcttcgtcgt	atttgttgct	ggccagggaa	Raccageres	6464466	180
++	coaccttacc	ttccagatga	gaccgaatac	LLLEBCLLCE	Ccacobasa.	
gactiguate		cataataata	atcaggctgc	tcctcgttgg	tgaatacatc	240
tacgcgtgta	gcgtttatgc	Cattgugues	-1110	agacattacc	gaaagatgat	300
cagcaacgag	tatagaagcc	ttccacaagg	aagttggtct	ggacgctacc	Gaaagaagaa	360
	actoggacto	aatoratoao	aaattttagg	LLLABBLLLB	645665-6	• • •
acacacege	400000000		tagtgcaagt	cttcatcgaa	tacctgcggt	420
tactttctgt	gcctcaccgg	Ctacaacccc	Lagiguage		cotttgaaac	480
gcgcggaacc	cttttgcata	tttagcgcgc	aagtigaigi	CCCggaccca	08000	532
5-5-55-55	casaastta	gaatcatatc	cttgacttcg	ctatgcttgt	cc	332
gcarrgrage	CEREERCECA	8				

# (2) INFORMATION FOR SEQ ID NO:818

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...2065
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:818

```
ggactgactc atcgttatcc gggatcggtg tattgttcct tatcacgggc caaatgttcg
                                                                        60
                                                                       120
atgtactgtc gtcattgtac ttcgccgtcg cttcgcagac agaaagatgc ttcttctcct
                                                                       180
totgagogoa togatogatg cattgacata tagocaatac acogacagto ogcgatgttt
                                                                       240
tgctatcggg aggcgagccc tccttgtcag cgacgaacgc ttggaataca tattgaagcg
                                                                       300
tctgccgaaa tacctcatgt ggagattgtt cgtataggaa gccgtacgcc ggtatccttc
ctcagcgtat aacgcctcaa ttggtggata tgctcaaaaa atacatccgg tgtggctgaa
                                                                       360
                                                                       420
cactcacttc aaccacccga atgaagttac cgagaagcag tagaggcttg tgaaagaatg
gccaatgccg gtattccgtt ggtaaccaaa cggttttatt gcgtggaatc aatgattgta
                                                                       480
cacatgtgat aagagattgg tacatttgct ggtaaagatg cgtgtgcgtc cttactataa
                                                                       540
tatgtatgcg atctttcgct tggaataggt catttccgca cgccggtact aaaggaatcg
                                                                       600
                                                                       660
aaattatcga aaatttgcgc ggacacacct cgggctagct gttcctacct ttgtggtaga
                                                                       720
tgctccgggg ggtggtggta agatactgta atgccgaact atgttgtatc tcagtcccca
cgacatgtgg ttcttgcaat tatgaaggtg ttatcacaac ctatacggag ccggagaatt
                                                                       780
atcagaggag tgtgattgtg aggactgtcg agccggtaag cataaagagg gtgagctgca
                                                                       840
                                                                       900
ctttccggag gtcagcagtt ggctatcgag ccttccgact tactcgcaaa aaacgcaagt
                                                                       960
ttgataagaa ctgattgaat gaaaataagc tcctcccctt tgcaaagcca ttggggagag
                                                                      1020
agtttgctta aagagagaaa agagaaaaaa ttgccttttg tagaaaaaat tatgcagagc
cggagcatac cattttcggg atggagaaga acaccggcaa aacagaaacg ctcaactaat
                                                                      1080
                                                                      1140
tatcaggcga ctcgatgcct atcggcatag ggttgccctt acttctaagg catagatggt
                                                                      1200
gaaaagagtg accaggttac tcagacggcc aagccgaaat agtggtacct aaagggatga
                                                                      1260
tatttgttac ctccgagctg catttctaca aaaagaactg attgcagaga ttattgatgt
cagcgaagat cggatgcgct gggacggctc atcacggcct gctctttgga acccggtaaa
                                                                      1320
                                                                      1380
atttgctctc agggccttcc acgacaggag ggttaagaaa aatgataact acctatcgaa
                                                                      1440
ctccggagtg caaacgacta ttgtagatgg agctctttct ccaagtgtct ggcatctcct
                                                                      1500
gtcgttaccg atgctatgat tttagctacc gagctgcttt gtccatcaat atacctcagt
                                                                      1560
tggtccgtaa aacggctgcg tgtatcaatt gatctcttta cccacagtgg aatccgaatt
                                                                      1620
ggcagagaat tagatcccat cgaacaaggc atatggggga tagacgaatc gggtaacttc
acgacttagg gattcgttcg gcactgctgt tgaatgcatc taacagaatg acctaactcg
                                                                      1680
                                                                      1740
cttcggcaac agaatttatg tgtccggggc cgttatgata acttattgga acagcttcgc
ctctctgatg ataaaatctg tctctcatca gagattttac acgtatgttt gctttgccgg
                                                                      1800
                                                                      1860
aagcagtaga tcgtttctac agagcaaaca tgagatcaaa tctctgtatg gaggtaagct
                                                                      1920
atggcccgtg acaatcaatc cggtagcacc cagcgggtac aaactgaaat cgaagtgctg
                                                                      1980
cgcagagaga tggaaaaagc cctcggtatt ccggtctacg tgtaagaggg ttaaacacgc
                                                                      2040
ttgaatgttg atgaaactac cgggaacagt aaatagcatt agtggctttt ccctatgtaa
                                                                      2065
taaaatgagt tgggccatca ttcat
```

- (2) INFORMATION FOR SEQ ID NO:819
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 564 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...5\overline{64}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:819

gggcattatc attgttgcac atcctattgc taatgtatgc caatcggtt	gatccaattc ggtgcgtcta acaactgctg ggacaaagat tgtaaattgc	ttcaaaaaca cgctgtcgtg atagtcataa atataaaaaa taaaaagcaa	gctcttggcg	cctgaatagc cgcttaattt aactctgaga aatagtcttt tgcgggcaat	ctcgccgaaa gtcaaaatta attagtcctc tttgactctc ttcctgcttc	60 120 180 240 300 360 420 480
ttttttattg agctttgcct gacttgtggc	cttatcagtt	agatttgtgg ttgcagtctt	ccgtgcttgc	tcttgcactc	ttcctgcttc gcctttttct tctttgcgtg	

- (2) INFORMATION FOR SEQ ID NO:820
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 426 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...426
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:820

atgcgtcccg cttattgttt ctacctctct aacatcgacc cggtcggatg cgtgccaaag	tggcagatga gcggctcttt cccgagaaga ggtgatggag	gttggccgct cgcgagtgta atccttcgtc gaggtggagc	tataagtaga gatatgctca tggctatccg	gtaggggttg gtggaggcat tcatattcgt gccctcttgc	tccctccaag gggttcctta caaaactgaa tacgggacag cagatggaaa ccctgctctt ttgtacatag	60 120 180 240 300 360 420 426
agggag				•,		•.

- (2) INFORMATION FOR SEQ ID NO:821
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 582 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...582
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:821

gatggagtcg	gctcaagcca	aactctattg	cgccgaaacg	gctatggatt	gactacgaaa	60
				tccggtagag		120
				gttcaacgct		180
atccaactta	ttaaaaaatc	aagcattaga	ctatgaatat	cgttgtttgt	atcaaacagg	240
tacccatact	accgaaatca	aattggatcc	tgtaaaaggc	acgctcattc	gtgaggtgtg	300
cccagtatca	tgaaccccga	tgacaaggga	gctttggaac	aggtcttcgc	ttcaaggaca	360
cacacaatgc	tcacgtaact	gtgatcacca	tggaccgnca	caggcagaag	ctatcctgcg	420
cgaagcatat	gccatgggtg	cgatcatgcc	atccttgtca	gcgatcgtaa	gttcggtgga	480
gccgacacat	ggccacaagt	tacacactct	cttcaagctt	tgagaaagat	cgaccacgac	540
tgattatcgc	cggcgtcaag	ctattcgacg	gtgatacggt	tc		582

- (2) INFORMATION FOR SEQ ID NO:822
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 549 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...549
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:822

ggacgtattc	cgctcaatga	aacggatcgc	tcgcccaaag	cgagtgtaga	ttttccatgc	60
gtgggactcc						120
caatateeat						180

gagtagcgat gaaagcttcc ttgccgaaag	cgggtaaaag gccagcgagt tcttcctatt	ggctctgctg accgaaggtg	aaaggacttg tgagcggcta ttcatgtact	atgatctgtg atgaagatcc tcggcaacta	atcagagccg tcgatttacc atgcaggaga tcaagatggt tctagccaag aagctcacgg	240 300 360 420 480 540 549
----------------------------------------	----------------------------------------	--------------------------	----------------------------------------	----------------------------------------	----------------------------------------------------------------------------------	-----------------------------------------------

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 524 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...524
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:823

			agaggttcca	gcatcgcgat	accaaggtgg	60
gggcttcctc	ttttcgtgaa	acccaatgtg	ggaggetteta	60000000000	accaaggtgg aagåggtaat	120
	acadetectt	ccggcaatag	aacaagccic	LUKKAABBUB	~~6~00	180
	atantatata	otaccoagtt.	accteceee	Catteres	444444	
gatagagege	tacatataca	gaagttotco	cacataatga	gtttttcgac	ttcgatgcca	240
gtggtcgcat	Cacciaca	gaageegeeg	опспаравто	agceateage	ccaccgattg	300
aatacacgga	gctgtagagg	aaattatat	ggcgagaacc	ababaaaat6	ccaccgattg	360
	+ asctaraca	catatacgag	Cttctcaacg	CLCEBECALC	22249-90	420
	+	tootaticcc	acctectera	agigaacaca	404000	7
accacacea	gagetttatn	cccapcaggt	tcgagcagcc	cggaatgġat	atgaaagaag	480
tgacccctac	gagetttati	ggatggactt	asstasascc	caat		524
otoctttgca	tattcattcg	ggatggattt	gaatgagace		t	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1165 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature

#### (B) LOCATION 1...1165

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:824

```
60
ggaagttggt cagaactcca ctgataatgg agtccatctc tgccaattcg attcgtgttg
gctgtttact gctgcaatag agtcatactg cattttcact ctttataggc actggagttt
                                                                       120
tttccacatg ataccaaggc aagagttgcg ctgtggcgat aaacagtttc ttcttcatgt
                                                                       180
togtaatact tttattgcgt gacacttcat tcattcttaa cttattgctt ctcttctttt
                                                                       240
                                                                       300
ctcccttcgg ggcggctcca cccacgatga gaacgaattc tccccttgga gggtgttttc
gaagtgagcc agtaattccg cgagtgttcc gcggatcacc tctcgtggag tttgctcagc
                                                                       360
tcccggcatg cagcagctgg tcgatcgaga ccaaaagtctc cacaaattgg gtcagagtcc
                                                                       420
tgagcacccg atggggcgac tataaaatat catcgtccgg agctcttcgg ccaattcttt
                                                                       480
cattcgagtt ggcggccttt cttgacaggc agaaaacctt cgaaaacaaa cctgtcggcg
                                                                       540
ggagtccgct tgctaccaaa gccggaatca atgctgtggg tccgggcaac attctaccac
                                                                       600
                                                                       660
tacacccaac toggoacatg ototgacaag caaaaaacgg ggtogotgat coogggagtt
                                                                       720
ccggcgtcgg agatcaaagc tatgcgtcac ctccggatat ccgttcggcc aatgacttgg
ccgtacgatg ttcgtgaatt tatgatggct ctggagcgga cagtgaatgt cgtaatggtg
                                                                       780
                                                                       840
gagcatacac tgctggtacg cgtgtcctct gccaaaatca ggtctgcttc.gcgagtacct
                                                                       900
tcaaggctct caaggtaata tcctccaaat tgccgatagg agcggcacga ctgtcaaacg
                                                                       960
toottocato goaaatoota oggitoagit ottotaogga agaaatooga cactaottoo
gcaaagtcat ttaccaccgg teetetgeet eccattgeat cegetgatge aaatagatea
                                                                      1020
                                                                      1080
tagcttcagc gctgacgaca gcaatccgag atgggcagag atgtctcgca taagcttgca
                                                                      1140
togtottgaa acaactocog totaaagoga aaaaaatoca acgtagaact atottotgca
                                                                      1165
aatcgaagcc tgcaggagag gtctc
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1008 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1008
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:825

```
60
gatctatctt gatgtccaag tggagttctc ccgcgtttgt tggcctgagg atcacctctg
                                                                       120
ggcatatttt tccggcatcg gaatagagtg cttcggaggc tggtcatgca ggtcttcgcc
                                                                       180
gaagttgcgg cgaaactcgt ccactctttt tttcagcttc tctgccggag cttcgttatc
ggcatagagg atattcccac ccgtcgatct ccctccgtaa ggcgaagggc caaccatctg
                                                                       240
                                                                       300
ctattggcgt atcgggatga aagagccgga tggattcggc caaagaatcg atcccgtatc
tatttcagta ccgatacttg tcagtcgatg cggagtacag cgaatatccc ttgggccacc
                                                                       360
                                                                       420
teggacaggg ecgacaggag ateggatatg ceteteega aegtgeaetg geteetaega
                                                                       480
cagggatgcc cagcctgcgc ggagacetet caggtcgate tetacgccgt tecgttegge
                                                                       540
ttcgtccatt gattggcaca taggacggca cgatccgtta tttcgaggat ttgcaggata
                                                                       600
gattcatatt ccgctccagt cgggtagcat ctgccacgat gagggtaaat cgggcttgcc
                                                                       660
gaagagaatg aagtcgcgag cgatctcctc atcctcgagg tagaaaggag agaataggtg
                                                                       720
cccggaagat ccactatett gtatgagage eggeataega gaatgeacet teggetttet
                                                                       780
ctaccgtttt cccggccagt tgcccgtatg ttgtttgagc ccggtcaggg cattgaatac
```

			aggegateg	tassatrata	tretrogoat	840
cgtatcttgc	ctgtattggg	attgccggca	agggcgacgg	cgaageegea	tegteegeat	900
+	acaccagaat	ttatttccgc	TETELECERS	gcaccegeeg	Caggeegaag	
Cgglglllal	gcgccggag.		tanaattaat	ctgaacgtta	ggtcttttac	960
aagtggtagC	actcttttc	atcattcgat	Lgaagiiggi	CCEAACECCA	8800000	1008
	ggatataacg	gcttgatcgc	gtcgcaaggc	gatggccg		1009
ctggatataa	ggatataacg	60106-1-6	0 0 00			

- (2) INFORMATION FOR SEQ ID NO:826
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 499 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...499
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:826

oggestegtt	ctatagrasc	aggtacgacc	atacggctac	ggggatagtt	tggctttgca	60
eggcateget	++++aatcat	togactgacc	tctcgataat	gaggagaagc	catttcatga	120
ccaaattete	teccaccac	ctttcaggag	taagatatac	ggtgaagtat	atggcttctt	180
accgcacata	tecgaacegg	ttacageag	actuacadac	agtgattcta	ccaaagcatc	240
gctcaatgaa	atccaatttg	teachanacac	acceacagae	agogrouptt	ccaaagcatc	300
cattcatata	tttccggctg	tgagtgcaac	acaacaaca	aaggccggcc	agagtcgaag	360
ccggatattg	gagcggattt	tagtagtttt	gcgctccgtt	agaatactga	atataaggat	420
gtttcaagat	ccaagaaacg	atcgtcaagc	ccgacctctt	cgacaagtat	tttgtctgcg	480
attatgctac	gtgtcagggg	attgctgcgt	ggaaggagaa	agcggtgctc	ctctcgaagc	499
gggtgaaagc	gattttgct					499

- (2) INFORMATION FOR SEQ ID NO:827
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 539 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...539
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:827

				tagecanate	agettageea	60
ggcaatgaca	atttgcaaac	gataacagtg	egtegeaata	tggccaaatc	ageteggeea	
tgaataccgc	caagctgaca	gaggtggagt	actctcttat	aacacctttg	acaaaggcac	120
cttggctcca	ttcgacccct	ccgaaacaat	ccagacttag	cattcaaaaa	agattttgtg	180
acceaeccee	ccggagtgat	tttgataatc	agaaagggtt	caaacctgtc	ggtcctgaga	240
atttctttat	pptttcgagc	gtaaaaattc	agttattgct	gcgggagaac	aaattcttgc	300
ctgatcataa	aaggcaaata	tcaaggtagt	aatgcctttt	cttctacaag	atagactttg	360
tocatoagga	CGBCBBGBCC	aagcettace	actcatacec	aatcacttct	ataaggtgac	420
cctaccagga	ctatttaaa	cagatttcc	acaatcgagg	cggctctttc	aggtgctgct	480
gatcaatgat	gractiaaag	cggattttt		agtettete	+ 000000000	539
gcgaacaaca	agctctctcc	gaggagctgc	aaatgtaccc	cgtctttctc	Lgacggaaa	239

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 529 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...529
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:828

gggttcaaag	agatattggt	accggccgat	aatttccggc	aggaggatgc	ggccgcttcg	60
gtattcggct	cgtgccggtc	agaaaggtgg	aggaagcctc	cgccatctgt	tctcgaaagg	120
aagagaatag	aaagaacgga	gaaaacacta	tcaggagaga	gctacaattt	ccaaaaacat	180
acaagtaata	atgaaaagaa	caaactattc	cgtatcggga	tacttgccat	cgttgccctc	240
ttgctacagg	atgcaagggg	agccgatacg	cattttatca	ccgatgcaga	cttcgcaaac	300
aggtgcaaga	agatctgaga	gtaaaacgcg	aagctctatc	cgaggcaatc	tcttcgaagt	360
gctggagcgc	gattcgctcc	gtaccgaaga	gccgaagcac	tggagttcct	gtatgcctac	420
atgacttctg	ccggacatcg	tgactactcg	ggcgacttct	acttgcagaa	tgtacgcgag	480
		atgtcgtggg				529

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 433 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...4\overline{33}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:829

		acttcaccca	gaaactggat	cagcccaatc	cgtaaccttt	60
cggagcgcag	ccgatageee	gcccacca	gactatetca.	ggagaacgag	atcggcatgg aacttcagac	120
gtaggcaaag	gcaaattgga	tgagatacgc	gcccacgcca	6606000000	pacttcagac	180
						240
						2.0
						300
catgcaaaac	gcaggtagaa	Ciggogoago	tataggata	agagtccggg	agaaaagcag	360
atggacccac	ctcgaaaggc	agcgaggcgg	LELLEGERALE	apabaaaa	agaaaagcag agaacttaag	420
ttogagacag	accgccgtat	cgtctttgga	caaatagctc	ggcccaaaga	agaacttaag	433
						422
ggacatagac	aag					

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2096 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...2096
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:830

	taatgagtac ctccatctt tcctgcgagc atagagattg gcccccaca agcgcggcac atagcaaccg tatgccagcc gaagccgagt cagctgggga tgccatggc aatagaccgg gcaaaccggt cagctcgaat ttgaagaccg gcaagccgagt cagctcgaat	aaacgatggt atagtccttt ctacagtcac aaagccata aaatcctgcg aaccggggat agagagcgaa atatgccaaa acaccttca agaccgcaaa cggaggagtt tacaagagtc tacaagagtc gctccgaaga cattcgtaga actacgtaga	cagaggttcg tccagcagct gcagccgtga ccggcctcat tgtggagcgg catatacac gccatatcgct aatgacacac aagagtaagg tggagccggc ggacaccaaa gccttgctgt aagagatagc aaactgttca aagagtaag	ctttactgta ccttgagaagt aatccgtaaa cggagcaaaa gcaaagccaa atcatggcga agaggaactt ccatcagc agaggaactt ccatagcagca agaggaactt ccatagcagca gcaaagcagca tcagctgaa tgtagcagca ccagcttgt gagaattcca gagaattcca cgaaagctcca cgtagagaa	ggatcgatcc cgaggaggac gtgagcatga gcattacagc agagacagta aaacggatcc ggaaagtctc gagagcaaag tcttaggcat tgaagtgaca tgtaccaaga agccataaa agccaagaaa accgaaaata accgaaaata taggtaaagg	aaacggcatt aggttgtc actgcact cttgagcgga gccatcataa atcccaagag acgatcgaga ccaattcgag accctgcaac aagccaagca gcgtaccgat gaaatactga acggcaaca cggtaccgat gaaatactga acggcaaca acggcaaca acggcaaca acggcaaca acggcaaca acatctctca atcatctcca	60 120 180 240 300 360 420 480 540 600 720 780 900 960 1020 1140
totacctact transcratca teacegtate caegeaacte getaacate	gctttcttct atacgcaagg	tgtccttatt	gcaacaaaac	aagaagetea cgtagagaaa tcaccgtatg	ccatagagga cacgcaacto	aaatcttcca gctaacaacc	

```
1380
ccgtgcggtc tcggcagcaa ccgcttcagc agcttcagct tcggtatcag gactgcagcc
                                                                      1440
ttgctcttga tcatcgaagc atcgaaagag aagtcgctcg ttcgggtggc agacagtttt
                                                                      1500
catcattaca agccatgaag cgaacaccac tttgatagag aatttggcag ggtccgtcac
                                                                      1560
ctgaattttc tgacggaaaa gacagtcttc tcgtaccatc tcagatccat ttcgaactgc
ttgtcgtacg gttgacagga gctttgtcag gaatagcctt accgacaagt ttggctccgt
                                                                      1620
cattttatcg aacaggaatt ctgtggatgt agggccatcc tcgggcgatt ttggtcataa
                                                                      1680
                                                                      1740
aggtgccatc cgggtttgat cgtggccgta aacacaatgt tttctcaggc gtgtcgctat
                                                                      1800
cctgaagaga ggttttccaa acgatacatc cttgataatc tgagcagatg ccccgatggg
caacatagag agaacagtag ggctaaagct accgtccatt tgctgtttct gtggttcttg
                                                                      1860
ttgtcattat tatatgttgg attattaaaa ttagtcagct acctatttgg acgtttttt
                                                                      1920
                                                                      1980
gtctttgata ttgtttggtc tgctgcagtg ccttcttcga atgtatcagg cggcgaaaga
gtttgggcaa aggcaactta tattcctgct atctcccgtt tcaggatgac ggaatacgaa
                                                                      2040
tcgcgttccc tgtagggcag acagtccaga tggcggaaag aactaccctg cctcaa
                                                                      2096
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 650 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...650
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:831

tagaggatcc	cctgtagatt	tctcgtcatt	gtatagctgt	ctgaaaggga	taccgctgtc	60
				gcagtttaca		120
				gaaagcttct		180
				aactcatcgc		240
				gcagtcagca		300
				agttaattga		360
tactcaaaaa	taaaatggca	gacattaaag	ctttgctgaa	caactggtta	acttgacagt	420
				atggcattga		480
				tgcagctgaa		540
				ttgcaggtgt		600
		ctgaaagaag				650

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1530 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1530
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:832

```
gttctttcca agaagaatta tcctccaggt cagcatggca ataaccgtct cgtaagacga
                                                                        60
gcgagtatgg cctccagctt cgtgaaaagc aaaaagcaaa tatacttacg gtgtattgga
                                                                       120
gaagcaattc cgtcatttgt tccatcggca cagcgcgcaa agggtgtaac gggtgagttg
                                                                       180
cttattcagt tcttggagca cgtttggata atgtggtgtt ccgtttgggg attgccccga
                                                                       240
cgcgtctgct gcacgtcaat tggtttccca tcgtcatatt accgtagatg gcaggttgtc
                                                                       300
aacatteett ettattetgt taageeeggt caggtgateg gegtegtgag egttetaagt
                                                                       360
ccttagaggt tattgctgat gctttgacag gttcaatcac agcaaatatc cttggatgga
                                                                       420
gtgggatcag tcgtcattgt cggtaagctg ctgcatatgc cggatcgtac ggacatccct
                                                                       480
gaaaatatta ggaacagctg atcgttgaat tgtattcgaa ataatccata gatcccatgc
                                                                        540
aatattagca tttcagaaac ccgaaaatgt attgatgatg gagacgtcga ctcgatcgcc
                                                                        600
aagttcgagt tcaaaccttt ggagcccggt tatggtatac cattggcaat gcgcttcgtc
                                                                        660
gaatactett gtettegett gaaggtttge gattactgea atcaagattg aaggtgtaga
                                                                        720
gcatgaattt gctacattcc gggtgtattg gaggacgtta ctaatattat cctcaatctc
                                                                        780
aaacagttcg ttttaagcag attgttccta atgccgatgt agagaaagct acattgttat
                                                                        840
ctctaattcg gaggtgttcc gtgccggtga tttgaatgca cactttcaaa ctttgaagtg
                                                                        900
ttgaattcga atcttgtcat ttgccacctc gtaagtcggc tacgcttact atggagtttt
                                                                        960
ccataaataa ggggcgtggc atgtgtcggc agaagagaat cgcgcagagc ataatgagct
                                                                       1020
ttccacgatg cgatcgactc aatctatacg cctattcgga atgtcaagta tgcggtagga
                                                                       1080
atttccgcgt agaacagaag actgattacg aaaagctcct gatggaatga ccacagatgg
                                                                       1140
ttcgatccgt cctgtagatg ctcttcgtga agcagccaaa tcttgatatc ccacttctct
                                                                       1200
ctgtttgcag agaataagat agcgaagagt atgtggatat agtcgatact gatgagttcg
                                                                       1260
atgaagatto totgatatgo gtoaactatt gaagtoaaag otttoaggto ttgacotgto
                                                                       1320
 tgtcgtgccc tcaattgtct gaatgcagcc ggagtagata cgttgggcga ttagtgagtc
                                                                       1380
 tgtcacggag cgatctgatg aagattcgca acttcggaaa gagtctttga ctgagcttga
                                                                       1440
 cgaactgctg gcaacgctga atttgtcgtt gggatggata tcagtaagta taaattagat
                                                                       1500
                                                                       1530
 aaagactaag aacgatgagc atataggaaa
```

- (2) INFORMATION FOR SEQ ID NO:833
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 623 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
    - (ix) FEATURE:
      - (A) NAME/KEY: misc_feature
      - (B) LOCATION 1...623
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:833

ggccagttcg	atattgcttc	ggtctgtcat	gctctctgcg	acaagctgac	tatcggcatc	60
			atgctgccaa			120
			tccgtcctct			180
			agaaagccgc			240
agcaagggag	caggtatggc	cgaaagttga	agaagagctg	aacgaagtcc	gagggctatt	300
gtcagtgaag	atcccgatgc	catggaagca	gagttcggcg	actgctcttc	gccgtggtga	360
			atatgctctc			420
cgacagccgt	ttctcctatg	tgagcagcgt	gccaaacagc	agggcaaagc	tctcagagat	480
			atgaggcaaa			540
ttccaagcgg	aaaaagctat	ctttgtaagc	acgatttagc	attattacat	aatgaacgaa	600
gacattaaaa	agaatacctc	ggc				623

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 753 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...753
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:834

agcggggcca	aaccttttct	ccacccttgc	caaaaaccag	cttccctttt	ctaagttttc	60
tattatagca	gaaataaatg	cattattttc	cagctccaag	attattccgg	gtataatggt	120
tgttgctttt	attgttttca	tataagatcg	accactctat	ctgcggataa	tttgctctta	180
gcgtaatctg	taaattgagc	ttacaccaac	cttttatcct	gtaggctgca	atggaggaac	240
aattttgagt	ctgcactcag	gattatattg	attgattgct	ttgcaaagat	tttcgttcca	300
agaacatttg	attgataata	ttctttcttt	gttgttcgtg	aaattgtgcc	gccaagtgaa	360
caattacatc	ttgtcctttt	acaaaatctt	cggagattcc	aagttcgata	aatctccttt	420
gataactttg	actttatctt	cattgtttct	atattgctac	tttcccttgt	caaacaggtt	480
attggtgtgt	tgtttttgac	aataattcaa	cgagtctgtt	tccaagaaaa	cctgttcccc	540
ggttatgcca	attcttatca	tttttatatc	attcataaaa	tatttcttat	tattatcgnt	600
ctctccaaag	agtgtagtag	gcgtacngat	atccatgcgc	angaaagcaa	gtatgggttt	660
				tttcttttt		720
ctgaaattcg	agaaagctct	aaagactacc	tat			753

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1247 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...1\overline{247}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:835

ggctccatca agcggagcac ggcagcaaac gaggcttcta cggctgtaat gattcgctac cgncggcatt accatcacag tatctccatt ctgatcgaat ctatctgctt gcgctccatc ctcccggaaa taccttgcct aatgtcgtat tctatatggt acgccaaata cctccctgcg aggttgaccg ttcgtctctc tatcctgcgc aacggactcc ggagaacttc tcacaccgcg aatccggtca aatacaccgcg	atcgaacgct ccgctgtgac atgtgctata aggaacgaat gacgaatcta aggagggcat tatcgtaacg gaagctcttc tgacagacac ccgcctctc	tcccgatggc gacgaatacc tcgaaaccat gagccgcacg tgcctccgga ttcggacgtt gctccagccg tcaagcaaaa atcctaccca tagaaggcgt aatcgaagac	cattaccttt gcgaaacaaa ccgcatcgaa tgcacgaaaa attgatgtgc tccttttcac atttggacta aggagaagcg acctccttct acaacgccgg ctcaaaaaaag gtatacaccc	ttcgcagtgg acaaaaggta gacgcctgcc gggctttccc ggaatgacca cttatacacc tcatttgaac atgaaattat acatatcgga tatctgctcc cagaagaaat atccagatta	60 120 180 240 300 360 420 480 540 600 720 780 840
aatgtcgtat tctatatggt acgccaaata cctccctgcg aggttgaccg ttcgtctctc tatcctgcgc aacggactcc	aggagggcat tatcgtaacg gaagctcttc tgacagacac cgtcccctct cagacctgca ccccttgggg gctatcggat ccgatggtat cggcgttttg tctgtcatca cttctggatg	gctccagccg tcaagcaaaa atcctaccca tagaaggcgt aatcgaagac cataccattc cgagttatcc gccggacgtt ccataggcta tctattacga gtacgattacga	atttggacta aggagaagcg acctccttct acaacgccgg ctcaaaaaag gtatacaccc gaagaaggct cgttcggctt taccgtcctt attctgcatc taggcatgg	tcatttgaac atgaaattat acatatcgga tatctgctcc cagaagaaat atccagatta tagaagaggt gcggatcgga tctttcatc ggaatcgaac caaataggcc	540 600 660 720 780

- (2) INFORMATION FOR SEQ ID NO:836
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1367 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
    - (ix) FEATURE:
      - (A) NAME/KEY: misc_feature
      - (B) LOCATION 1...1367
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:836

				teattettea	tottttagca	60
CCGGCACCEC	cggtgatgag	aatatgacgt	cggaagttta	Legitettea	tgttttagca aagtgtttt	120
CC888		gaatectoce	agtgagggtg	ctgatgtcga	aagtgttitt	120
gattcagaca	CgCagCCaaa	gaaccccgcc	-6-6-66-6		aagtgttttt atattcatcg	180
astasgogto	ttatccaaga	cggaatatgc	ggccgtctta	CCCCCECCE	atattcatcg	
446446464	•					

```
ctatggcaag ggctgacctg catgctgtat gaccactcat tcgggcaatg gccactgcaa
                                                                       240
agtogaccag gagoatacac ottogttgot aaagtgatac agcoccgtot taacggoagt
                                                                       300
tgtcctatag ccagacggtg tatgaaagca gccaagtccg cagataggta ggagtaccga
                                                                       360
cctgatcgaa gactacgttt aatgtatcgc gtcagctgtc agccgaagca tcgttttcac
                                                                       420
aaaattattg ccgaacgatg atacagccac gatgtgcgca gtatcatgta tcggcagtcg
                                                                       480
gctgccagca agcctgttct ccttttagct tggtacggcc atacgcaccg agaggagctt
                                                                       540
cgggatgtct tccctatagg ggatattagc cgtaccatca aatacatatc cgtagaaata
                                                                       600
tgtatcagca gggcatcata cttcgcagca gccgctgcag atgagccgca gcttggtgat
                                                                       660
tgactttctc ggcagaggct tcatcgcctc agctttgtcc acagctgtat atgcggcaca
                                                                       720
gttgataatg atcccatgct atattcctcc ataaaacgga ggacagcatc tttatctcta
                                                                       780
atatcagttc cgctaagtcg gtgaaaacaa aacggctgtc agccgaagcc aacaccgaag
                                                                       840
ttcactaccc aactgaccat cggctccggt taccagtatt cgttcattcg tataagtctt
                                                                       900
gattgtaggg gaagagattc cggaaatcct cctcgatatc aattccgtcc atgacggatt
                                                                       960
ggcctgatct ttagctgaga gataatgtcc tctgcaggga ttttccactc aatatctaag
                                                                      1020
ttcggatcat ccaggcaatg gctccttcgc tttgtggagc atagtagttg tcgcatttta
                                                                      1080
ctgaaatacg acttcgtcac ttagcacgac aaaaccgtga gcgaatcgcg cgggataaac
                                                                      1140
aactgtctga agttcgtatc ggaaagctcc actgctcata tttgccgaaa gtaggcgatc
                                                                      1200
caaagcgaat atccacggca tagtcatcac acacccacgt actactcgta ccagcttgct
                                                                      1260
ctgggcatga ggagtttctg aaagtgaagc cctcttagta caccatatcg ggatgccgat
                                                                      1320
tcgtgtcttg tacaaaatta atgggcgaat acccgtttct atctctt
                                                                      1367
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 855 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...855
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:837

tcagtccatg	aagaataggc	agcggatcca	ctccgacaaa	cgaacggcat	catcttgtaa	60
gatgggacca	tccacgtagt	cgttcgggtt	cggccgatag	taacgatcag	ctttttctgc	120
tcctcggcac	aagcctccat	cacataggca	gcgtactgat	ataagtaaag	aagcgagtcc	180
cgacatcctg	catatcaata	gcagcacatc	gacgtcggcc	aacattcgag	gagtaggttt	240
				tgacatcccg		300
				aggcctaaga		360
				gctccgtccc		420
				aggcaggagc		480
tctctgcacc	acaactaccc	gtacctcctc	tcttggggtt	gcgaccgaaa	tctcctgctc	540
gaatgagcag	tctgactccc	gacttcctca	ctcctcgacg	aatgcgctcc	cctgcaactt	600
				caggctaatg		660
				tcgatgatct		720
				tttgatggcg		780
				gtgctgcgta		840
tggcagcaag						855

- (2) INFORMATION FOR SEQ ID NO:838
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 687 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...687
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:838

			tanatacast	gataccogto	actatccaaa	60
gaagccaaca	actgttatgc	aagcaattcc	tgaatacgat	gataccages	testancton	120
+	++acctacaa	gtaaactccc	aaacgaaact	LLEBLLLECE	CCacaaca	
250000000	accattaaca	ttaaogtagg	actgttgatg	cagtcgatga	tgaaaaccta	180
gacaagcaaa	gggattaaca	****	atgatactct	togccccgaa	tcggaagaga	240
aacggacgaa	taataggaat	ttttacccca	atgatactct		++cgcaaacc	300
+	++000000ttt	tactctccaa	agcctccgaa	gallitegate	CCCECAGACC	360
aatgaaatat	ccatcgactt	aactgttttc	aaagatttgg	Cigillaale	acceaaaago	_
aatgaaatat	-t-castana	acastetest	acgtgaaaaa	atgacactga	aaaagggaga	420
attgtaattt	atacggcgag	acaaccccac	tobogantos	2222222	ocatoocaaa	480
cttaatgacc	aagccatttt	taaaggcctc	tataaggtaa	aagaataaga	6000660	540
accastsate	coacoatage	agacgttttt	gaagtccaat	Lagalaalig	Caagaagaaa	_ :
gegaataata	-8-80 00	atoacacaoc	tcaacagtag	cgtaatacta	cttttgtgga	600
ttcagtacat	Cgcaaacgac	atgacacage	occasattta	cccacaaata	agggtgattt	660
agaatacccc	ttggactgtt	ctccgatctt	agaaaattta		agggtgattt	687
tatgcacata	cagtcctccg	atgggga				00.

- (2) INFORMATION FOR SEQ ID NO:839
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 789 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...789
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:839

aaccggctgc catccggcgg atcaactcga caaagtcgga tccgattcga gcatgacgac ttccgtttcc ggatctccca tacggcaatt atattctaca cataaggatc tcctcctaca

```
ttcatcagtc ccacgaagat gaatccggat aatcgattcc ttcggctatc agtcccgata
                                                                       180
togtaggoog gataatogot ottocacott cogcatgaat gottoatogg ogaaaggtac
                                                                       240
tggcgaacgc tccccattcc gccggtattg agcccggtat ctccatctcc gattgcttat
                                                                       300
aatctttggc gactggaagt atgtgatagt ctttgccatc ggtgcaacaa atacggagca
                                                                       360
ttctatgcca tcgagaaact cttcgatcac caacgacggc ttgcagcacc gaatttgcca
                                                                       420
ccgagcatct cagccaactc cgtttggctt cttctgcagt cggagcaata atcacccct
                                                                       480
                                                                       540
tgccggcggc aaaccatcgg ctttcagtac ataaggagcc tgcatcgtat ctatgaatgc
ttgcctgcat ctgtttggtc agccgtgaat gtctgataag cggcagtaga atcccgtgtc
                                                                       600
gtttcataaa agacttgctg aaatccttgc ttccttcaac cgtgcaccct tggcatcggg
                                                                       660
ccccacaatg aggagatcgt gcagtggtcg tgatttcgga agtagtccac tatgccacgt
                                                                       720
acaaggggtt cttcagcccc actaccagca ggtcgataga actcgcgctg taccacttcg
                                                                       780
                                                                       789
gcaacggca
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1914 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1914
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:840

```
60
ggcgttttat gaaagagtga tttaatgccg tttggtttat tccggtcgca aaatatgtgc
                                                                       120
agctttttca tggcaaagaa aaaatcatcg aatgttttat ggcttcatag atacagacta
                                                                       180
tatcaattca ggctttcttt ttctcagaag gattcgcccc aaaaaagtta tcgatcggag
                                                                       240
cagtataagc atgaaactcc ggcgaaaaaa ggaaagaggg ggaaaatcgc tcgattggcc
                                                                       300
gagggtttgg cggaaaaagt gcctgtttct ccgtattttt gtcccgtttt gaataaaaat
cacacaaatg atcttatgaa acgaaccctt gttttcttat ttctgctgcc gttttggctc
                                                                       360
                                                                       420
ttcgggccga ggcacagtct gcacccgagc aaccgagacg aaggatttca tcttctcgcc
                                                                       480
ccaaaaggag atggtgtacg tgccatcggc tatccggcag gaatcggatt gccctctctg
gataattata cgtagaaggg gcttcggctt cttttgccgt cggctacgaa cggggcgtaa
                                                                       540
                                                                       600
acaactcgca gaagggcttc tgctatccat ctatgcggaa ttggattggc ggcattcaga
                                                                       660
totgtatotg acaaaagato cotgootttt totgatgtto tgcgcagaat cggtttcgat
                                                                       720
ttttagccgg agcaggcgtg cacaagggct caacccgaat atcgaactct atgcaagagg
                                                                       780
tgcagtaggg gcgagttttt cccggaaaac aacggttcat catcgagaga actaaagggc
                                                                       840
ggattaacgt tagccttagg gtcggactga gttgctcatt gagagacaat ttcccgtctt
tatcgatacc gggacatccg acatcgtgcg cggcggcctt gcttgatgtg gtagcagaag
                                                                       900
                                                                       960
cagcgtagga tttaccggaa ggtatgaagc cctactgacg gtcgtttgtg ctattattct
                                                                      1020
cctctccttg cctctcggtg gcagacggtg gtgcccgaat gggatgaata catagcagag
                                                                      1080
cagatagaac aggtgcactc ggggaggacg agggagccga atttctggaa cggtggatgt
                                                                      1140
gcagaagcag catccgctgg acatcaatac ccttacccgg gaggactgga gcaattcccc
                                                                      1200
tttctcaatg agtttcagat cogcogttto otgotoacog acatgotoat cocgaggggt
                                                                      1260
tcgacagcat ttgggtgctg agtgaattgc cggctgggac agacgtacct gtctgctctt
gtggccgatg ctgaggtgca gaagcggagc gagtcggctg ccgcctcttt tcgcgagatc
                                                                      1320
                                                                      1380
ctgcttatgc ccgtcacgat gtatcggtgc ataccgatgc catcctccag cacaggaggg
                                                                      1440
ctaccgtccg gatagccggc atccgtatcg gggcgatccg tgggtggcgg tttgcgctgg
                                                                      1500
agctacgcta tgggcaatcg tttttcctta gccttactgc gtccaaagac cggggagaac
```

		nagacttcga	cagctattcc	gcccacttct	tcatggaagg atacggctgc	1560
						1620
gaagggggtg	tgcgagccgt	ggcactcgga	cctaceccta	tcctcgggcg	gaaccacgct cgctcttgca	1680
tcgtcaatca	ggcctctttc	atgggaatgg	cttcagcgcg	pppccgctac	cgctcttgca	1740
gcgacgtgcg	tttacctatg	ccgaggacaa	CECCAGOGO	gatcgacgcc	cgctcttgca	1800
		tttaccacac	LEEKCLECAL	~ B ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	0 0 0	1914
cocgaaacgc	tgccacgatg	acaccgaagc	acttncgtct	gctatatgat	BrcB	_

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 661 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...661
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:841

cgatgcgaaa ggttttgccc gtttcgcgat tgactatggc acgaaggagt cgaaattatt 60 gaaggatttg cttactccga tatgctgctc cacgatctgg acgtgaccac tcccctacta 120 tottgtgtta tgagaatgag ottgtocgot cattoatcaa ottotocaga toattgcoga 180 ggtaatcggc cagcattatg ccacttcggg cgatacgctc agtttcttgc cggcagcagc 240 cgacagatga agtccggcat cttatagtcg ggtatggtct cggacacgaa tacttcccga 300 acttttcagc cttcgtatag aaagcctttc gcttatcggg tttttcttat aggcaatgac 360 cagaatcgta gtatcgggga aagtgccata attgcttcga gcaagtcgat attgtccact aactgcgcct cccgaacgac gtcaactgcc tccggcccat catcgggaaa cggcgcgctt 420 480 cgttcgctat tcggctacgg aggttttgtc gccgtagagg ataaccctgt tgaaagtcca 540 ttcatctacc ggcaccacgt gcgtctccag cagagtggcc aactcgtcat atagaagggt 600 tettteggee ggeeageaga tagaagtgge gaagaatgge acttacgtae agaategaca 660 661

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1086 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1086
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:842

```
ggtcagtgca gagaccagtg gtgtccgcgt aggcatatcg ggacattgca cctggagttg
                                                                    60
ctggacaagg atacatccgg ctctcaagta acagcccgat gaaagccatg atatgggctt
                                                                   120
cggactatgc cacattatca ggacgettca gagagaaacg ggcgaaacat tegatteegg
                                                                   180
totocacgtt ctggtatggt aagtgtatoc taccatgagc aatatggact aagcottogc
                                                                    240
attotgacat agaccoctco tacacaatgg gggctatggc togcaaacgc aaaggatcat
                                                                   300
cgaagaactg cgccggcaag gtctatacga cctcaatcgc agctgtccct accccgcccc
                                                                   360
acceaacgea ttgccatagt cteateeggt gegetgeegg ettegaagat tteategeae
                                                                    420
                                                                   480
accttageca tteggeegag etttetgttt etateeegte etetteeaag eegtgatgea
aggagcacaa ccgaagcatc ggtgttggga gctttggagc gcatcgcata tcaccgggat
                                                                   540
ctttcgatgt agtggtcatc attcgcggag gaggagcagt gagcgaacgg cagctttcga
                                                                   600
660
cacgacaggg acgagacggt ggtggactgg tagcttatcg ttcgctcaag acacctacgg
                                                                   720
ctgtggccga ttttctgtaa actgccagcg cgaagagtgg aaattgatcg acgaccttcg
                                                                   780
ctccgtgctg ccgaaggact tcgaatgatg atgatgtact gccacgaacg gctattcagc
                                                                   840
                                                                   900
tategeteeg cacaceggee atactgaaat catetgtteg tgagaacace ateggataaa
gtccgtagaa gatcgcatcc gattagccgc taacagcgga tcgccttcgg acttcagcaa
                                                                   960
ctccaaatag caagccgcag ctgccggcct tgatgaagag cgaactgaaa' caaaatacgg
                                                                  1020 .
gtcaattggt caggtagcag cccgactgcc tttattggtg acagccaatc tgaagaacac
                                                                   1080
                                                                   1086
aatcga
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 696 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...696
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:843

aattgctctc	acgttccttt	tgcatcgact	ctattcgtgt	ttggttcaģt	ègcgaaaacg	·60
				cggccataga		1/20
ctgtcggccg	attctcctgt	acgagccgct	ttttcttata	gaaagcactt	ttgtaggcct	180
ctacttcctg	tcggcgggta	gctcttctcc	ttggagtaat	atggccaagc	tgtcaagtag	240
ctcgactcgg	tcatgtccgc	caaacgggcg	tttacacttg	ttttactttc	ttcgctgatt	300
tggattcgtt	t.tccaaagga	gtcggatctg	ccacttccag	gcttgagcct	ccggcaaccg	360
gtctgttgtc	gtaggtttca	attcttcgga	ttaggctgtg	ccattgaatc	cgtgagaggg	420
ttcgtagggt	tttccatacg	tactgcttta	atgttcactt	ccaccgaaaa	cctcctgtcc	480
ggagagatac	attcggtact	tttccaatac	aacggaaggt	aattatcaga	taatgattcg	540
ttttcaaaag	accaaattaa	agaaaaaata	ttgacagacc	ataatttgaa	ggtgtttgca	·600
gggcaaggca	ttcaaaacaa	gcattctata	aagtttttag	tecetteaat	gaagtccgtc	660

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 951 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...951
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:844

			gatgaatcgg	coortracca	atgcgactcg	60
ggtctttcca	ttcaattcgg	acticgigat	gatgaatcgg	gatgaagetg	ctaatcaccg	120
gtaggtatcc	actgcttcct	atccatcigi	acctctgtcc	tcatttagaa	ccgtatccga	180
cagtattttg	cggattggta	attacgaaac	cctgtcgttt	graaatcac	gtagtcatga	240
atgtgccagc	gaaatatgtt	ggtacgcgaa	tccattgtgc	Pegaaaccabs	tttttacaac	300
cctttagcag	ttggcggact	tccgctaatg	ttttggagaa	agatotocat	cttctctttc	360
cagagagagt	gcgatagcct	gattatcatc	gttatgttcc	catagacaca	ataatcccca	420
tctttggcca	cactgatctt	gaaaatagct	cgacgatcag	atcagatcac	ceettcccet	480
	0000+33000	aaocataacc	gagugugata	B C C B B C C B C	0660000	540
tagatcatgg	atgtctgctc	ggcagctccc	aggcccggcg	ckacacaca	ggcaccggaa ccgttgtcag	600
	~~++a+aaaac	atodatatec	CLECCACEAA	g cgcugucu	000-00	660
	0000000000	ccatagccag	taggttcagg	Laaguccccc		720
	2200000000	racttgatcc	CCaccgagia	aacgaacagg	40046000	780
	assetetata	cotcappate	cagatttatg	CCgaaacecc	C C C C C C C C C C C C C C C C C C C	840
	- aaccaaaata	acccccaaag	aaattttgaa	gattttt		900
natecetaag	ocaatcgtta	cggcgaccaa	gagaatggag	LECCACTOC	ucuco8	951
caagtcatta	agccattgca	tattcatcca	acagettata	gtagtcaata	R	,,,,

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 567 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...567

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:845

gatccccagt	tttcaagacc	aacgttggta	agtatatagc	ggtatttacg	tccttattca	60
tttcgctgac	ttgctcgcgt	actatccggt	acattttcca	ttggcttccg	cctgtttgtt	120
ggccaaagct	tgtgtcatgc	tgagttcaat	ctttggcctt	cttcttgcat	cttcaggatt	180
ttctcctgtt	ccactctgca	gcatcttcgc	tggtgaatgc	attcgtccga	agacggcgtt	240
ggaaacctcc	gcagctttct	gcatggcagt	catcttggta	gccaaggttc	tttgttctgc	300
tcagcttcgg	ccgcaagttg	tttgttcatg	tcccgaaagt	attatattgc	gaggccaggc	360
tgtccatcct	tacgaaagct	ataggcagag	tgcggcagct	tgttctgcct	tatgatttgt	420
tgtcttggct	tttgatgccg	agaacgcggc	atcataatga	agaggatgat	gatggcaacg	480
gccagtacaa	cctcgatgac	ataatggatc	tgtttcattt	gtgaatggga	tatgtttttg	540
-	ttcgagttct				·	567

### (2) INFORMATION FOR SEQ ID NO:846

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 662 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...662
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:846

ttatggttaa ag	gacggcaac	ctttccgcag	aaaaaaacg	caaggcctaa	ttaaccccaa	60
ctaccagaag ag	gggtgtgtc	aaaattcagt	ttcaagcagg	ggccgggatc	atcgtttgta	120
tagaaaaacc go	ctatcaaat	caatagttcc	taaatgtttg	cttagagggg	ggagtttta	180
gtatgagagc tg	gagtcctcc	aatacaagac	ttttgggatt	tgagggggat	cccctgcct	240
acggaagagc tg	gattttgtt	cttccggcgg	aggcgaaaag	ggttcattga	tccatggcct	300
tttcttacgt cg	gagctgacg	tgaggttatc	aatcgcatag	aaatcgaacc	gaaaatcgcc	360
caaatctgaa ac	ccaaaatcc	cccaaaaatg	gtcgagaatc	ttttcgttct	caggcgagat	420
tttttcaact co	ccgaaccaa	ataaaaattt	tctcagacca	cgtttttcag	aactgaaata	480
caccggattt to	cagtacacg	tcaatcattc	ggaagcgaaa	aaggcagtct	gaatgaaaga	540
tgcgccagat tg	gtcaagttc	cggaccctgt	ggcatcggat	ttgtcgttct	ttcgaccgaa	600
tagaaccaac ca	aaccattaa	cggattataa	tccactagag	tagaaaggac	caatcggggt	660
aa						662

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1259 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...1\overline{2}59$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:847

gcaatataac cacggaagac aaatggctcg gtcaggctct ttgtattgct cggctgaagg 60 aggeceatee geagacaatg gtgaaagtga tatecagetg agaatataat egecaatetg 120 cttacccagt atggctatac caagatttca aatgttatga tccgggagta actcctaaaa 180 acattattga tgctttaacg gaggaatctc gttggccaac tatacgggcc acggaagcga 240 aacagttggg gtacgtctca cttcggcacc actcatgtga agcagcttac caacgcaacc 300 360 agctaccgtt tattttcgac gtagcttgtg tgaatggcga tttctgtaca acgtaccatg tttcgcagaa gccctgatgc gtgcacaaaa agtggtaaac cgacaggtac tgttgctatc 420 480 atagogtota ogatoaacca gottgggott ctcctatgog ogggoaggat gagatgaacg aaattotgtg gaaaaacaco cgaacaacat caagogtact ttoggaggtg toaccatgac 540 600 ggtatgtttg ctatggtgga aaagtataaa aaggatggtg agaagatgtc gacacatgga ctgtattcgg cgacccctcg ctgctcgttc gtacactgtc ccgaccaaaa tgcaggttac 660 720 ggctccggct cagattaatt tgacggtgct tcagtcaacg tatcttgcga ttataatggt gctattgcta ccattcagcc aatggaaaga tgttcggttc tgcagttgtc gaaaatggaa 780 cagcacaatc aatctgacag gtctgacaaa tgaaagcacg cttaccctta cagagttggt 840 tacaacaaag agacggttat taagaccatc aacactaatg gtagcctaac ccctaccagc 900 ctgtttccaa cttgactgct acaacgcagg gcagaaagta acgctcaagt gggatgcacc 960 gagcacgaaa accaatgcaa cactaatacc gctcgcagcg tggatggcat acgagaactg 1020 gttcttctgc agtcagcgat gcccccgaac ttcttcgcag cggtcaggcc gagattgtct 1080 tgaagctcac gatgtttgga atgatggatc cggttatcag attctttgga tgcagaccat 1140 gatcaatatg gacaggttat acccagtgat acccatctct ttggccgaac tgtatgtccc 1200 ggccaatctg ttcgctccgt tcgaaatacg gttccggaaa agcagatcct tcttggtcc 1259

- (2) INFORMATION FOR SEQ ID NO:848
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1271 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1271
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:848

```
aaccgataat gatcatccaa aagagcggag aagccaaatc gtcatcaaca cgactatcac
                                                                       120
acggatagca ttcacattcc atctcgttat gcagcaatac cgctacacac gccacacaaa
                                                                       180
acggcatgat ccatgtgcga taaaacttcc gcttcggagc ctccccggac atgtatcgat
                                                                       240
agoctaagtt totototoot totgaotgta acoggoocot goagaatato oggogtogta
                                                                       300
ctgtcttcat tggaagaaaa gtgctctccc gtattgatct ttttatgact tcacgaatca
                                                                       360
                                                                       420
ggccgatact tattacggcg tgttcgctat gcaacgcacc accatcatgt cggacaagta
ggcttcgaat tcctcgatcg tttacaatcc gtatggttct cccgatcgaa atgtgaggct
                                                                       480
aaattgtgca atactcctcc agcaggttat aggcatcctc gtcgatgtgg aagaccttgc
                                                                       540
tcccagattc atcgtgagcg tttttttcat cttgtttttc cgttaataca gattcttctt
                                                                       600
cgggcttaat atcgcgcacc aatagttgca atgatttttg ccgttgaatt cgttctcttc
                                                                       660
tatogtgtag caaagacgaa atgagcgttt ttgatotoat cgcaatgaco ggcotgatta
                                                                       720
aacgcaatcc cactcccgga tggcgttcgc ccgatcccac tctcacatct atcttcaggt
                                                                       780
gttcgaagct tttcctacag ccctgctacc accggcatca tacagttgtc gggtataaag
                                                                       840
accggcttgg agttttccgg gccgaatggc cccatccgct tgggttgtcg agaagtttgt
                                                                       900
aattgacctc ttcgatggat atttcggcat cacatctatt tgtggcacca atagttccgg
                                                                       960
cgatacagcc tcttcggcat gtccgtaatc atctttcgga aggtttccag attctcttct
                                                                      1020
ttgatcgtcg accggaggca aaaggatgcc ctccgaaatt gaccagcaag tccttgcatg
                                                                      1080
ttcgatggct ttgtacacat cgaaccctcc tacggatcga gccgagctga aatgaaatca
                                                                      1140
ccgctcttag tcatcacgat cgtcgggcgc gaataggttc ggtcatcctg ctggccacta
                                                                      1200
                                                                      1260
tgccgataac gcccttgtgc cattcggccg gtagataacg aggatcttct tgtccacatc
ggatagctcg c
                                                                      1271
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 356 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...356
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:849

gctgtccgtt	tccctatcct	ccacgggcgc	atggcttggg	gtggagtatt	tccgagagct	60
tggctcgcag	gcatacggca	cctcttacga	ggagggtacg	gcttcgtaga	taatatcctg	120
tgggcggaag	tagtagtaac	cattgtcctc	agcagggcac	tgatggtctg	acgctcttcg	180
tgcagctttg	ccaaatgaac	tggtctcctt	tcctgatcaa	agacggagtc	tgcctgtaag	240
ccagatgctg	tcggggaaag	tgctgatcgg	taagggaatg	atgctgtcgt	aatgtaagga	300
gaggccatat	ccaccgtata	ggagattttg	gctttgagcg	agtcttttc	agagtg	356

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1642 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1642
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:850

```
tagaggatcc cctggaaaaa attccttttc atttttgacc gcctgtcata ctgatcgcta
                                                                        60
tgccttttta gcaacgtttc cttcacttgg gcaaagaaat tatatctgaa gtgaacagaa
                                                                       120
cagcetttte gtttttaat atagagegag cataateega eeteggeeat tettteagaa
                                                                       180
aaagcgaacc gcaatccaga aataatggaa cgagaatctg aaaaatctca cgccacaaag
                                                                       240
ttttcttttg gtttgaaaat ttttcctttc cgacgcagga aaaaaatatt ttaccgcgac
                                                                       300
tttttgagtc ctcttaagta aggtatttt tttaacatac ttgaccgaat tatgcatcta
                                                                       360
accatagigt agaatcetca teigtaggia attgeacega acaacegati igicagtaca
                                                                       420
ttatgtctga cgaaacgcgt attttgactt caaatgaaag aaagattgaa ccaaaccgta
                                                                       480
cgctattttc gcctatactc ttcgcagtat atgccggcct ggtcatatct ttcactcact
                                                                       540
ccatatcatc aatggcgtga tcatcgtcca ctcccacgta cagtgggggga caacgaaagc
                                                                       600
gatccgcagg acaatccgca ttcggattcg gaattgatct gtacaatcag ctttcggcca
                                                                       660
tattcacgac ttatttggat acgccgccat agacttgaaa gaacctgtga gggttgtcgg
                                                                       720
cgtcgttcct ttctttgcga taatcttact gctctcattt cggagctaac tccttccaat
                                                                       780
catccagggc tectecegta geetgateca ttettacett attteggacg atcatteatt
                                                                       840
cggatggtat tgcgcgcgct tacaatgaga tccgttgcat cgcacttgta gatctgcctt
                                                                       900
tctatgctga tttatcaagg ggatcgaatg tcatccatag ccgtgatgca aggatttca
                                                                       960
teettettaa taeegatett tegtgggata gggagtggga caeaetetee taaeeteaaa
                                                                      1020
aaccgactaa aaggatcgga ataaggatac cgaacagaca ctatatccat atcaagccat
                                                                      1080
caaaccaaaa aataaaatga aacaactaaa cattatcagc ttcatcatgc tttcctattc
                                                                      1140
ttaggaacga gcgcatcggc tcagcaatcg ggcggaccgt tacaggtacc gtagtggaca
                                                                      1200
aaagctcaaa agaacctatc gcatagtaca agtattcgtc aaaaggaacc actctcggaa
                                                                      1260
cttccacgga tgcacggaaa ctactcgatc aagggaatcc cttcgggtaa tcaaactatc
                                                                      1320
gtacccgact catgggttac tccacttgcg aagaaaaagt acatatagaa aaggtggttc
                                                                      1380
cegecacgta gacetetate tgacegaaga gattetetet cenatggggt agtggtatet
                                                                       1440
gccaatagaa acgagacttt ccgccgtcaa caccctcgtt ggtaacggta ctgtcgccgg
                                                                       1500
aacttttcct caaaaccaat ctaccaacct gagtcaggga cttaagttcc agcccggtct
                                                                       1560
 gcgcgtgggg acaactgtca gaactgcggt ttcaaccaag ttcgtatcaa tggactcaag
                                                                       1620
                                                                       1642
 gagcctattc gcaaattctt at
```

- (2) INFORMATION FOR SEQ ID NO:851
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 919 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...919
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:851

```
catcgaagtt ctattttcat caagcgtcct tacatctctg ttgtgggcat attcagaaga
                                                                       60
agattctcgg agaactttcc aaaggtgaac gctccagtat ggctttatag accgcattct
                                                                      120
atttgtgatg cctaatcttc agcagaagcc cgatggagca gaaccgagct tccagatgat
                                                                      180
acagagaaac gctgggaggt attattcgac ggctcataga cttaccatgt gccaaggatg
                                                                      240
aagaagggaa gttacccctg agattattcc ctttgaagaa gatgccaaag ctcgctctat
                                                                      300
atgtggcagg aagagcatgc tcgactatgc gatactgagg ctatgaagta cttgtaggag
                                                                      360
tctattgtaa attagaaatc tacatcatcc gttttgtctc attattcagt tggctcgatg
                                                                      420
ggtatgtggc gaaagtgaaa atccgctata gacctgacat ctgtggagcg agccatcact
                                                                      480
cttaccgagt tttccgccat tcggcacagc aagtacacgc agagatcgca ggtgttcagt
                                                                      540
cactcagcaa cagcaacaac tccttgccga gctaccagca tcttttcaac tgccgaagcc
                                                                      600
ctgagtattg cccaaaaatt ggggatgaaa gaaagagttt taaggatttt ctcagtcgta
                                                                      660
atatoggaca cototttgot aaggaagaca oggactttac cataaactca atatgtaacc
                                                                      720
gagogoactt totgottato agoatttogo caccoottat taaacogaaa gtgtacaaag
                                                                      780
tgcaatagtg tgccattcaa atcaatttta tcaatgagca attatagatt caattagaac
                                                                      840
catacaaagg tgtgcggaca cggcatacct gcccatcgtg cgacgtcctc gatgcttcgc
                                                                      900
tcgctatatt gacacagag
                                                                      919
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 936 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...936
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:852

gaagacgatg	tgacggagga	ggaattgctg	gcctgcgtgc	atcgcctgat	caggatccga	60
cggtagatgg	cttcatcgta	cagctccccc	tcccgaagat	atcgacgagc	agaaaatcat	120
cgaagcagta	gacccgcgca	aggatgtgac	ggatttcatc	ccatcaacgt	aggccgtctg	180
agcatcggtt	tgcccgtttc	gtctcggcca	caccgaaggg	aatagtggaa	ctgcttcgtc	240
gctacatatc	cctaccagag	gcaagcattg	cgtagtattg	ggacgcagca	atatgtaggc	300
aagcccgtat	cgcagcttct	gctccaaaag	ggagagccgg	gcgctgcacc	atcaccatct	360
gccatagccg	tacccctaac	atcaaagagg	tagtctgacg	gccgacatta	ttattgcagc	420
tttggggcag	cccgaattcc	tacagccgat	atggtaaagc	ccggagctgt	agtagtggac	480
gtaggtacca	gcttgtaccg	gactcgacac	gcaaaagcgg	tttccgtctg	acgggcgact	540
caaattcgat	gaagtggccc	ccaagtgctc	gtacatcact	cccgtaccgg	cggagtaggt	600
ccgatgacca	tcgtatcgct	catgtccaat	acccttcggc	aagtaaagga	ttgtaccggt	660
aaaccctcct	tcccttattt	gccaacacct	tatcgaagag	gcccgtcatc	aatatcggtt	720
cgtccggtat	gatgacggcc	tcttttctta	ttgacagtgt	gtcatcatgc	gcaaattgct	780
gcgtgcttgc	ggcattcgtt	tcttagcgcc	ttgnacttta	cgcattctta	cccctaaaa	840
tggggtatgc	caaaaccgaa	ttttgacacg	ggctccctcc	tecgatactt	tcaagaattc	900

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3434 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...3434
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:853

```
60
tgcaccaacg gttcgccttc gttggaaaaa gaccttcgcg atggcttgga tatggaaagg
ctcatgactg gaaagcgtga acagcgtacc tacgaaagtt gtttcatacg gctgagttcg
                                                                       120
                                                                       180
tccacggcat gtagtaagaa cgggctctcc cagatgcccc atacgccatc gaaatcttca
togtgggcat actotgcttg cogaaataac gtttgtagco ggottgtttg acaaaagcat
                                                                       240
cgaagccatt gatccgtttg gtgcaccatg caagaaaatg gattgataac cgatcgcccg
                                                                       300
agagccgtcc ccaatccttc aatctcattg cccgaatagt gagtgtaatg aagtgtgagc
                                                                       360
ggagggaagg caacgagctt aatatggacg gctggcatcg atactcttgc gcccgttggc
                                                                       420
aaaagcctgt tcgaaaaggt acccttttgt gaaatcgagt cgaagcaggg tgtatatcct
                                                                       480
ttgtaatcgg aatgtcttgg ttcagccgtc ctacgtattg gcgagcaaag ctttcgatgt
                                                                       540
tatcaccatc acgttgcgtc cacgcaactg actgaaacga gctgtcgttc cgtcgccaaa
                                                                       600
                                                                       660
tgatgaatgg gattgaatac ttgctccaac tccttttgga ggcataaaaa cgcttttcct
ccaatccctg tttgccaatg gtacgatgat gctgtagggc gtgttcagta ccaaagccct
                                                                       720
                                                                       780
atgttccact ttgtcaccga cagattggca taactcattg tcataggacg ccacgacttg
                                                                       840
gcaaactgcc tnctcgtata ccccatacga taaatgcaat agcggcaacg aggctaccaa
cgtgaactgt ataataatgt aggctgtctt tcgcttcggc atggtgcgta ccggcttgac
                                                                       900
ccgatgatat agccatacca tagcagcaac gggactatag ccagcaggct catataccag
                                                                       960
taattcagga gaagatgcca atcagtcctc cgccctcatg gctgaattca gagaaaaccg
                                                                      1020
tcgaggatgt cgtttcaagg tgtatggata gtaaatacaa tcggccagac ctgccgccgc
                                                                      1080
cccaaagcat ttggcacgaa aaaggtccag tcggtcagga ttcgatagat cgcttggcac
                                                                      1140
gaaacctgaa cggcagaaag ctcaacagaa taaaaaggca ttcaaataca aaacggaagc
                                                                      1200
cgtgtcgaac ctaagccctc ccatcatgca cgccatacct gctcggcagt catgtcggca
                                                                      1260
aaaaagcgat agttaagagg tagaacagtc cacgggcaat accgaaaagg aaataagcca
                                                                      1320
atgcatacga taggcaaaag cccaccagct gttcgttcgt atcgtccgct taaaatattc
                                                                      1380
atatctcttt gtgtgtgttc tattcggatt ggaggcaggg acgagggtaa tgaatgattt
                                                                      1440
                                                                      1500
cggtcacata tccccccaat tgagcctatt catgattcgg tgcacgatgt atcccgttgc
                                                                      1560
accggcattg gatctgatga gtctgctgct gcgcgggatg cggcgtccct ataggccttg
tccgtttgat tcgcttgatc aggttgccaa attcctctgc tgaggatacg gagaagctcc
                                                                      1620
gccgacatct atcaattcac gggcttcctt gaatttctca tatcgtgtcc gaaaataacc
                                                                      1680
ggtataccat agactgcggc ctcgggtgta ttgtgatgcc tttgccgaat cctcctccga
                                                                       1740
                                                                       1800
taaaagctac ttgaccgtag cgataatgga ggataggaga ccgaagctgt ctacaatcag
                                                                       1860
acaatcctgc cggcaatatc gctttccgta gcttccgaaa gtcgtatgaa aggccgtcgt
                                                                       1920
attgcgatat gatctgaagc aaatgttcct tgtcgatttc gtgcggtgcc atatgagttt
                                                                       1980
gatcttggga tttcgattga agtagcgtac gagtatctct cgtcgggagg ccaactgcta
ccgcccacaa tgaccaaacc gtcttccgga cggaagcagc aaaacgctct atcagcggaa
                                                                       2040
                                                                       2100
gcgatttccg agcttcatta cggagatcac ccggtcgaag cgcgtatctc ccgctacgga
                                                                       2160
tacatggcta toccatgctt ttcaagtagc aggcgtgaag cettgtcctg aacaaaatgt
```

```
2220
gtgtaaagca gtgtagcaaa cgtttgtatg ctcctccata ccagcgaaaa acagctgtga
                                                                      2280
cggtcggaag atggatgaaa ccagataggt aggttctgcc tacgctccaa ttctgtcagg
aaacagggcc agaagtcgta tttatgaaaa tagccatctc aggcttgacc agatccagaa
                                                                      2340
acttacgcac teggeaaacg atetgeegge aaatacacga teaegtegge acettegtaa
                                                                      2400
                                                                      2460
tcttacgtac ctcatatccc gaggggctga agaaggtaag cacgatccta agtccggata
ttcgcttcgg atgcgttcta tcatcggtct cccctgctca attcgcccaa agaagctgca
                                                                      2520
tgaaaccata tatagcgccc gcccggcata tgccctcacg cagctgacgc cacaccttcc
                                                                      2580
atcgcccacg aaccatctgc gggctttggg attgaacgga acggcaagtt tgatcagcga
                                                                      2640
agaataacca atccgatcag gctgaaaagg aatcgcatat atttcgaaaa aaattttgct
                                                                      2700
gicagoctaa gacticgatg goacgaogta tgogtocaac ggtocttoac goocgagoac
                                                                      2760
ttccatgatg tcgaagatat gaggtccctt gcttcgccca cgagtgccaa ccgagtggca
                                                                      2820
ttcatgatat tgccgaggtg atgccattgg tctcgatcca attcttcaca gtgggttcgg
                                                                      2880
                                                                      2940
ttgcttcggc tcaaacgatc ggtgagagtc cagcaattcg gctagttcgc ccaactgctt
                                                                      3000
gccgtatctt ctttccagcg ttttttcact gtttttcat cataggatac ggtgcgatga
agaagaatcc ggcttgctcc catagctctc cgataaagtt acacgttcct tgacgaggga
                                                                      3060
gattacatga gctgttttct cgtcggtgcc actactccat tttcgcgaag gatgggacgg
                                                                      3120
aagagttogg ccaactogca ttgtoottac gotggatata ttggtgattg aaccagogto
                                                                      3180
ctttccgtag tcgaacttgg ctccggcctt gctgcatttt tcgatgtcga acagcggatc
                                                                      3240
aattogtoca tgotoatgao atootgatoa ttgoooggat toogoocaga agogogagga
                                                                      3300
agnttaccac tgcttcgggc agataacccg cttcacgata acctttggat atatctcccg
                                                                      3360
                                                                      3420
tttggggate tttecactee aeggaaatae eggaaatnee aaaegatege categegttt
                                                                      3434
gctcagctta cgtt
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 420 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...420
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:854

cctggcgaat	tggtgaatgg	ccgtttcgag	tccggtaaac	atggattcga	gtccgtctgc	60
				atagatcaga		120
				ccctcgtgca		180
				gatcgagacc		240
				cttgatgtat		300
				ttatgtgcag		360
				cagacgatca		
420		J	•			

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 529 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...529
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:855

cctgcaaatc	gcggctctct	atatcaattt	gctcttccgt	caggaaatgc	tcgtacggca gttcgcgtag	60 120
		+ cacaaacaa	CVLAALLEAG	EECCH		180
					acgaacaact agccctcgaa gtagagaaag	240 300
						360
gttgggatct	ctccttgctc	ccgaagagac	gccgcgaagg	tctggcctcg	ctcgtgcggc	420 480
-toottooga	roctcageet	cctgccggai	acagcaacgg	ccuccio	cgacctcggc	529
aaggagtatg	cgccatcaac	cccttcttct	CCgaacagcg	gaagaaaaa		

- (2) INFORMATION FOR SEQ ID NO:856
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 571 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...571
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:856

			antatotact	cotaagcata	tattgtagcc	60
agagaaagat	tcttatgaaa	agaccttgct	gatgtttgtt	t-cot-G	tattgtagcc cgctttcgcg	120
	+ acategee	20200CC0AT	CLECLAAAEL	4555 C 65 C 6	-0 0 0	180
		Cattoooooa	CACCECCEAC	agecee	00 00	
atguagagau	46660464	gcaagtagca	ctteccettt	tgctcaaacg	atgtggtgta ttattaaaaa	240
tgcggatgcc	talgaggacg	gcaagcagca	teatacaaca	octtettate	ttattaaaaa	300
gatacactga	gatacgtacg	gggcaggatt	Ligigiagea	at a at t t t a C	ttattaaaaa atgctctttg	360
	ancactetet.	+ occartcec		CLEUCCCCO	0	420
	+ -+	CAADACCTTT	CTTCALAPRO	aaacccgucc	5-5-0	
		tatagatatt	actatccgca	cggcagattt	ggcgcatact	480
gcaaatagga	gagcaggcag	tacagacatas	atcagatcaa	aattttggcc	tttggcattc	540
catctgcaaa	acctactgat	tcgacgacga	gccggaccga	1	tttggcattc	571
ggatacgttg	ttgtgaaaga	tccgatcgtg	g	•	•	

- (2) INFORMATION FOR SEQ ID NO:857
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 600 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...600
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:857

tatattgaaa atcggtgata atatccttaa catataggaa gttattcgac aatatctacc 60 atcttgacga atagttgatg tttccacgat tgaaatcagt acccgtcctc tgattttgta 120 ttaaaaatta agcaaccttt atccaaggtt ttgtactcaa gcctaactga ggtttgatgg 180 aatattetee attttetagg ataeggttaa aaagetatet ttagettetg ttttgagaag 240 cataatgcat caactgtttc attgttaagc atgcaaccat caatgtaaat tataaaaact 300 caccattagc aatattaggg tgtatgcttt gatcataaag gtgctagcaa gattgttaga 360 ttgttcaact atatcatctt tgtcatcaaa ancttgtgta caaatctata tgacggattc 420 atgtctaaag actctataga acaaactgac agaaaacatc aaacttgaat gtgttttta 480 ctaatgttga ataaatccag aagcaaacga catatcatct gctttagaag aaaatgctaa 540 ccttcttctt ttaacttatt gccaaccttt gtactgtggc gattgtagga ctcctaatta 600

- (2) INFORMATION FOR SEQ ID NO:858
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 534 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...534
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:858

agaaggtcac tgcggtattgacattctgc gcgaagctattgagaagaggg tggaaagagggaacttctttc gcatacaccc ggagtttatgaagccgct acaaagcccgct acaaaagctcagatgaatt taccgcaga	gacaaacgca agcggttaat ctgacctcga ataattggga	ggaagcagca ttcaatgatc tggcaaagaa tgatgtcgag	gaatggcgtg tttacaaggg gtgtatgtgg cgcaaacaga aagagcctat	taactctatt tctggaccgg gggattcaat gaagacggag	120 180 240 300 360 420 480 534
-----------------------------------------------------------------------------------------------------------------------------------------------------	------------------------------------------------------	------------------------------------------------------	--------------------------------------------------------------------	------------------------------------------------------	------------------------------------------------------

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 703 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...703
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:859

60 cgaccccttt gatgtcggac aaacgtgctg tcagttctgc cagacggttg caccgtacag 120 gtcgaggccg tagaaggtaa gatcctgagc aatcagttga actcccgagt cccatgcttt 180 acgagcatcc gtacctcttc gactaagcct ccatcgggcg cgaccgatgc cggccggtga taatcggtat ggcgcatacg aacagctgcg atcgcagccc tcggatattt tcagataggc 240 300 ataatccgcg gagtggtcag tttgcgcctg ttctctgcct cggcataata agactcccca 360 aatgagaaat gagttgcttc cagtcgaatt tgccgtagta agctccactt cgggtatctc 420 cttcttcagg tcttcccgaa accgctcgct cagcagccca ttacgtacag gctgccgata cgtccggcct tcttcgcctc cccatctcca gaatggtatt gacagactcc tcctgtgcat 480 540 cgcctatgaa ccgcaggtat tcaccaccac gatctcgccg cataccgaag ccggatcgta 600 tgcacggtat agccgttgga caggaactgg cgcatcagca cctcgctgcc accagattct 660 tggagcaccc aagcgtaatg acgtctactc tgtttctctc attcgccaaa ggagagagtc cacgaattcc ttcttacgga agatctcagg tcgtcttatg ccc

703

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 697 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:

### (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

### (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...697

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:860

tgctactgat	cgtttattgt	tattgatgat	cgaagtcgtc	gatgcacagg	ccacaaaaac	60
	_			tcgcgcaagc		120
				attccatctc		180
tcctggaaca	ggaagtattg	taggggaagc	gcgtgatatg	gattgcctta	gctctctcgt	240
acaaagagct	ttcagagcat	ccatcccggt	gcctttcttc	gccgagacga	acagcagtca	300
ttcccgagtt	tggccatcca	ggtctgttgc	agctcctcgg	cactatgttc	tcttttgttc	360
ggggagtaag	gtcgtcttcg	tctttgggtg	tgaagagaac	gcatcgatct	tgttgaagag	420
aagaagcatc	ggcttttctt	ccctgccgtt	atctccgcca	gagtctggtt	caccacctct	480
atttgctctt	gaatgccgga	tgcgacatat	ccaccacgtg	caccaacaaa	tccgcctctg	540
cacctcatca	agtgtacttt	tgaaagattc	gaccaactgt	gtgggcagtt	gcggataaac	600
ccgacccgta	tcgctcagca	agaaaggcaa	attgtcttga	tcaccttgcg	caccgtcgta	660
tttcaacgtg	gcaaaacagc	ttggttcggc	gaagacc			697

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1133 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1133
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:861

```
tgaaaaaggc atccatccca gcatgagata gatgcctttc cttttatcgt ttgatccaat
                                                                        60
tatttcgctc ctttggtttt acacgtatga tatctgctct accgtattag cttccatcga
                                                                       120
                                                                       180
tgtgtagtat ttttctttta cctgctttaa gcagcgagag ccttgtcgta ttgtttgagc
                                                                       240
tcttcgtata cgcgacggct ttgatgagac agcccggtgt aatggcatcg ttagaggctg
                                                                       300
cggcccagct ttctcaaaat agcctacggc ctcttcatat tttttgagct gtactaacag
tcaccgataa gacgagtgat agatggtgct accatatttt cctggaggag aatcccttca
                                                                       360
gatgatcaat ggctttctga tattctccga ggtgtagtag caaatgccgg cataggcttt
                                                                       420
tgccagattg gatgcatccg accggagtat tttttgatta ctgtcaacaa tcccatttcg
                                                                       480
tttgcaccgt tccatttaag gctgcgctgt ccaattcctg aatgaatttg tcttcggcag
                                                                       540
gtataccttg gcagcagctt cacgagcttt aggttcgctg acgaaacgtt gtaggcaaaa
                                                                       600
atacctgcca caatgataaa aacgcccaga ataaccagcc gattttggtc atgttctttt
                                                                       660
ctatgaactg ctctgagcgt gaaacccttc tcctacgtgg ttgtccggtt gttgattttc
                                                                       720
ttttttagcc atatttggaa taattattta tttcttttcg gtcgcacaaa ggtacgcgtt
                                                                       780
tggcgtgata tacaaatgtc ctgtccgaat aaatatacga tatgtaatgg ttgtcgaaaa
                                                                       840
cgtttcttct cttcttgcct ccaatatccg atttacttgt ctctcttgag ccgtcaggta
                                                                       900
gccgaaaaga gagctattgc caatccacta accgctcttt acggcatacc gtatcagttc
                                                                       960
ggctgcattg gtgaatccca tttgtgcaga atattactac cggtgtgttt ctaccgttcg
                                                                      1020
```

gtaactaaag tgcattttt cggctgnttc tttggcagaa tagccatcgc acagatatgg 1080 1133 actacttctt tctctcgttg ggtcaagctc gagaagtccg ttctgctctg tgc		
(2) INFORMATION FOR SEQ ID NO:862		
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 398 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: circular</li> </ul>		٠
(ii) MOLECULE TYPE: DNA (genomic)		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: UNKNOWN		
<pre>(vi) ORIGINAL SOURCE:     (A) ORGANISM: PORYPHYROMONAS GINGIVALIS</pre>		
(ix) FEATURE:  (A) NAME/KEY: misc_feature  (B) LOCATION 1398		
cgactotoga ggatocooga ggagacgacg galaggoba tattttoca tatactalle	60 120 180 240 300 360 398	
(2) INFORMATION FOR SEQ ID NO:863		
<ul> <li>(i) SEQUENCE CHARACTERISTICS:         <ul> <li>(A) LENGTH: 1362 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: circular</li> </ul> </li> </ul>		
(ii) MOLECULE TYPE: DNA (genomic)		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: UNKNOWN		
<pre>(vi) ORIGINAL SOURCE:     (A) ORGANISM: PORYPHYROMONAS GINGIVALIS</pre>		
(ix) FEATURE:  (A) NAME/KEY: misc_feature  (B) LOCATION 11362		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863		60
(xi) SEQUENCE DESCRIPTION.  ttgcaatagc aacacataga taagccgggg tttgagaaga agattcaaag tcgccatagt ttgcaatagc aacacataga taagccgggg tttgagaatcaa ttttgcgatt attctctccc gagagattat atattattct ttatcagatc aacgaatcaa tgtgccgtta tgctttttgagtcttggggt ctttacagcc ccagtctgaa tgaggcagta cgtgccgtta tgctttttga		120 180

tgctttcgtt	ttggcaccgg	ggcagagtat	cagctcctcc	atagactcaa	agaggtcgtc	240
				ctcccttgag		300
				ggattgtcga		360
accgaacttc	tcctcataat	actcgataaa	gggattagta	gtgcctcacg	agcaaggagc	420
				tgccttttga		480
gccattcgcc	gtgcttgaag	tattctctga	gatgatgcga	agctttctgt	cgagcatacg	540
atacgttgag	gaatagggat	aaactccccc	gtagtagtgt	catacctgtc	acaagataag	600
gagcttcgcc	acaagtaatt	tccatacgcg	tggagcaaca	tagtctttcc	atgtcttacc	660
ttcggggaat	gtaataggtt	cggtagtgca	atccaagtct	ttgtctcggg	ttgctcaata	720
ttaaacacat	ccttagacca	aaccaagcct	catcgatcag	attattctga	gcgttgcaaa	780
				ttggcttgtt		840
ttcagcactc	tgggctgtat	tacagtgtca	tgctcccctg	tatgctgtca	gtcgtaattg	900
gtgcatcgta	tttggtacgc	atctcccagt	gagtatagtc	atctgtagcc	caaaagatat	960
				ccttcggact		1020
ttcattctcc	taatgtcgac	ccccatcttc	atatcgctca	cgagtaacct	ctttgcattg	1080
acaagcagtg	gttgtcaaat	tactgtatac	catatagaat	tgccatttgg	gcacagatta	1140
gaaataggca	cgacaaatct	gcccctactc	ttagccccgg	ttggggacat	caccaggaaa	1200
				taagcaaagg		1260
ggggcatact	aacgagggaa	atggatattt	ctttaccgag	tagatcaaag	tgcaacagat	1320
		cgggcattcg				1362

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 750 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...750
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:864

ccggtcgagt	ttcatgagaa	gaagatcgcc	gaagccggga	aagaccggag	gttttcgagg	60
			accaaaaccg			120
			aggctgaaag			180
acaggcggag	agcacagccg	atcggcgaat	tatacggctt	tcaattatcc	gtcaagagcg	240
			ggataaccgg			300
agcatctatt	atacttacaa	caacggacat	ttggctgaag	acccaaactg	gcctgcatga	360
actttctgaa	tgccttggag	aagattccca	gatcgtcgag	agtcatcgga	aagaactggc	420
tgcgacacaa	gccaagatac	cacgttcgaa	acgatggttt	ctgccgtatg	gaagaaagag	480
gaggaattgc	ggagctgaag	agacaggccg	cggagctgga	tcgcaagatc	gccctttcgt	540
caaaaaagag	gacaacagcg	aagtgaaacc	ggaagaaacg	gtcgctccga	tgcgacaatc	600
gcatcgatgc	gcccttacgg	gaggagctaa	aaagggacgg	tcttccgagc	ggaatcatac	660
cgattggaaa	gaaatacggg	aggatgaaaa	atcaaaccct	gcataaagcc	tggaaggtgg	720
tgagagatac	agagaatacc	tgatactttc				750

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 665 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: circular		
(ii) MOLECULE TYPE: DNA (genomic)		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: UNKNOWN		
<pre>(vi) ORIGINAL SOURCE:     (A) ORGANISM: PORYPHYROMONAS GINGIVALIS</pre>		
<pre>(ix) FEATURE:     (A) NAME/KEY: misc_feature     (B) LOCATION 1665</pre>		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865	60	
gggctccaat tcctgtctgt tcgatggtcg ggaagatcaa agccaacgtt ccccactggg cgagctccaat tcctgtctgt tcgatggtcg ggaagatcaa agccaacgtt ccggcagcctt ctatatcctc ggagagtagaag ggagctggcg aagctttcct gcaggagtat ggcctgacgt tctatcgaagtg tctatcgaaa gcctttccc aatcgctct tggccggatt tccccttta tcgccgaca tttggacatt ccggctgtat acagatagtt ccgacgactt tcttgtgcgc acgtgtccc acggctgtat acagatagtt tcttgacgactt tcttgtgcgc acgtgtcat acggctcc attaccgctct gaacgtccc attaccgctc gtagcctttc acagagggact ttaacgctcg gaagatcaa gcgtcaacaa aggttgagta gcgtcatcaa aaaaaagaggc attaacgctcg gaagatcaa tccctgtacg acgacagga accaacaca tggagggact tatacaatat caccacaacaa tggagggact tatacagtga agaaaagtca accaacaga agaaaagtca accaacaga agaacaagac ccagaagaa tcccgaacac atcaaccgc aggaccagga aaagtggcga aaagtcgaaagcc ctggtccaac acaacaacaacaacaacaacaacaacaacaacaa	120 180 240 300 360 420 480 540 660 665	
(2) INFORMATION FOR SEQ ID NO:866		
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 402 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: circular</li> </ul>		
(ii) MOLECULE TYPE: DNA (genomic)		
(iii) HYPOTHETICAL: NO		
(iv) ANTI-SENSE: UNKNOWN		
<pre>(vi) ORIGINAL SOURCE:     (A) ORGANISM: PORYPHYROMONAS GINGIVALIS</pre>		
<pre>(ix) FEATURE:     (A) NAME/KEY: misc_feature     (B) LOCATION 1402</pre>		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866	,	60
(xi) SEQUENCE DESCRIPTION (xi) SEQUENCE DESCRIPTION (xii) SEQUENCE DESCRIPTION (xiii) SEQUENCE DESCRIPTION (xiiii) SEQUENCE DESCRIPTION (xiiiii) SEQUENCE DESCRIPTION (xiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	1: 1 2	20 80 40

catctacttg accaggaaca taccacaact go ttcagctcat atagaacgaa ttggggtacc ca catgtactta ttgagaccna agaaaagctt tt	aattincca taigtaccoo taitaggcaa 360
(2) INFORMATION FOR SEQ ID NO:867	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:         <ul> <li>(A) LENGTH: 568 base pair</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: circular</li> </ul> </li> </ul>	:s
(ii) MOLECULE TYPE: DNA (genomi	.c)
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMON	NAS GINGIVALIS
<pre>(ix) FEATURE:      (A) NAME/KEY: misc_feature      (B) LOCATION 1568</pre>	е
(xi) SEQUENCE DESCRIPTION: SEQ I	ID NO:867
ggcttcgagc cgttccagct cctgcttctc ctt gcgtcggttc ggggcttttc gctttctgcc tta gcctttcggc ctcttcctgc tgtttgtttc gcg cttcacgatg ccgttccctc gaacgtgaag aga cggtctgcga gacgacgagt acgcatcctt tga cagcgtgagg atatcgaggt cgttggtggg ctc atcagcacgg tgcagaggta gagcctgcgc tgt tatattgctt ctcgggcggg aaaggaactg cgt gtaccatcct ttattccgaa tcacctcggc gat gtttcgtcaa actgcatgcc cttctgac	acgtgtga gggggaagat tcgacggtct 120 ggtactgg gtgtagttgc cggggaaatc 180 atggttca ctaccttgtc catgaagaag 240 aattcgct caggtagttc tccacacgtt 300 cgtcgaga atcggaaatt ggggttcttc 360 ccgccacc gctcaacttg tggatcggcg 420 ccagcaag gcccgatgcc cgagagaggtg 420
(2) INFORMATION FOR SEQ ID NO:868	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 672 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	

- - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...672
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:868 •

		-costgaggC	tooctaataa	gaccataaga	attttcgtcc	. 60
tagccattgc	tgttatccga	agcacgagge	costagecaa	CCTTACGCAG	agcacattcc	120
		aggeratyc.	Cagiggocau	CCCCGGGGG		180
						240
		+~+arararavi:	LLALUCCEAG	u chhacaaa	**	
	++++	Caarccuaii	LECTERAGE			300
tgaaagatcg	LLLLLacego	ttoggetteg	agcagtccga	atccctgtcg	tcttggtggt	360
gctcggagtc	tettegettt	LLCggcttcg	ageageate	ccgacaaget	cggcaaatgg	420
	++~~~+~~CCC	toactattaa	Cagagiaica		- 66	480
		++aroocaaa	CYYYAAAKAA	CCGCGGG		540
	+	aattaaaaty	CLALKICAAC	Eure con and an	0 00	
		CEEGGEAUIV	LUMUEARUUR	Fabor 20	- 0 0	600
tatgcatact	gracega	-ceggeage	tteretecea	atgtggcaga	agaccatcaa	660
tttgcttgct	gggaaaacct	acgaractgg			agaccatcaa	672
acaaagaatg	ct					

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2760 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...2760
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:869

```
ttcggcctcg tagaagagcg tccgcgtctt gagcgatgcg tttccggcac gtctttctgt
                                                                        60
gccagctcat agagagatcc ccatgtgccg aggtctgcca gccgaagtcc acgggcatga
                                                                       120
ccaagacatt gtccgccttc tccatcagcc aaagtcgatg gaaatgctcg gacagtaggg
                                                                       180
gaaagcctga tcgatgaacg ccgctcttca ggtgtattga agtgtgccaa gccattttcg
                                                                       240
agagagaggt tacttccggc agatgcttgc ggaatgcggc aaggatgctc tccagttcca
                                                                       300
tacgaacatt ccactattcc acaggaattc tccactggcg aggagatgct tgccatctcg
                                                                       360
gcattgggct tctccgtaaa ggttttcaca cgataaaatc accggtcttt tcttcagcca
                                                                       420
tttggatata tccatagccc gctccggacg ggatggacgg atgccgagcg tcacgagatg
                                                                       480
ctcgtgatcg ctacgaactc caacgcttcc gatgcagcac gcacgaattc gtcttcgcga
                                                                       540
ggatcagatg atccgaagga gctacgatta tgttggcttt gggattgccg cgtaaatgtg
                                                                       600
atagotggca tatgogatgo agggtgcogt attgogaggg toggttogog caggatttga
                                                                       660
teeggttega teteaggaag etgtteegea eettgteeac gtaaagttea ttggtaacga
                                                                       720
ccagaatgtt ttcccgggga taaaccgtgc gaaacggtca tatgtcatct gcaggaggga
                                                                       780
gcgtcggtgc cgaagaagtc gaggaactgt ttgggatggg attcacggct gnaggccaaa
                                                                       840
ageggettee tatteceet eccataatga egeaataatt gtttteacag ceatagtege
                                                                       900
tattctattt ttaagttctt agacaaaact atcaaaataa taacgtcatg tctcaagaaa
                                                                       960
atcgtacttg tggttcgtaa taatttcata ggccaatgga ggattttttc cctcctcaca
                                                                      1020
tegittegeg acttggtggt titteteta etttageggg eggaaaaatt attegeaaca
                                                                      1080
tattttttt ctccccaaac tctttgcttt tttcgcaaat gccaaggtcg atcgaaaaat
                                                                      1140
                                                                      1200
ctcattctaa aatcaccaat aattatcacc aatacagtat gaaaagaagc agacttttag
                                                                      1260
gccgcatcgt agtactatct ctatggttgc cacaattccg gcttcggctg tcagccaacc
gcagatgacg ccctgcagtc gacacacacc tccgatcgtt cgttcggcag gggagctcag
                                                                      1320
cagtagetga egaatggagt geegecatge eccaaaceac atggageage cagetgatgt
                                                                       1380
cagttggtac acggcagacg gcacggaatt cactctcacc atgcggagca gtttgcaggc
                                                                       1440
```

```
1500
ttggccaagc tcgtcaacag cggaaagtcc tgaagggtgt gaccatcaag ctgggtaatg
acgtggactt ctcggctaac gcttcgatga ggtgatcggc aaggataatg acaacccctt
                                                                      1560
                                                                      1620
ttccggcatt tcgatggagg caaccataca ataacgggcg tgatgatcag cgatccctct
tgggattcat cggattcttc ggacaaacca acgaggccat tattcgaata caatcatccg
                                                                      1680
                                                                      1740
caatgctacg gtcgtaggtt cggccccggc aggtgtctcg tttgcaacat ttacaacaag
                                                                      1800
ggactcgtaa gcaactgcca tgctatgact gtcgaatcgt ttccgctcca tacgaaacga
gcttcggagg cagggtgcag ggtctttggt tggaggcctt ttggatgaat ccaagataga
                                                                      1860
aattgctctg ccactcgtgt ggaagtctat agccagagcc aaagcggtgc ttcatatccc
                                                                      1920
aggcatacaa totgtgcgaa gtaaagaatt gottogtaac gacagcaaga taatogcaga
                                                                      1980
cgttgggttg atcggtggat ttgtcggcaa aactttgctt tcttccccgg aaccgagtct
                                                                      2040
actttctcca actgctatct ctcaatgtgg aagtcgtatc gcttgacagt ggtgatcaag
                                                                      2100
ccgttctgga gggtttgtcg gtcaggtatc agccaacttc attgccaagc actgctcgtg
                                                                      2160
tcagccaaag taacgggagg aaaaaatccc ggtgcttttg tcggttgacg gcagatgaat
                                                                      2220
ccatgaactg caaatacgac ggttgcttct acaaaacgaa caaaacccgg gtatggtcgg
                                                                      2280
cataggaaac gggcgtcgaa atactgccat cgcaggtatg ccggaagcgg caatgaagac
                                                                      2340
tgccgatatg gcgccaagct caatgcagat caaaatcctg ctccctggct tcaggcaaac
                                                                      2400
gcgcaaacaa cggttggccg tacctcaaag acaacaaacc ggtaataacc ctctggccgc
                                                                      2460
tcccatttcc catgagatcc gtatttgggc tactgccggc ggatattcat tgcgggtgct
                                                                      2520
                                                                      2580
cctgcgggca catctgttca ggtgtacgta tgcaaggaca tcggatttac aatgctgccg
                                                                      2640
tgcttgcaga tcatgacttg cagttgcatc cggtgtatac gttgtacgag ccggtgacag
cacagcaaag tgatcgttcc ctaagagaga ggtcgatagg aaaaagttgc atcctcatga
                                                                      2700
gcgatttgtt tgccgcaagt cgtttgtgca ggattctttt aatgttgtgc ccggggatcc
2760
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 556 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...556
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:870

```
60
agagcaagtt ttccatctcg ctgcctcgtc tgcgtcctgc cacgggcggt gggagcctaa
                                                                       120
agatcctatt gacgatgtcg gtatggtaca gcttattatg ccttccgtct gttggataag
gatgtcgaga tcagcctgtc cacacggaga gtcgtgagtt tcgtgaccac gtgatgccgc
                                                                       180
                                                                       240
teggtateae eteggtagtg eeggeageaa gaeegaaeee ggaggatatg eegaagagaa
                                                                       300
tgccgtctgg agcaattcgc catcaacgat gcccgcagtc cggccgaaat ggctccgatc
                                                                       360
ttcgccgact tggctacgag ccggtttgga aagactggga tgcttcatgt aacagaagat
                                                                       420
tcttaccgta acgcctcgcg tccgaagcga aggatcttca taagaataaa ggcttgctct
                                                                       480
ccggtcgagg aaagcagcct tgtccgtttt tggttttatc gtttgaatcc ttacaagcga
                                                                       540
atacctaagc tacgtggaaa gaggtattct ttcagcgtag cctncaagtt tttagtctcg
                                                                       556
gtttaatggc tttacc
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1368 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION  $1...1\overline{3}68$
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:871

```
acttccgttt tatccagaat gttcttaatc ctcggatcgg attcgtagtc gacagcagat
                                                                        60
gttctatgag tcggagcagn accacatatc cggtcgttcg tctccgtgca tcgtagaagt
                                                                       120
atagagcacg cgaggctttt tccctgtttg gcagaggacg tcagcttgca aatcatcagt
                                                                       180
ttacgatcct ttacggcttg ccaatgacgg aagtagtaca aagtgatgga tactttgttt
                                                                       240
ggaacettee ateatgetga tataggette ataggtgggg taageattee attetatttt
                                                                       300
totoctgago ggtagtogaa catotogaca gogogotgoa tggtggagga gtcaagaatg
                                                                       360
taggettgag cecatagege aggaatgeet egacteetet tegetggeat aggeaatgge
                                                                       420
ttcattggtt acggggtcaa atcgtcgatg gacatgatca gagccagctc ttgtagaacg
                                                                       480
gccctatcag cactttgaat gagaagtagg cctcgcccg ttcgtcaaag ttgaaataac
                                                                       540
tttggcctgt tgtgcctgca tgctgccgat gaaagtcagc aaagcaacaa aatgccaaga
                                                                       600
agcaaaaaat tottttott cataaatagg ataattagtt tgttattgga ttottgcagt
                                                                       660
atcettttge gagaaaaagg tgetegttt tgeataaegg tatggeagtg ggageatatt
                                                                       720
tttcgggcta aatgtctcgc aaagataaaa atattcctat gccattatct ttttgagcct
                                                                       780
aaaagtcaat tgcatattcc acttagttga tagtttcagg atgggatgtt cccaaaggag
                                                                       840
attgttgcat gggagtttca ttgagctctt ttgctgcaga gcgattctta gtgtcttcgg
                                                                      900
gaaaggtcaa accttcggta tatggacaca gaagcaaaca gaaatttcat caagtttcca
                                                                       960
ttagagaagt actcctttcc cgtcaaatca atgcttgtac cgataggcga gaaataagga
                                                                       1020
atgattgtcg ctgattcttg cttcctgcac gatgcaggac gcgattgtca gctgattctg
                                                                       1080
cttcctgcac gatgcaggac gcaattgtca gctgattctg ctcccgtaat gcgctaacta
                                                                       1140
                                                                       1200
tcagctattt gcaactattt tataggactt tcattgagtc ttttgccgca gagttgattc
ttaagtgttt ttcagattac ttgagtttgc agagagatcg catgaagctc tcctttcttc
                                                                       1260
                                                                       1320
gtcaaatcaa tgcattatct gncttgatca atatgagggg ggaagggtta ttgtataacg
                                                                       1368
gtccaaaagt gccttttccg gatcaaagtc caaataaaaa ccttgcag
```

- (2) INFORMATION FOR SEQ ID NO:872
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 589 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVÂLIS

### (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION  $1...5\overline{89}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:872

tacacgtgtc	aagcccgtgc	aactntccgc	tttgctcgta	acgatacacg	tcccgaactc	60
		tcgcgatagg				120
		tagcatgact				180
		tggcatagtg				240
gatatcggcg	tgattacctg	ttggtagcca	aagtgcttct	gtatctgctt	cagaagtctt	300
ccaaacgcaa	acggagctgt	gtgcctcgcg	gtagccaaag	cggaagccgg	cacctacatt	360
ttgggagaaa	gcgaagagtt	cgagctcctt	acgatctttc	gatggtcgcg	cttcttagcc	420
tcttccaaaa	gctcgagata	tcatccaaca	tctttttctt	tgggaaagag	attccataga	480
ttcgtgtcag	tgttttctct	tttcgtcgcc	gcgccagtaa	gctccggcta	cacttaaaac	540
ttgatcgctt	taatgtaacc	ggtattgggt	aagtgaggac	cgcgacaag		589

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1123 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1123
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:873

aatgatccgg	aagccgatga	agcgcgtctt	tacggcgcaa	tcccgatatg	caggcgtcat	60
				aagccgcttt		120
				agcgattcgg		180
				ggtattgccc		240
				aagcaaatca		300
				tactctgcgc		360
				aacggagtgc		420
				aactgagcgt		480
				ctatgtggtg		540
				aaagcgagga		600
				gcttatccgt		660
				cgcgaaggcg		720
				ggaaagcttt		780
				gtcggagaag		840
				atctatcgac		900
				ggaggaaata		960
				gataggagtc		1020
				cgcggtgtcc		1080
		gcgcaagcgg				1123
				7		•

- (2) INFORMATION FOR SEQ ID NO:874
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 579 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...579
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:874

ggttcctccc caccatctat	•••	agccagtaaa	tagccgcgtg	ggatcactgc	60
ggttcctccc caccatctat	aaggegegee	tetestagg	agttroctc	ccttgtcgaa	120
cccgaatact tttgataaag	gcggatgcta	Lactataggg	tagtostasc	gagecogtet	180
+++-0++003	90000000	allittice	CAACGGGG	0-0-00	240
	aggregagga	LELLCARCAR		6 00	300
	teterroay	Lacaggacga	CC66	0.0	
cgatcgatag ccctgtgtgc	caagtagrag	cagatectea	tcatttgggg	tttgagcaca	360
cgatcgatag ccctgtgtgt		atacttchaa	actoggattt	tcggtcgtgg	420
tagacctgac agcgcgatag	gageggaege		aantgaatcc	tecteactet	480
	+c+coctcta	CEECLECCAIL	aaguguucco	-00-	540
toctgaaacg tgtatctcgt	cgatgaagag	gatggtgtgt	cctcctttgt	Cgaacaggag	579
ccacgatgga ttcgatgtcg	gctattactt	cccgacttc			3,7
ccacgacgg 0 0					

- (2) INFORMATION FOR SEQ ID NO:875
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 581 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...581
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:875

		antangacct	ccggacacat	acagaaatca	60
ggctctaaac ctgcaaaccg	ctttcgagca	gataagacct	CCBGCCCC		120
tertone atagatgata	tcttctatgg	aagcagcact	gigaalggua	600000	
gcgtgatgca atggatgata		tagatagaat	titctttcga	ttccaatctg	180
ataatctttg ccgagacagc	gaaaatcatc	LCERTECE	caccete g	, •	

cacacataca	aatgagttcg	ggcttcgtcc	ggctccatga	aactccggct	cttgccaaac	240
cgcagaagag	atagcagcag	ctatctcttc	gcagtcgccg	ttatagacaa	tagttgacaa	300
tggagaaaca	agcggagctt	ttcctccagt	ttcgttttta	tatcgggaag	ttctcctgat	360
gagcacctcc	tatattcgta	atgataccat	acaggggcat	attatgctct	ccaaacgttc	420
catttccccc	atttgcgata	tccggcctca	aatataccga	gagtgtgttc	ctccgccatt	480
gccatacgga	aggggtactc	ctatctgcga	gttatagctt	cggggcgagc	ggacaatgca	540
tagtccttgc	gcaataactg	ataaaggaac	tctttgacga	t		581

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1029 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1029
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:876

ggatgatttg	gccaaggctt	atggcgatca	ccaggtgttt	tccggagctc	atacaccatc	60
gaaagaggcg	aaaaggtggc	tttcgtaggc	aaaaacgggc	cggcaaaagt	accatggtca	120
agtgtatcat	gggagagctg	acagactcac	cggcaagctc	gaactggggc	acaacgtgca	180
gctgggctac	tttgccaaaa	cgaagcccaa	gagctaagag	gggatctcac	ggtattcgac	240
acgatgaccg	tgaggccgtg	ggcgacatcc	gtctgcgcct	gaacgatttg	ctcgggcttt	300
tctcttcggg	ggcgaagcat	cggaaaagaa	agtaagtgtc	ctggtggagg	agaacgagca	360
cgattggcta	ttatcaggct	tttgctacag	ccgctaactt	ccttattctc	gatgagccga	420
ccaatcacct	cgatatgcgc	tgaaggatgt	actgaaagag	gcgatcaaga	acttcgatgg	480
gactgtcatc	tagtatctca	cgaccgtgag	ttcctcgatg	ggcttgtcag	caaggtgtag	540
aatttgcaga	tggacaggtg	aacgaacacc	tcggaggtat	atacgacttc	tccggacccg	600
ccgtatgcag	acgctgacag	agctggagcg	aaccactcga	tcgaaacaaa	aaccacacgg	660
gaggctatac	ctgaaacgga	agccaagcgg	actaccgtcg	gcaaaaggag	gtagccaaac	720
agctgcgcac	gttgggcgaa	ccgtagcaac	ctgcgaggag	cggatcggaa	aattggagtc	780
ggaatacagg	caatagagat	gctactgcaa	gatccgaaac	atgcgactga	cgcaatctgt	840
tcgagcgata	cgccggcatg	aaacaagaac	tcgaaaaggc	caggaggact	gggaacaggc	900
ttccgaagct	ttatccgaag	cccaaggata	actcaacctc	cccctctct	tctctcctcc	960
tttaccaaga	gaccatctca	caccaatcta	ttagaagctg	agacaacctt	tcgccatccg	1020
tccgaaagc						1029

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 545 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION  $1...5\overline{45}$
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:877

tgaacaaaga agctctgtcc tatcgtttgg ccggcaagga cattgcagag tgaatgcaa	t 60
tgaacaaaga agctitgtit tategittes best agta agcatctatt ggatacgca	a 120
ggacatcaag actettattg aatgggtaga teetetggtg aacatetgtt ggatacgca	g 180
acceptant the characagat actgagagaga tacggacacg cutsession cutatagat	6
tggggttgga gtacttacga tgaaccgagc tgcagcatcc ttatccggag gagaaagcc	a 240
tggggttgga gtactagga gataggaga aaactggttg apptcttgta catatggat	g 300
gcgtatcgtt tggctacgca gatcgggagc aaactggttg aggtcttgta catatggat	t 360
aaccgagtat cggtcttcac caaagggaca atcttcggtt gatcattcgc ttcaggatt	c 420
and the tart of the contract o	
gactatgtaa tagacttagg acacgagccg gcagacatgg tggtgaagtg gtgtttgca	g 480
gactatgtaa tagacttagg actagagg gactagg gattatataa gtggacgaa	g 540
gtagtccgga gagatggtgc aggctaatac cctgactgcc gattatataa gtggacgaa	545
cgtat	545

- (2) INFORMATION FOR SEQ ID NO:878
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1088 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1088
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:878

						,
atcasattac	atagogaact	cggcgggtgc	cttgtctttt	ggaatgagtt	gggaacctta	60
***cgagccgc	ttcatcatag	gagaaaatgc	tcttttgtcg	aaaccggatt	ggcatacggt	120
neatagraca	aagataatag	pagagtegge	gtaaggagca	taaatggatg	aatatacgcg	180
ttcattatta	agccotttta	attoggatga	taagtgttag	gatagagata	tttagcttcg	240
ttgaatcott	tototttto	caaatgtagc	caattcctgc	gacttccaag	aggctgatga	3 0,0
actatatata	tratttotot	ctgtcctgtc	gattgctcat	aagagggcag	gggatggccg	360
++ act cases	togaaataag	agagetttge	tgatgctaca	taaggtgttc	tatttggtac	420
catatacaaa	gataggettt	gttttttccg	taagtttgta	ttgatattgt	ttcttgcata	480
gacgtacggg	ctattgacag	categcaagc	gaaagaaaac	tgaaaaagca	gataaccggg	540
ccatttccga	agtetttact	gatgcattcc	tgctcaaact	ctttgtgaag	aggaaaaaaa	600
cacagaggtg	paaactatcc	tcaatcgtat	tctccaattc	aagataccac	Cattgctaag	660
attogttgca	acgacggtaa	gcacaacctg	cactcgtaaa	gaaatattat	Caccaacca	720
togatoattt	CaaggagagC	tgtccgagat	cgtgaagagt	atttcggcgt	gracaccea	780
taatgatttg	tcacttacgt	gcattaagca	gaaatagcgt	aåcatataga	ggtttttgaa	840

gtttttctca cgattgttgc tcaggatgat gggctggaaa gcctcgtccc atctgcaaat 900 ccgctccaaa gcgtcatttg cgtggctcct ctaccagcaa ttacgacttt ttgctgggca 960 aactctacta ttggtctatc gtcggaaagc cggcttcctg atgaaaaagg aatggtttt ctccctttg gaccgatctt cagggctatg ggaggtatcc cgatcgatcg ctcgaagcag 1080 gttccact

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1856 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1856
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:879

				:		
agccggtatc	gtagtgaaga	aaggattgct	gtaccgcaag	agaaatggta	cataaccctg	60,
ttcgagcaat	tctatggcat	gccatttgtt	gtagaactcc	ctatcggctc	catacgtacg	120 ;
		cacccctccc				180
tgattaccgt	ggccagatac	ccatctgatc	tcctttgaca	cggtcgaatc	ccttggcggc	240
accgccactc	cgcggaagat	attgcctcct	ccgatgacga	tgccgatctg	tacgccatgg	300
cacaagcctc	cttgatgtcc	gaagcataat	cggccaaccg	attgggtcga	tgccgtattg	360
		caccgctcag				420
		tcaaagaaaa				480
acgctgtcga	tggctgtttt	cactccagac	gagagagcat	ctcttcgccg	agagcacgct	540
tttccggatg	tgctccacca	cctcgacgat	gaagggattg	ctttcgaatc	gcctcgcacc	600
tcatcgaaat	cgcggtgttt	catctcccct	accaggttat	tccgaagcct	acctgactgt	669
gcatttggaa	ttccttcttg	gcatcccata	gagcatctca	tccaagcgaa	tcaccgaacg	720
		ggctactttg				780
taccttcgag	cagagcgttg	tatgcccagc	accattcata	gtcgtagtat	cggtatgaat	840
ttccttcatc	cgctcattca	cctccgcaag	gcttttgatc	ttccttctt	gatcaaggag	90∤0
gcaaggcggt	ggatctgttg	ttgtggagcg	acatgccaca	gatgtccacc	cagctgccgt	960
ctccctcatt	gtgagtcggc	tgagagcact	cagcacctcc	tcatccgtac	ggcaaggaca	1020
atcttcaagc	gtttgatgat	ggaattgccg	aaaaacttgt	tcagccccat	ctcatagaca	1080
tcagcccctt	gtccaaggca	gaagaacgta	tgcgcatatc	atgatagcat	aggtttgtcc	1140
ctcactgccc	agtatcttgc	gtagcttttt	cagcttcgac	tgccgcgcat	catcttgccg	1200
		attgagttga				1260
		tggcgtcacg				1320
cggaccaaat	acgattcgtt	acggtcctct	atgatataag	agaaggggaa	ggcgagctgt	13 _į 80
caatatggtg	tacgtgtcga	cccatcacca	acgtgaaaag	gcctattctg	gatggccaaa	1440
ggatataaga	gtcgctcgtg	gtcttcgagc	gcgctccacg	atgccctgat	ggatggggcc	1500
gagcttgtag	aggtgattgt	ctggttagag	ccgctgccgg	cattgaggaa	agagtataga	1560
ccggcaatag	caggctcgac	ttgtgcatcg	acacggtata	tggcccggca	aagacggaca	1620
ggcctcgccg	ttttcgcctt	ggcagttggc	aaagaaaagc	gaatcagtgċ	agagaaaagg	1680
		ccctacaaaa				1740
tgctgcccga	acagagaatg	aaatgcggca	gacgacattg	tagcctaccg	acacgggggc	1800
ctctttcttg	ctatgatact	gccgttgcag	agatgcgagg	cacccggtga	tctcgg	1856

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1025 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1025
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:880

```
ccttagctgt cccgtcgagc ttggtcacgg caagggcatt cacttcagtg ctgcggtgaa
                                                                        60
ctgccttgcc tgttcgaaag cattctgacc ggtggatcgt ccaataccaa taaaatctca
                                                                       120
tgcggagcgt cgggcactac cttctgctca cacgcttgat cttcgtcagc tcgttcatca
                                                                       180
gattgacctt attgtgagac gtccggctgt atcgatgatc acgacatcga cgccgttagc
                                                                       240
cacggcgaac tgactgtgtc ataagccacc gaagccggat cgctacccat ctgcgcttga
                                                                       300
tgataggcac tectaetege teggaceaga tetecaactg etcaeggeeg cageaeggaa
                                                                       360
ggtatcggca gccccgagca cgacgctctt gcggcctgac gaaagcgatg tgccagcttg
                                                                       420
ccgatggtag tggtcttgcc tcgccgttta cgcccactac catgatcaca taaggtttgg
                                                                       480
                                                                       540
taccggaggg aggtcgaagc tgtcgccatc ggccgatccg ttctccgtga gcagcgaggg
atctcttgac ggaggatagt cgtcagctcg gaggtggaaa catatttgcg cgagccactc
                                                                       600
gttcctctat acgtttgatg atcttcaatg tggtatcaca cccacatccg aagtcaccag
                                                                       660
cacgttttcc aattcgtcca agacctatcg tccactttgc tcttaccggc tacggcacgg
                                                                       720
gtgatcttgg cgaatcgttt tctttggtct tggacaggcc ttcgtccaaa gtctcttttt
                                                                       780
                                                                       840
tcttttcgag aataatccga ataatcccat atcgtatata ctgttatatc tctccttagt
tcattctgtt cttgtaatcc tcataatcga accggcgcaa cactctttct tcccgtcggt
                                                                        900
gcgcagcagt acgatgtccg gatggcgtgc acgttgaaca tgtcgtcttc accgcggtag
                                                                        960
tggagcatgt ctcgaatatc gtcatcgcca ctgcacgcga tcgaaactca gtcaccgatg
                                                                       1020
                                                                       1025
aagcg
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 490 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...490

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:881

ggggatctcg ttctata	ctt ttcagacgat	gagttacatt	atcgacatta	tcgaggtcag	60
gtgcagcctc taaaacg					120
tagccggccc catcgtc					180
ggaagggagg gaatatc	cga <mark>a</mark> gccctgatg	ttgataatgg	gaggtctctt	caagaaagcg	240
atcattcgga ctatatc	agc ctgaactttg	tggatcgcgt	gttcgatgct	ccaagcttta	300
caccggattg gagaacc	tta tgggggtgta	tggctacgcc	ctaagatcta	ttgcgacttt	360
tccggttatt ccgacat	ggc tatcggtata	gcctggtgct	cggcttccgc	ttcaatatca	420
atttcgattc accttat	cag tggccaatat	caccgagttc	tggcgcaggt	ggcatatctc	480
tctttcgtca					490

### (2) INFORMATION FOR SEQ ID NO:882

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 648 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...648
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:882

gcaaggagtt	cggcttcggc	tttcgctatg	gaatcctgcc	gagctgcttt	atcgcagcct	60
	ttctatttcc					120
	agaactaaac					180
	accgactcgg					240
gggagaaaaa	tttcacaccc	ccccaaagaa	ccgacaggca	aagcgattat	tcttatcttt	300
	ttgattgctt					360
gtactattgt	attcgggatg	gaactgtacc	ccacgaacca	gcggcaggca	ggcacttcca	420
cggcttctac	caagcccgtc	tcggattctc	gcccacacat	tgcataccgg	ctttttcgaa	480
agcttcgcga	actggctgtt	gaattcgaag	cgatggcgat	ggcgttcgcg	cacgaattct	540
tgccataggc	agcagccaat	ttcgatcctt	tgcgcagagc	acagtcgagc	gcccaaacgc	600
atggaaccgc	catatccgta	accgctctgt	cgtcatcggt	cgtgacct		648

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 386 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION  $1...3\overline{8}6$
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:883

- (2) INFORMATION FOR SEQ ID NO:884
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2415 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...2415
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:884

			ttoctac	ttatccacga	eccettetat	60
tggtttccac	ttgactccaa	gcgtattgac	ggcttcctgc	- tescents	atgattacto	120
	cccaactaaa	tagcaggaca	aaaactgcat	aatggcaatg	~ · · · ·	180
*****	catattcatt	CHATOTTACE	ttactattax	guuduuugu		
+	nacaggettt	totattat	gaccgaccag	CCgaaacagc	06-60	240
Lacgacgeet	Baca Babaca	atoroaatat	gccagcaggt	ttgctttctc	catacgaaag	300
cccaacgaga	agraticge	a c g c g a a c a c	caacacaaat	attaccacat	cggccataaa	360
aacctgtctc	cgggttgata	tattgittgi	cggcacggat	actetatect	gaccggcgat	420
catgtcatgg	ctaccgagtg	gaatgacctg	tctaccttgc	acticacgot	atctcaacaa	480
+000000000	aaddadrttt	ptcagcttgg	CCEECTCCAC	ggtaaggeet	6.00.00.	540
+	teettaceea	AACGGACACC	gcaccagtcc	gilligilige	CCGCBCCBCC	
-++	+ casaccoss	chogodacto	tctttgatga	gagtatagag	66666666	600
gragicaggi	ccaaaccgaa	atagacaact	ggctgcaatc	gtccccaccc	aactggccgt	660
ggcgaatact	gacatageac	ataggegget	enect cacca	atatooccop	tagoggatag	720
aagcaaatta	taatcctccg	gccggggcca			tagoggatag	780
	caaattccaa	tottatotoa	ttgtttcatt	Cilagadade		840
+-+-c-actc	astacaatca	ccegctagtt	ttcgctcgca	gragicgeac	-6-666-6-	900
	tetateacae	poaatceget	ttgcatcggt	LULLELLEE	00000	
Cigiliagea	220000000	acceacaatc	teteteetac	ttccacctga	cgtttttcta	960
ggattcggac	aacggacgag	+ c+ + c c c c c c	cacattcaaa	ocastaspag	cgatgcggtt	1020
caacttcata	gtcccgaata	cgcccaggcg	Cacacccggg	6	cgatgcggtt	

```
1080
caatteetet ettegaaagt ettgteetet atettgataa eteetttega accatggeee
                                                                      1140
gactgcgcaa attgttgccg atggtgatcc gcttgtccaa atcatccgtt gcaggagagt
                                                                      1200
agccaccttg aacagtttcg tcggggggat atggtcatca cgatgccgtt tctaatcgcg
                                                                      1260
gcgacgagca tttcttcctt tttcatacaa tatctgctta gtttgcaacg tctatgccga
gcacttcaca aatgtggact gcctcgtata aagcccgttc agtgcttgcc ggataaagta
                                                                      1320
ggcttgggat tgtcatccac atcataggca atctccccca cacgaggtag cgatgcagta
                                                                      1380
                                                                      1440
cgcgcagatt cggacggctg tcggacagca tagcgttggt cgcacataga catctttgac
                                                                      1500
ccgttcatat tcctccagat ccgtaaaccg tcacgttgta ctcgtgtcat gtagagaatg
tcgcagttgt tgatcacctt tcgtcgaaat gtttggtttc cgtataaggc agatcatgct
                                                                      1560
                                                                      1620
ctcgacaaac tgcttgtatt cttccggaag agacagctct tcgggagcaa cgaagataaa
cgagggcgga agtgcgacat accetetate agagaatgga tagtacteea taettgagat
                                                                      1680
cccctaccat agcgatagtc ctgtcataca gcgtgcctgt gttttgcgaa tggaatagag
                                                                      1740
                                                                      1800
atccaataaa gtctgtgaag gatgtggttg gctccatcgc cggcgttgac taccggcaca
cggcttacct ccgagcataa cgagccgccc cttccagata gtggcgcata ataatcagat
                                                                      1860
                                                                      1920
cgcatagttg cccaccatgg aaatggtatc cttgagcgat tcgcctttcg tgagctggag
gtggatgcat ccgaaaaacc gatgatacgg cctccgaggc gttcacagcc gtctcaaaac
                                                                      1980
tcaggcgcgt acgggtagaa ngctcaaaga aagagtggct acgaccttac cctccaaaag
                                                                      2040
gtgccgattc ggattctttc gaatagctct gcccgatcga gaatgcnaag aatgtcctcg
                                                                      2100
gncgaacctg gtcaatagat acnatatgct tcatctttta aggagtataa ttgattaatg
                                                                      2160
                                                                      2220
atatggacgg aagcaaagct cacttcaaag cgaaagaagc cttaacgtta tgcttgccgt
cttcatcttg gaagacgtat tgaacgaacc tcccagctat aatcttcgnt cgagttgagc
                                                                      2280
                                                                      2340
cccactatct ggaacacgcc catgaagaag atagcatctt acccacggag gaaccgctcc
                                                                      2400
cctccgcaat gacgaacacg attgaaagcg tcttcgaggc attgcgcagc atctccacct
                                                                      2415
tagatcattg agctt
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1116 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1116
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:885

```
tcagcagatt tggttggctt ttacggccaa aaagcccacg ttgggctatg cctataagta
                                                                       60
tcagnccgag cgagtaggta ctcgtctgca gcatgtaact atcaagtagg gcgtacgggg
                                                                       120
                                                                       180
neggteacae etgtggeeaa tetegaecag tactgatate eggtaeggte gtgagaegeg
                                                                       240
ccagcttgca taatgcgatt ttattgcgga gaaagacctt cacgagggag actttgtcta
                                                                       300
tgtggaaagg gtggagagat cattcccaag atagtgggtg tggatacgga tgcagcagta
                                                                       360
togatggcag acctatagtt titacagtgc totgtocaga otggctacac cattggtacg
                                                                       420
cgaacaggga gaagctgcct attattgccc gatgccgagg gctgcccaca gcagcagaaa
                                                                       480
ggacggctcg aacactattg cgacgcaaga cggcagacat caatatcggc ccggagacga
                                                                       540
togaattgot tatagoogca atatgattog taacgttgot gacttttatg coottacgga
                                                                       600
gagcagctac tcactctgcc cggcttcaaa aaacgggctg ctgccaaatt ttggacagta
                                                                       660
togaagooto caaagooogt cogtatoagg coattitto ggattaggta tiogottigt
                                                                       720
cggagaaacc gtagccaaga aacttgtgcg gtctatcctt ctatcgatgc cctggctgct
                                                                       780
gcgacgagcg aggaatagta cagatagacg agatcgggga aagaatagct gctgctgtac
```

togttggaag ctgagacagt ttccgtggcg gtttccaatc gttagctgga aaaacggttg tcgttggaag ctgagacagt ttccgtggcg gtttccaatc gttagctgga aaaacggttg ttatcagtgg tacatttgaa aagcgtagtc ggatgagtac aaaagctatg gtagaggaca ttatcagtgg tacatttgaa aagcgtagtc tccaagaact tctttcattc ttgccgggat atggcggacg tatggcccgg tcgggtttcg tccaagaact tctttcattc ttgccgggat atggcggacg tatggcccgg tcgggtttcg tccaagaag ctcggtgtgc cggctgatag	960 1020	aacggttg 9 agaggaca 9 gccgggat 10	aaaagctatg	ggatgagtac tccaagaact agctgagaag	aagcgtagtc tcgggtttcg agagagagaa	ctgagacagt tacatttgaa tatggcccgg	tcgttggaag ttatcagtgg atggcggacg
------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------	-------------	-----------------------------------	------------	----------------------------------------	----------------------------------------	----------------------------------------	----------------------------------------

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 621 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...621
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:886

gtgtggaagt atgtcccacg aatgccatcc atagctgaac teedstated aggaataaat 480 ggagccggct gtcgccacag agctgccgca ccggcacaag agactgtcta aggaataaat 480 aacaacaaag ccacatagaa ttattatgtt gaggactttc cgaatcggtg gtattcaccc 540 aacaacaaag cacatagaa ttattatgtt gaggactgt tgcctatccc tnacagtagt 600	cgatgctatc gcatgtggtg cctaagagcc aagctgtagc	cgcatcaacc cttgtgtcaa gccgtacttt aatgcttgta	ggcctgtcca gttagctgcg tcggctgctc	gaccacacca	cgaactccgg caaaggcggt aagcaatgcc agttcgcatg	aagaaagggg gtcgccaaga aattgaggct tgccgcaagt	60 120 180 240 300 360 420
gtgtggaagt atgtcccacg aatgccatcc acagctgaac ttcccaccga agaagaatagt ggagccggct gtcgccacag agctgccgca ccggcacaag agactgtcta aggaataaat ggagccggct gtcgccacag agctgccgca ccggcacaag agactgtcta aggaataaat 540	cctaagagcc	gccgtacttt	gttagctgcg	octotectte	aagcaatgcc	aattgaggct	360
conceptages thattatort pappaclice charcobood of	gtgtggaagt	atgtcccacg	aatgccatcc	ccggcacaag	agactgtcta	aggaataaat	480
catcoctctt ggtcagcaca t	aacaacaaag cccgaaaaca	ccacatagaa agttgtcggc	aggcaagccc	gaggactitic	Charcesses	0	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 582 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...582

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:887

```
cggtttggat ttggctctcg gtgtaggcgg ttaccctcgc ggacgtattt cgagatatac
                                                                       60
ggaccggaat cttccggtaa gaccactctg gctatccagc cattgccgaa gcgcagaaag
                                                                       120
caggtggctt ggcggccatc atcgatggga acatgctttc gaccgcacct atgccgaaaa
                                                                       180
gttgggcgtc aatgtgataa tctctggata gcacagccgg acaacggtga acaggctttg
                                                                       240
gaaatgccga gcaactgatt cgctcttctg ctgtcgacat tatagtcatt gacttgtcgc
                                                                       300
agccctcacg cccaaagcgg aaatagaggg tgaaatgggg gacacaaggt tggtttgcat
                                                                       360
gcccgtctga tgtcgcaagc actgcgtaag ataccggagc catcagcaaa tccaatacaa
                                                                       420
cctgtatctt catcaaccag cacgagagaa gatcggtgtt ttgttcggca atccggagac
                                                                       480
caccacaggg ggaatgcact gaaattctat gcatccatcc gcatcgacat tcgcaagaga
                                                                       540
                                                                       582
caccgatcaa ggatggcgaa gagatcatgg gacacctgac ca
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1545 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1545
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:888

gccggcaaaa	tcctgattcg	aagcgatcta	aggaaaagaa	agaaccctcc	atcatggcaa	60
				cgcagggtca		120
				tctggtacat		180
				tgcctcccaa		240
cctgcccgta	ccgctggctc	ccgctacgtc	gccctggaac	agtacacgcc	cgtcaatgag	300
gcgggataga	aataggccaa	agcgagggct	atgaaaagga	gtagaccgca	gcataaggta	360
				acggttccgg		420
cggcttttcg	ttttcttca	tatgtcgttt	gtttttcggt	tacaaagtta	aaaaaccatg	480
tgattggctc	gcctacgacc	aactgcttct	ctgaacgttg	agcagagaag	tatcctccga	. 540
cattgttatt	gtatgcaaga	ggtcagaaaa	tgagcagttc	aaaccttgga	caagctctct	600
ccctattcta	tatacatatc	tgaggacaaa	gcgaaacatt	gaggaaagag	gcggcatcca	660
tttgtttctt	gccgggcatt	tggagcagag	tatacgtatg	acccctttgc	gtgtcatcac	720
gtcgaggttt	ttcttgccca	tatgatggag	ccgaatcggc	ctctgtgtcg	cggttctcgt	780
ctatacttgg	gtaccgtata	ttttcagcac	gatggactca	tccttggacg	atgagcttgg	840
tccaagctgt	aggagcaggc	gatatgctgc	ggatgaaatt	gttacctctt	cagccggttt	900
gtcccaatcg	atacggcagt	cgtctttgaa	atcttcggag	ccggtcgagc	atcaacatag	960
cccggaagtt	gctcctgagg	atggagacgg	gttctccttc	gagaaacaag	tccactgtgt	1020
gcaccaatag	gatgcaccga	gagtagccat	acgttcgtac	aattcgccga	aagtctctca	1080
tgtcctatag	gcaacttctc	ttgcagcagt	acttcacccg	tatctattca	tgccggaggc	1140
ggaaggtggt	aactcccgtt	tccgtatcgc	catggctatc	gcgtggttga	taggggctgc	1200
tcctcgatac	atgggcagca	gagagcatgc	agattgattg	ttcccatggg	gggcatttgc	1260
catacggagc	gaggagcata	cggaaagcca	ctacgatttg	caagtgcggc	tgataagtcc	1320

tcctgtgcgt	atagtttgac	catactggga	crracellal	accaaagctc	gcgacccaat ataggcttgt ggagtgccgg	
aacagcaaaa	tcggccgttc	Cataaaaacc	aaccacagee			

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 626 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...626
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:889

		actatatttt	ttcgttagag	gtggagtaca	60
gtggctccgg aagcgatcac	agettettgg	accacacca	ctatcaatag	agtagacctt	120
	acacaagacc	CCaaaaacka	CCUCCUGGG	-00	180
	+ totottgat	ttaatattig	gccaccaacg	00-00	240
	atoocttcga	Cattkkrrrr	atttcaact		
stacataatc	toaaccgata	ataatagaag	aagaccgcgg		300
ttaatccttt gngagcacta	estatesass.	trraaatoat	gttgatgaca	attcggataa	360
ttaatccttt gngagcacta	agtatagaga	cccatacgat	800000000	ttacgtatat	420
taccgtgggt ggagaacgct	cccataactt	Cogalcacce	200066000	ctaatctta	480
	totocoggac	atacaccgac	aaagaaagac	0.00	540
catattccaa	ctttggcata	CCEALAAKKA	aggegueege		
ctttcaaga tcaccaatct	aatoapatac	agatgggatc	aaatacgaga	cattactctt	600
Ctttcaaga ccaccaacca	tatata	- 6 000			626
tttatggttg gagttggnca	Lacgia				

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1327 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1327

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:890

```
60
ggccgactgg gcttcctcac cgatgtcgat tgccacgagg cttcggagcg atcacacgcc
                                                                       120
tgctggacgg cgacttcacc atcgagaccc gttccctgtg gaagtgaccg aagacaacgg
                                                                       180
ctcctctccc tcctacgccc tgaacgagca gccatactca agcgtgaaac cggttcgatg
attcgggtga atgcctcctc aacgacgact atctggcggc ttacgatgcc gacggcctcg
                                                                       240
tggtgccacg ccctccggct ccacagccta ctcgctgagc gggaacgggc ctatatcatg
                                                                       300
cctgcctgtc ggaacttcgt ccttacgccc atcgcccccc actgctgaat atgcgtccgc
                                                                       360
tggtcgttcc ggacgacacg gtgatccgcc tcaagtggat tcgcgcagtc ggaattacct
                                                                       420
cttggtgctc gacggacgaa cagaacgttg ccctgcgata cctccatcct gctcaaacga
                                                                       480
gctcctcaca gctgcgaatg atccgtctgc gtccgcactc cttcgccgaa accctgaggg
                                                                       540
taagctcatg tggggagcag ccgtaagata aagacacttg cgacggtgac aacgagccaa
                                                                       600
                                                                       660
cggacactta ccatagacta ctcccataat ggaagaaata caaccatggt gctgcgcacc
                                                                       720
gaagatctgg tcaaacgcta ccggaacgta cggtcgtgaa tcacgtatcg atagaggttc
                                                                       780
ggcaaggaga gatcgtggga ttgttcgggc cgaacggagc cggcaagacg acgactttct
atataccacg gggctggtcg tccccaacga aggacggata ttcctcaatg atcggacatc
                                                                       840
                                                                       900
acccaatacc ccgtctacaa acgagcgcgt gccggcatcg gcatctggca caagaggcat
                                                                       960
ccatattccg caaaatgtcc gtggaggaca aatcctctcc gtcctcgaaa tggccggact
                                                                      1020
gcccaagacc tatcagcacg aaagctggaa agcctgatag ccgaatttca ccttgagaaa
                                                                      1080
gtacgcaaaa ccttggcgac cgcctctccg gcggcgagcg acgccgtgcc gagatagccg
ctgcctggct atatcgcctc gcttcatcat gctggacgaa ccctttgcgg tgtcgatcct
                                                                      1140
atcgccgtac aggacattca ggccattgtg gccaaatcaa ggacaaaaac atcggcatcc
                                                                      1200
tcatcaccga ccacaacgtc cacgaacgct tcagcatcac ggatcgcgct tacctccttt
                                                                      1260
                                                                      1320
tcgagggcaa agtgtgtatc agggcacggc cgaagagctt ggctgcgaac gaagtcgtaa
                                                                      1327
gggaaag
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 316 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...3\overline{16}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:891

gggtttctca agaagcacgg gtggatgtgt ccttcacctg ttcgtggagc gcatcaggag ctgtctgagc ggcgactcat gaactatatt cgaagacatg	ccacatgccg ccggtaccgg cggtgactgg	gactgtctga cctgcccaca agtttcgatc	gatgccttac tacaggatag ggccgttgca	aaacccgtca gcggatgcag ggtgggcgat	60 120 180 240 300
gaactatatt cgaagacatg cacgccatcc ggacat	ctccactaca	cgacggtgaa	gaacgaccat	gttcacggtg	300 316

- (2) INFORMATION FOR SEQ ID NO:892
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...2872
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:892

					anatattana	60
gctcgggacg (	gatttccgtc	ggcacctgga	aggtagcacc	accgatacgc	agasttstst	120
++-++	aaaataatat	tatogagago	CECCLLCCaa	LLLLBASSS	abaccccc	180
	acttcatctt	cacgatgcca	aagcaccgta	gaagacacca	444646464	240
+-++c++cc	atrataatta	ootoattaac	gaacttagtt	acccccacac	02002-0	300
	aastetatet	ttttttaggt	LLLECTION	CCACCECCC		360
	++~a++a^^a	tttcarrii.	PICILICAACE	CLCCECCEE	60000000	420
	andectatee	aattgaactc	aaacceggicc	LLaaataatt	-6666-	480
+	ataacacaat .	TTAGATTPEE	Paartratte	g ccc ccaccg	6	540
+ + c c + c c	aaccaacaaa	TCCCCTTAGC	ggctcttact	CCCCacccc	~6~66~~660	600
+	cttcagacac	TTOOCACCEL	attiggaacg	acguigue	6600000	660
acctactata	traggrater	cacgaacaat	gtgalaggla	Caccagacaa	60000000	720
accept coac	TRACCAGCAC	gatgettgtt	CCTECAAELL	gigacicic		780
	++c+tagaat	trotragace	Cacacgcgcgc	accitacgea	cageegaace	840
+	acateateat	ataaacgcgc	acacaaacgc	CKCKACKCC	CPPC#CP==+	900
++	castttoctc	ttatccgcga	aagatttatg	acc c c c c c c c c c c c c c c c c c c	000000	960
	9+++c++c+	rctttaaaac	Ligatialaa	CCACCCCCC		1020
+	actatacgag	agtggcgcaa	aggtacatat	attitutua	cccacaaoag	1020
1 <del></del>	+++++++000	- <b>00CAACOCEC</b>	taatactcaa	Laglallace	- Pagaratar	
	++ccacccaa	ocoapapatc	Cgaaaaggug	gatgegeeeg	uuuu66-	1140 1200
~~~+~~~~	CAGCCCGAAA	aagtgagata	Caguguagu	Cacagaaaag	444644	
00+0+0++C2	Cagaaaagaa	acgcatgcat	atattaatgt	acgegege	6~6~60	1260
acconcact	attrotrraa	agagagaaa	Cggaacggaa	aaggacaacc	accca6	1320
acattacaca	ccacaatttt	ctgtttcgat	gctccgcaaa	acgreece-6	554000000	1380
atttaatte	aaaaataaa	aaattctcgc	gccacgagga	aaaacccccu	caabaccc	1440
	CGCGCGCAA	tragagraat	atggttcgag	aaaattagat	Cggaacacac	1500
0000000000	acaaaaaaat	agctatgaag	Ctgtaccgac	agectegate	gccucuu-	1560
otaccatc	2000220000	tcagagccaa	gaagagcaag	Caacagacca	caacbabaa	1620
atconceana	agetecocca	ccaagagcag	aggaataget	gullguguu	cagcaaaaa	1680
a a a a a a a a a a a a	gagraatgra	ggtagcccgt	atagcacccc	accegggeat	CBC CB C CB	1740
acatacaca	agaacgttca	gcaaaatagc	tggcaggcia	LECALECTE	ugc bu cu- vo	1800
+actccatca	oststatoct.	CCGGCTCCTT	tttgttggaa	agecgeece	60000000	1860
caasstaaas	agaatactga	tgatcctgac	agccttgttg	CCCCgaaacc	account	1920
aggetecata	ttrttgaaaa	gaaagggagg	gattitaatt	acticices	00000	1980
acctcattto	tttotaaaaa	aaggctcttt	. ccccgtgtgt	. Cgcccggcaa	CCUCCCCCC	2040
actatogoto	rrgactgott	attctcctt	. tgcaaggagg	acacccccc	cegacours	2100
costacttto	acecetaage	tcttcgccaa	tgggcttttt	. ctgcaaggga	LCaggicgat	2160
caattataca	aagatgatgt	acagagaggo	cagcacgaaa	agggctgaaa	gggacggaag	2220
+202022000	tettgecace	gataaagtcc	: cgtacaaata	i accegggege	, cagageage	2280
cagacaaccc	acacccasas	ccgtgtcgat	attggtgaag	ccgcctatca	catttcggat	2340
catctaccaa	aatoatacce	tccggtgcga	ı gaggtttgt	: Cgcagcggci	, gcagaaacog	2400
cattletes	atctccccc	ttttggcata	tatgtatgta	tgggtctgca	gtggagtcgc	2460
totacacac	atragtrtra	actcgaatgo	geggattega	ccgaaggg	g aaagagaagt	2520
Letgecaege	accagicaca		5 55 6			

gattgcaacc	gctgatcgat	ctttcttgca	gtagtctgcg	cttccgtagg	attgcccaaa	2580
aagccagccc	ggtaatgcag	atattcccca	ttgtcccgaa	gtggccaaat	cttctattgc	2640
caaccaagga	gcgatgcaag	catgaggatc	tgcaatgagt	tggccatttt	tctctcgaat	2700
gcccatgctc	cccgtttttc	tgtttcttcg	aagtactatc	gcgcaacctt	ccatttttt	2760
cttcgttttg	ctactcgttt	gcattatctg	aattcacttg	cttgcgtaca	aatatagtta	2820
tgacaaatgg	agggcgtagc	acctcggttc	ggtcgcttac	gggtgagctg	cc	2872

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 542 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...542
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:893

gtaagaacgg	gatacagggt	cgaaataggg	tatgcttatg	gcgggtatgt	aaactttccc	60
gtctgacggg	gtaccacata	atactcgatc	gtacgctgcc	atcggcaccc	gaagtactta	120
tgcgaaggct	gctctcggcc	ttggagtgta	ttgttcgaag	ctgtcgggaa	atctcacttt	180
gggatctccc	atcaactgat	atttccgctt	ccgttaatta	cgagcttgag	tgtaagggct	240
tcgttgtttt	ggcctgacgg	tcattgaaag	aggctgagat	ccgataatta	ccaaagcacc	300
atcgaatcct	tggggtttcg	gttcaggcaa	gggagcgaca	tctttgtgac	cggattggtg	360
gtcagagtcc	tccgcacatt	ctcatacggn	tgagtacaaa	gaagtcatct	atgtcgtcta	420
tctcccgtcg	gaccgntact	agacacgaaa	gttgcccgat	ggaatagtca	gcttaccgct	480
tttttgagga	agagcaacga	ctgcttgaga	acggttgtct	gatagttccg	tccttcatac	540
tc						542

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 865 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894

		-totostaac	aagaactect	cccctcgaa	gaaaggtgca	60
gtcagattat	gtgcagcctc	ctgtggtaac	at accept	COGRAGAAAC	cgatggtttc	120
ctccatccgt	atcggtacgc	agaagatgaa	atacggcacg	teacteteac	atacgagtcg	180
						240
Lattigeogu	catcagatat	actccttcca	cggattgcac	ttcgccctct	tccgtcggga	
						300
tgggacgcca	tgcgggtcga	aaagcggatt	acttatatat	gccttcgctg	ggttcatagc	360
						420
						480
						540
						600
attgacgggc	agaccgtctt	CCCCaaaga	acage	catocttcta	ttcggacaga taacttctat gacaaaagtg	660
						720
						780
Cttatttlat	Cgaagaccog	ongacaatto	catttcttcc	tgactattcg	.gcatgacgac	840
tccgagcgga	grgcttetac	aagacggccc		•	. gcatgacgac	865
tgaaatcgtc	caaaaagttt	cacac				
-						

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2749 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2749
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:895

```
60
gctccgagga aagccaacag ccctcctccc ataccgcctg cagctccagt cccgggatat
ggactatate etgeccegta tgccggtgta taacggcace aaatgetgca tegaatcate
                                                                       120
caatcgggcc accatctcct catccgcccc ttctgaggag caaaggcaaa agcggcacct
                                                                       180
toggggcogc aaaaagattg ogcacatogc aggccacogt aaaaagogaa toggccaaag
                                                                       240
                                                                       300
ccggagtgcc gaagagtcat cgatgcgata gacctccgac agcaaaccgc cgcaagggcc
atgccctccc ctatatctct cccatcccga tcgtagaagc gaagcccaat gcctgtagca
                                                                       360
                                                                       420
tececagtee ggeategttg gtggegetge caegateeeg acgataaaqt taegacaace
togatocaga goatotttga tagototoco gttocgaacg tggtagtotg dataggattg
                                                                       480
cgccggtctt cggcacgaga ggcagtccgc tgatgctcgc catttcgatg aaagccgtcg
                                                                       540
toogtoagog gatatacoat aagaagooto gogoatttoo attagtggga gtgtgcacga
                                                                       600
acggctatgc gctgcccatc tgtggcagct atcagtaatc ctgcatcccc tctcccccat
                                                                       660
cagctacggg cagtaccatt acttctcaat cggacaggct gcccgtacgc cctcagcagc
                                                                       720
tgcttctcct gcctcacaga ggagagacaa cccttgaagg agtctatggc tatcacgatc
                                                                       780
                                                                       840
ttctcattcc gcatttagtt tacaacaaaa tccggaagca ctgcaaagca tccaacaaaa
                                                                        900
attccaaaac ccaagagaaa aaacgataga caaactaact cgatggctct taggtttttg
                                                                        960
ctctcattct gtaaacctgt atccggaaaa gcaaattccg gtatcaggtg gagattgcta
toggaaagga ctotttaagt catcaatttt ttattgtgot gttcgcaaaa aaacagcgac
                                                                       1020
actcagaata ctttcgtata tccatcgaaa ggaagtcttc ggctctgaca cctccatccc
                                                                       1080
```

```
gagaataaaa googattggg gottgaagga atgggaaaat ttgtocacoo gtotgtoott
                                                                      1140
ttctctgcat tgcttttcac ctcaatggca acaacaaacc tttcttgcgc aggacgaaat
                                                                      1200
cgacttcatc gtctcgttcg cgccataaaa tacctcgaaa cgatgaacaa aagcctgact
                                                                      1260
gacgaggtag gctcaatgcc tgattcgaag attcgccccc aggacttgcg atcaagcatc
                                                                      1320
gctgttcaaa ggtaaaaggg ctatacacca tcttcaatgc attgttatag actgcagttt
                                                                      1380
gggaatactt gccttcctcc ttgccatatc ataaccaaac tctgaagtcc acaaagcaat
                                                                      1440
ccgctttcat ccaacagatt gatatatccg ccaaggtcac cgtattaccg gcatcttgga
                                                                      1500
gtgagcctaa catcttgtta aagaaagtaa ttctcccgaa taggcagccc ccaattcgaa
                                                                      1560
agtccggcaa gcaaagccgg tttacctatc ggtgtaccca tcagaatgtc cttattgtag
                                                                      1620
ttgcttcgat aatggcagct tgaatatatt ggctgaaacg gtcgtctcat cggtcaggga
                                                                      1680
agcggcaccg ggatatcccc cataaaacag atattgttga gcgagaaacc gaagcagtct
                                                                      1740
ttcatctcct gatagctcca atggtcatgc gtatttcttc gaatcgaccg gccagcgact
                                                                      1800
ctgacaaccc ctttccaaca acacacgact actgcccaac agcaacacct tgatattacg
                                                                      1860
gtatggaacg tatcatcgtc ccactctttt ttcacgactt cactccaatt acaatctttt
                                                                      1920
gtatctcgtc gatcacaaga ataatgctct cccactcctt gcctccttca ggctacggac
                                                                      1980
agcageceaa caateggaaa tecaageaeg tteacagteg gaacattate ggetgagaag
                                                                      2040
aactgatagg gtgcatccag tccttcagca cctgcttgac aaccgttgat tttccgattt
                                                                      2100
gacgagecee attacgaett gaatgaatet eeteegatet ttaagaegat etgtaacaca
                                                                      2160
tgatactctg ctcttttata catatccgca cattttactc agtaggtgag tattttact
                                                                      2220
cagtgcaaat ataataaaga catttgattc ataacaatct cttacaagtc aataaaggca
                                                                      2280
atgtgattat cccataaagg gtggattatc atgtattttc caatagtaaa tgcaacaccc
                                                                      2340
tataaacaaa aataccccga gggataatcg ctcggggtgt gaagccaaca gcccacctcc
                                                                      2400
ctaccgcctg cttctcctgc ctcggcagag gagagacaac ccttgaagga tctatggcta
                                                                      2460
tcacgatctt cttcattcca cttccggctt atttgcagcg atagtcggca; gtccgcaagg
                                                                      2520 🛫
atgcaagcat gagaggaaaa gccaaatcac aaaagagcca gtatgatccc ataaggcatc
                                                                      2580
caaagactct tggagaaagg caacgccaat agttcatctt gatcttacga acatccatat
                                                                      2640
cgtagattcc ttgtgcggac ggtcttcctc catttttgct acgcttcgtt tgtatgctcg
                                                                      2700 🕺
cgatacttcc tttccagttg caagtagaaa gcatccacca aggccatgc
                                                                      2749 🕴
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1167
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:896

```
gagacaaaat aatcaccgca ggcggtatac acggcaccat acgcgaggtc gcgaaaaaga
                                                                        60
tttcttnntc gaaatcgcca atggcgtgaa catccgcacg ataaagggtc tgtatatgta
                                                                       120
tctgctcgcg aagcggaaac agacatgcca acaagaaaga ctaagctgca taaaagcaat
                                                                       180
ctatcggagg aactgaagag acgggtaggt attacgtcca ataacacttg gcataaggca
                                                                       240
cccccatctt tcagttcctc atcgttctcc accaaatccg ctaaagggaa tgaactcaat
                                                                       300
ctcctcaatg ccgatcggaa aaaggggaaa agtatagaca aggatccgct ccccgttcac
                                                                       360
gccgtgggag gaacgtcctt gtctttttcg ctttgtggtt ctctctgccg ttttttggtt
                                                                       420
tatgcagagt ctgcaggatg ttacaccact tcattttcga ttcccatctc ctattccgag
                                                                       480
ctgccgccgg cataggagtc tcaggcaggc tgcccgaccg cttggacatt atgctgaaaa
                                                                       540
```

			annagatte.	tetecgataa	tatctcccca	600
tcagggtatc	gtgcttctga	cctataagci	gaaggggttc	constaggst	ctggtcgaac	660
						720
						780
						840
		a+a+caau:(CPLEAGLACE	EURUPCCCC		900
aagtgcagaa	gcgttggcga	gcaccgggcc	ataccccat	coatgatate	gttatcgatc	960
ttggagagcg	atttctccgg	tgacatageg	acgeeeegae	gascaascot	gttatcgatc tcgaactgcc	1020
		+0000000000	V.aac caace	Fac		1080
		+ ~ = = 0 0 (1 1 1 ()		0000000	0 0 0	1140
tacageteae	actneceaca	togoactaca	aagaagtatc	ggaagctatt	tgcaaacagc	
Lacageceae	ccgtcctctc	cggattc				1167
cgttttctat	CCECCCCC	- 66-34-				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...522
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:897

gggcaaacac aggtctcctt tatcggcaca cgcacaaggg acatcggaaa tgcaaatcgc ctacgacata atcgtcagga	gtcgaagttt atctgaaatt gcacatgtcc ggagaggcta tttcgttagc tactttgcgc agccaggtcc	acgtatctga tctcactagc aaaagacgat tatcggtcga gacagcatca tctccggcct cccggtgaaa	gagatattca tggccaagaa ccacggcatt agagccgttt cgattgtgtc gtgttaccgg	gctccacctt gtcgtgtgtc gcagtcgtcc taacgcatta atatccaact taatataagt	ggcaatggca ttgtttccgg tcttacagtc tcaacattgg	60 120 180 240 300 360 420 480 522
atcgtcagga attcgcccct	agccaggtccactgatcgaa	caacaaggag	ggtaaagatt	gg		522

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 619 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898

```
ggcgaaggcc cggaagtctt gacgaagctt ggcaatgacc cttcggccaa cctttgaatt
                                                                        60
gctgaccatt catttcaaag tcgaacgatc cgtccgnact atgtgttctg cgggaatatc
                                                                       120
gctttcatag gcttcgtgta ctacatcatt ttgcccgtga atgtaccgga gagattgatg
                                                                       180
gcgaagtgct cggtagacgt accgtagcaa cgaaatagcc gtacagattc ggagtgcgta
                                                                       240
catagettic acagagatet eggettgtee egttgttitg teegetteea eagegtatag
                                                                       300
atgetteegt ageggettet etgeeatgta eegeegaget ggagtegaae gatttgttgt
                                                                       360
aggogattot tocotocaga ttoacaccat atcottogat actocatoot tgtogttgta
                                                                       420
gatggtacga atgatccatt cttgccatcg ctcgtggttt cgaccttatc ggatggtttg
                                                                       480
aactgattgc gataaaggtg gagaaggctt ctcccatgat attgaattgc caattcgtcg
                                                                       540
ctcttgtggg taataatcga aagaagcact gatgccttcg tggaacgtct tctttcagat
                                                                       600
tggggggaaa ggacacgct
                                                                       619
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2762 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...2762
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:899

ggtagtactc	tgcctttcca	aggacctgcc	ttttgcacag	gctcgcttcg	tggtgccgaa	60
				actgctttga		120
		_		tcgtgccgtc		180
				atcactcaag		240
				ccaaatattt		300
				ctacaaacaa		360
gcccttctct	cttatcataa	aagaaaaagg	ttgaggaatg	gctgtaaatt	gtgaagagag	420
				agtatttggt		480
ttttctgtcc	aagacgaaaa	gaatggagtg	cttcatcctg	cagtatcggg	atgatcggat	540
agagcggtta	tccataggac	gagccagctc	ttgatagata	aaatcgtctc	gaatcctata	600
tcggcagcat	cctgccgatt	gttgccatag	aaaatccatc	tatgcgtgcc	caatagatgg	660
ctccgaggca	catcggacac	ggctcgatga	agtataaatg	gtacatcccg	aaagatcgaa	720
agtgccgagc	cgcttcaagc	catacgaata	caattcactt	ctgcatgcgc	tgtggggtca	780
ttgtgagggt	cacacgattg	ctcgtcgctg	caatgatctc	tccatcttt	acttcacagc	840
				aacggatcgc		900
				gttcaattgt		960
caggttgtcg	gcttatgctt	gggagtagat	acagtttcat	tcagagtgat	tgccgtagga	1020
gtgatcctgt	caaacggcga	cgatagagca	ttccgacagc	cattttgaac	gttttcttct	1080

```
cataccggta tgttgcataa tttcctcggg cgaactctta tccccgaggg aagccgaccg
                                                                      1140
cctcttcttt ggagcatgtg tagcagtcgt tcgctccgga gtcaatacgg tcatagccta
                                                                      1200
toggtttgag cgagaggtcg attttccatc gtcacggagg cgaatcacga aagctttcac
                                                                      1260
ttgtgcccg atagcaaagg catcggtagc gtatcggaat agatcatccc ccaatgggta
                                                                      1320
tgaccacgat catgcgataa cccggatcga ttcgttcgta aaccagtgcc gaaccttgtc
                                                                      1380
cccaggggag taggatgggg gaatgttgcc caaatgtttg gcaatttcgc cgagccaacg
                                                                      1440
atcttaccgc tcacatgatc gatataagca agacgaaata gcgtccgcct tctcgaatga
                                                                      1500
gctgcgtctg ttctcgaaag gaacgaagag atccttgtgt atgccccatt ccatatacgc
                                                                      1560
cccactattg tgacggagac ggcatgcagc agagccacct gtcccacttc gacaagcgcc
                                                                      1620
gcatggtggt ggcgatgagt ctgccttcat tgtcatgata gacgaaacct ccacttccat
                                                                      1680
accaggtgca gcatctgagg ggaggtagcg attggcaaca aaatatccgt atcgcctcca
                                                                      1740
tegagatatg ceccaatgga tacgtaeggt egatggteag acgaectatg egteegaget
                                                                      1800
ggtatttgct ccgttcatcc tccgggatta ctcaagcgta actgacgatt cgtcgcgcag
                                                                      1860
gagggttgca ccaaaataga ttcgggcata ccatcgcgct gcacctgaaa gcgcacgaag
                                                                      1920
taatctgctg gtcgtttacg tacgaacgga agaagaaaag taggcaaaag ccggcttgta
                                                                      1980
tttgggctga gccatcatgc gtgcaatctc tcgtagttct tgggtgacca ataacgacac
                                                                      2040
ccggccaaac cattggcacg gtgaaggtgt cttcctcagt acggtacttc atgctctttt
                                                                      2100
tgatgaatct ttgtaagcag aggagtactc ttcggatccg gacaaagcag gaatacgttg
                                                                      2160
atactgatga tacggtctcc ggctttcagc cctgcctttg ctgccgagag tcggggtcga
                                                                      2220
ctgctgccac gagcgaaagg tcgttggcct gatatacagc cccgtataga agtaacgctg
                                                                       2280
actocgoaga oggaacgtog ggtotoacga tagogaataa acgggaacto catoatoato
                                                                       2340
aaaggcacgt tgatcgcgca tattctgcca actccaaagg tgtggaaagg aaatcattcg
                                                                       2400
atcgcattgc cagaaaattt ggagattgtt cctggcattg atcagccgta gccgagctgg
                                                                       2460
attacataag gagcattgat ctcctgtgtg ccggccggct aatgggggatc gatatcatcc
                                                                       2520
tcttgtcacg cggagaatac tgccaagatt atgaggggcg gaactattga atgaggtaaa
                                                                       2580
 gagettgttg ttgtcgacag ataataacaa tcgacgatta catcgggatt gttcagcgtc
                                                                       2640
 tecttettee catggeacte agatatttge ceaettettt gtagacaget atateatete
                                                                       2700
 ctcgttgtcg ggcgaagaag ctgcgaaaga gtatgtacgc agatggtaaa gtccgctttg
                                                                       2760
                                                                       2762
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...573
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:900

		~~~~	tratactest	caategcaag	agatttgttc tcctgatgat	60
nagttgctgt	gcgcaataat	Ragagragga	CERCECCE	cocatttaca	tectoateat	120
antanttate.	+ a t t a t t c c a	tcatgcgtcg	caaggaatgg	gcgacccgca	200-00	180
+-+a+aa+aa	agacgattgt	gactacgaat	tgatccgcga	Lalagegaag	uuu6-60	
	coattotaca	ccootttcaa	atggatagca	gccgtaataa	gagagaatga gggagacttt	240
tgagcatgtt	Cgattgtata		nananttato	gatttttgtg	gggagacttt	300
aggtctcgcc	gctatatagg	aggiggagag	gagageeacg	stantages	acttaggett	360
attcgagaca	agagttcggt	atctgcttgt	gcactcttct	grgaarggra	gcttgggctt	420
+ + 0 C O C C	catogototo	tatogactca	tcgcagcatc	Lattiggaat	4088	
LEBUCCEUGE	accettagtg	tntocotaaa	ppcaaatccg	gågcagaaga	gatagaagcc	480
ctacgaaaag	ggacttagtg	curegegeann	88		_	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2571 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...2571
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:901

tccccgagga	gatcccggtg	gacgaagtga	ttgtaagtat	cggtgtatcc	ccaatccgct	60
	actatttccg					120
	cagctctccc					180
ctgtgatatt	ggcgatggcg	atggacggaa	agcagcagct	gccatgcacg	aatatctgaa	240
	agccatgact					300
tcctcattcc	cttggctctt	gagggtagtt	ttcactaccg	attgccgagg	ggttagccga	360
	gtggggatgc					420
attatcatcg	gactgtccga	caacgtccca	atctgcaaat	ttcattcaag	gaggttctct	480
tcctgcctga	gataagccgt	cagttactgc	ctcacagctg	agtctgtggc	agtggctgtg	540
gcttattaca	tatgtacgca	gggagaagta	ctccgtgctg	ctctgcctca	gcattactac	600
ccgagagcca	taccgtcatc	cattataata	cggacttgaa	gccgacagcc	ggcttagtcg	660
tgatgaagag	gagctcctcg	atatttggag	tcggcaaaag	gacgaaccta	cacgcttgac	720
gccctgcaaa	aggcttcggc	aaacgagcga	ttcgcgcttt	tacctccttg	gtcgaacgag	780
gggcatacgg	ctggaggaag	aagtaaaaag	ccgttataag	cccaagtcag	aagattcgtt	840
cgtctggcag	agcctttccg	gacggaaaag	acttttgcct	cgttctggat	agtttgcatc	900
gtgctcccaa	gcaatccgcc	cttttgcttc	atgggcagag	ctgataacag	agcactccct	960
cccatattcc	tctccgatgc	gcaaaggcta	ctggcggagt	ccgatcctca	tgctacagtc	1020
accctttccc	tttgaaaaag	aaagggattt	ttctatccga	atctgttaca	cactcggtat	1080
	ggcggaggtg					1140
attcaatcgg	aagagagttc	tacagactcc	gcagtacggc	ttctctacct	caaaaacctc	1200
tttctctcct	ctatacgcat	gacttcgacg	caaagaaaaa	caactcttag	aatggacgga	1260
	cgttaggagg					1320
	tctgtccaca					1380
tgcctttgaa	agcgatgcca	aaagggtgga	agtgtggaac	aattggccac	aacggaatat	1440
ccttgcgtgg	tgctgggtgt	tcgatcggca	ttttcctgcc	attccgtcgc	ttgcgattga	1500
ttatcgtgga	cgaggaacag	aatacctcta	caaacagcag	gatcctgccc	cccgattcca	1560
tacgcgacgg	tggcagctcg	actcggccgg	atccacgact	gccctgttgt	gttggctcgg	1620
ccactccttc	tgccgaggtg	ctccaccaag	tgcgccacaa	agcctggaac	tgatcacctg	1680
gccggacgat	cgggttcgcc	cccgattcga	tttggagtca	tagacatggg	caagatgcgc	1740
	aggtcggtgc					1800
agacgattcg	gcaaaaaaaa	tggccgtcgt	cctccaaaat	cgaaggggct	tcgctccgta	1860
	gctcttgtgg					1920
	ttcctgtatg					1980
					gcaacctgtg	2040
gggtatggag	ccgaaagata	gaggaagagc	ttaaaagacg	tttccccacc	gtctctatcc	2100

		ccatgagccg	aacgaagatg	gacgaagctc	tggcgctctg	2160
tcagaatgac	agcgaracgg	CCatgageeg	accounted	t caannocaa	atctataaco	2220
gaagcgaaag	aggtggatat	acttgttggc	acgcaactga	tcaagggcaa	geetataag	2280
aacatotago	tottotaged	gtcacccagc	tggaagcata	ttgggtttcc	eggattteg	
	caaacttatc	agcactctat	cagctcatgc	ttaggagcgg	agcctcccgt	2340
cgcccacgaa	cgageccaet	ccaaccaact	cctttccgga	tttattgcga	gaaggtgatt	2400
ctatacatac	aacgaacaac	CCggccaacc		cttttcttcc	accttttagc	2460
aaaggctttt	atcggaaaac	aattggagga	aaggcaaacg		accttttagc	2520
cooctoatac	gaatcgagtt	cagagcaggc	gaagagagct	cgtggagcga	atcgcttccg	
CBBCCBGGG	ctctttggcc	occcatctcc	ggagcagagt	ctctcccccg	t	2571
actatgccgc	CLCLLEBECC	600000000	99000	•		

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 584 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...584
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:902

ggggggggt	tttctctgtg	ttcgatgcgt	ttgcaggaac	catcagcacc	aaaactacag	60
gggaaggcac	canacatacc	ggcagatcga	toocotacta	cgcacatagt	gatgcgcaga	120
atataacatc	gaagegeace	becagacega tecetace	nengeetett	-00	tagaaagcct	180
ttcggaaatc	agtegeeget	tgcgtgctcc	acageeeee	cgggggccag	accatatora	240
tcggtacgag	tcttgattcc	acaacgacca	gttctctgga	cgtggatgcc	acgacaccca	300
gctcgagccg	ccccgactgc	cagttcaggg	cttctatctg	atagccttgc	tgccgaggtg	
tttcagcgcg	atctcttcgc	cttggcgtcc	gcggtcgtta	tgacggccat	tgctactgtc	360
gagacetttt	ttttcgttcc	ggctgaggat	gagctctcta	tgtgccgttg	ttttttctct	420
gagaccccc	+ = = = = = = = = = = = = = = = = = = =	atgatator	coetttecte	cacctctccg	aaagactcat	480
tccaggatci	Lacctacage	acgaatatge	ngacaaagct	atatatocac	ttacgagana	540
tcactgcagt	ccgaaaacac	geatettegg	agacaaagcc	atatatgcac		584
gggatattga	tacccagctt	gcgcacttct	atattgagag	tull		304

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1075 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1075
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:903

cgacgtagct	tgtgtgaatg	gcgatttcct	gtacaacgta	ccatgtttcc	agaagccctg	60
atecetecac	aaaaagatgg	taaaccgaca	ggtactgtgc	tatcatagcg	tctacgatca	120
accaptotte	ggcttctcct	atgcgcggca	ggatgagatg	aacgaaattc	tgtgcgaaaa	180
acacccgaac	aacatcagcg	tactttcgga	ggtgtcacca	tgaacggtat	gtttgctatg	240
otogaaagta	taaaaaggat	ggtgagaaga	tgctcgacac	atggactgta	ttcgcgaccc	300
ctcgctgctc	pttcgtacac	ttgtcccgac	caaaatgcag	gttcggctcc	ggcaaatatc	360
totgoototg	cacagacatt	cgaagtagct	tggactataa	cggtgctatt	gctacgctct	420
ctgacgatgg	tgatatggtc	gcactgctat	cgtgaaagac	ggtaaggcta	tcatcaaatt	480
aaatoagagt	togotgatga	aacgaacttg	acgctcaccg	tagtaggata	caataaggta	540
ctotoataaa	ggatgtgaaa	gtggaaggta	catctattgc	cgacgtagca	atgataagcc	600
ttatactota	gctgtatcag	gtaagacgat	aactgtaaaa	gtcctgctgc	cgggctgacg	660
atcttcgata	tgaacggccg	tcgtgtgcta	ctgctaaaaa	ccgcatggta	ttcgaagcac	720
aaaacggcgt	gtatecettc	gcatcgctac	tgaaggcaag	acgtatacag	aaaaggttat	780
agtgagtaat	tcacactgca	attctctaat	aagggctgtg	ccgaggaatc	catcggcaca	840
gccctttttg	aattattggc	actacgccaa	gagactgttg	agaatcaggc	gagaaaagag	900
gatgctaaag	gtcgtaaata	acggctcaaa	ccaatggccc	gttcatctca	taccatggtg	960
cocaappoct	acagaccata	acttgagatt	atgtgccata	gtgcttcgtt	ttaggtggag	1020
atatggtctt	tattgaggaa	aaatattctg	gttatgagag	agaaatcttt	ttttg	1075

- (2) INFORMATION FOR SEQ ID NO:904
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 723 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...723
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:904

cccaatccgt	cectccetta	agaatagagt	tgatctgccc	catcggtaga	acctgtactt	60
ccgtgtcgaa	atcgaatttc	ttgataaaga	tgttattgct	ctgacgaacg	ctaccatccg	120
gccatcgggg	ctgaatgtag	ggatcatact	ttgccgacat	gctcgctcag	tggttttacc	180
aaatteceec	gaacatatag	tcgtagacgg	cagcacgata	cgaatgccga	tagatgctct	240
ccataccgta	aagagcaaaa	tatgatgtcc	ggtactgctt	acctcgtagt	tctgatttgt	300
ttaaacgggc	attcgcgtgc	tcgttcgaca	ctgaagagcg	tattaccgcc	ttgccggagg	360
cataattgta	gcgaatgata	gccgttcgct	caggttcatc	tccgtatagt	gttctccatc	420
cggcatggag	cgtattccac	tcctgcactg	cgagcataaa	acattccgct	cgtgatttct	480
ttcaaatcta	gggtttgttc	cccgtctgag	ccatggcaca	catggttacg	atgccaagtg	540
cagaattatt	accggtcttt	tcataagaaa	gtgtattgta	tcttcttaa	gtggtttatt	600
gcttagcgtt	tcaatgcacg	atccatctct	cggcgatatc	tcgctctttg	atggatgcac	660
gtttgtcata	attgnttttt	ccctcggcca	atccgatttg	cagcttggcc	aatccctttc	720
atg	C			1	•	7.23

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1306 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1306
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:905

```
gattttcaac ggtttgctct tcggcgacag cctgatggat tcctcttcgc ggagaatgcc
                                                                        60
atggaagget atgcacagat getgggagaa gactategte taacaatgee gaagecaate
                                                                       120
tgcaagggct tccttctgac cttttggcta tatctacaag caggaaaata ccatcgctta
                                                                       180
ttgcgatacg ggattgtctc cacgcgcatc aatacatata cttacgaagg cggtgcacat
                                                                       240
acggaaatac agtccggttt gccaacatcc ttcgcaccac cggcaaggtg ctcgagagcg
                                                                       300
agatatattc aagatcgact atgcggaaag gctgtccgca ctctcatagg acaattggtg
                                                                       360
cacgatttcg gcaagaccac acctgccgaa ttgatgcaat aggtttcttc aacgcagaag
                                                                       420
aaatacagcc caatggcaat ttatgatcga tgacaaaggt ctcacatact gtttcaatga
                                                                       480
gtatcagata ctgcttatgc cagaggtgct gtctatgtcc gtctcggata tgacgtattg
                                                                       540
ctcctttgct aagggatgat tccccactaa agcgttactt gccgtagccc ctccttttgc
                                                                       600
ttcgaccgat atgaccaata tgcaggagat acccgaaagc cgctgtccca accggcaggt
                                                                       660
accgagatca togagaaata cttocccact tgtocgaacg gcaacgcgaa caattogago
                                                                       720
aaatgggagg gctgtcacgc attggaatgc cctcatcaat gtcatttccc gaaaggatat
                                                                        780
agacatttgt atctgcacca tgtgttgcat tctttgggga tagctcgcat gctaacttca
                                                                        840
aacccggcac aagtgtattg gatttgggta cgggtggagg ttccccggta ttccactggc
                                                                        900
gattttgttc cctcaagtct ctttcctgct gtggacagca tcggcaaaaa ggtgaaagtg
                                                                        960
getteggeeg tagetgaage ttggggettg acaatgtgeg cactatgeae tgtegggeag
                                                                       1020
aaagcatagt gagaaattog acttoatagt cagoogtgoa gtaatgaago tgagogaatg
                                                                       1080
gccaagatct gcaggaaact catccggcgt gaagatcagc naaatgcctc ccgaacgggc
                                                                       1140
                                                                       1200
ttatctgtct caagggtggc gagcttcaag cacgagtact gccattccgg aacaaggcna
tgacagagga gctatggccg accttaagaa gagtatttca aacataaaag tgtctactac
                                                                       1260
                                                                       1306
ctctatgaca cgacgaagta aagatgtcac ctcaattcgt gcagaa
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 603 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...603
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:906

ggaacttcgt	ctcctgatcg	atagcggacg	ttatgacagg	gctttgccct	agcccaacag	60
ttggtggcca	aaaatccaaa	gcatgccgat	aataactaat	gctagggctt	nttctgtaca	120
nggctgaacg	ctacgaagaa	gctattgtcc	ccttcgggtg	gccgtaagcc	ggcggagtga	180
tecctateae	atgttgcgga	tgcttatgcc	aaagagtatt	tcttctccga	agctcttgct	240
gractgaaaa	acagaaggtt	actcttgtga	agaaaaaaca	ggaaacagtc	tccaagatgc	300
Consatagac	cotatocoac	gagctgtgcg	cttactggac	agaccgaatg	ggtggaggtg	360
of a care	tacogacgaa	taaagccgat	ctctgtcggc	ctacaatctc	atagccgata	420
acagacagcg	caestagata	aaggaaacca	8000080000	acttcttttg	tcaatgggcg	480
acggicggct	cgaacgggcg	aaggaaacca	caccatocac	tttncagcct	gratgaagnn	540
cggcgaccac	toncatgat	ggagaaaggt	teceeteas	assactcatt	cccattcaa	600
	tggcaaatgg	ggcaatgcga	LUCULUE	aaaacccacc	cccgacccaa	603
tga						005

- (2) INFORMATION FOR SEQ ID NO:907
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 595 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...595
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:907

					tanaaacata	60
acagagggag	ttcggaaccc	tctccttcgt	tetecatttg	catcttggca	Lgagagtata	
taagagagtt	tgagctatgg	ccgtcggatg	ttttttgctt	ttcctgctat	cgggtgttgg	120
aacataagat	cccatgagcc	aagctcttgg	tggtatctcc	acttttgtag	tccactatgc	180
gccgacattc	ctcattaact	catcaatgcg	gtctatgatt	ccgtgtaacc	gaacccggct	240
accatgctaa	gggagaagct	gcctttgact	ctgcgctccg	agtctatgta	gcgaagggag	300
ccaatgattt	gtnatgctcc	aagatccgcc	gtacatactt	ctcatcatga	tgcaataaag	360
				ggagatattc		420
				caaccaccga		480
				aacttcatgg		540
				attctctccg		595

- (2) INFORMATION FOR SEQ ID NO:908
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1072 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION  $1...1\overline{072}$
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:908

			accogggaato	ctccgattgg	gcgcgtattc	60
ttgcaaaagg	agctattcaa	aaaaacacga	accegaaace	aatttttt	ttcccacgcc	120
						180
		CCGCGTTTUA	VVAVLARCAA	40666	00	240
						300
						360
						420
						480
		ataatcaaca	CPACEALLUL	EE COMPOSED		540
		2002220021	ITAALLLLLL	ECECHODO-	0-00	
						600
	+ +	tatattaaac	I CCCCCCEAA	CCCCCGGGG	00.	660
		20111707777		CCCCCGGGGGG	D00	720
		0077770000	T D D L L L L L L L	CEUUECCCC		780
agtgaaatag	agailtggit	tanganttt	caaattccgt	gccgatgatg	agctattgag tttgctgata	840
tttttacgat	ggtattcaag	Cagogecee	ctaataaaat	tcactetttc	tttgctgata	900
gttgtccaca	taggtcttca	ggtgcttacc	gragegaac	ttcataaatc	tttgctgata ataacgtctg	960
acaggagcca	. gtgcatcgac	cgcataaggc	aggaaacgag	antotaaaar	ataacgtctg	1020
		ttaataattt	PLALLERANC	agegeadad	-6	1072
aattttaac	attataagaa	catgatgaac	ggaaaaaggt	Lyaalligg	,	

- (2) INFORMATION FOR SEQ ID NO:909
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1010 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1010
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:909

```
ggctcaagag attctggcca agatggataa cagcctgccg cgtctggcca atgcgacatg
                                                                        60
                                                                       120
acaagagctg accggtagct tccgaggtat gggaccggaa aagcagtcac cgtgatggca
gcaatggaac tgtcccgccg tatccctcgc aagagatgcc ccgcagagaa tccattaccg
                                                                       180
atagtcgaat ggcctacgaa ctataagccc atttctcaca gacctgccgc aggaagaaat
                                                                       240
gtggggttac tcctcaacca aagcggaaag ataatcagca tggagaacct tagcgaggag
                                                                       300
gtgtatcgga gacttcggcc gatgtccgtc tgatcatgca caagccgtct ctcatcttgc
                                                                       360
                                                                       420
ctcggcaatc attctggcac acaatcatcc ttaggaacgg tacgcccaag tgaacaggat
attcagctta ctcaaagggt gaaaaggctg ccacattgct cggatttcga ctgaacgacc
                                                                       480
atctgatcat ggtgacgatg gggcatattt cagtttcgct gacgaaggcc ttctctgatt
                                                                       540
                                                                       600
ttctctgaat ccatacaagt aaatagagag tcggactctt tcttcttgtt gaaaccgatg
                                                                       660
agaaatcaac caccggaaca aaaaagccgg gtcatccttt atatcgccgc atagcaagag
tacccggtgt cgcataggcg acatttaggc agatagcagc ttctactttt gtgtcatcaa
                                                                       720
agaacaatga togataacat aagaaggaga otogacaatg gaaaagaaaa tgttttgota
                                                                       780
                                                                       840
tcaagccagg aaacagccgg caataaggga tgtatcctca aagggtatgc cgtaggactt
                                                                       900
tagtacaget aatetgatgg attgetegte tttaacetea aagtattgee ateataatga
                                                                       960
cttctatgag gcgtgccgga gtgaaagccg aaccgaaagg ctgcaaggcg atcatggaat
                                                                      1010
ctctattgcc acaataccaa gccaactcga ctactctcca tagccaacgt
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1274 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1274
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:910

gaatcgacta	ctctctattg	attaaggaag	ggctttttgt	acttttggcg	acagaaacga	60
taaataactt	cgaaacgatg	accaactcca	actccttaac	gagagactac	agacagcgga	120
ctcattcttc	ctgatggccg	gcccctggcc	atagagagcg	aagatatggc	actgcgcatt	180
gcagagcgaa	tagtagggtg	acttcccgac	tgggcattcc	gtatatattc	aagggatcgt	240
accgcaggcc	aaccgctcgc	gtatagattc	cttcaccggc	ataggcgacg	aaaagcactt	300
cgcattctgg	gcaaggtagg	ccgggagttc	ggtgtcccga	cgggacggac	atacatgaga	360
cacacgaagc	ggctatggct	gccgagtacg	tgatgtactc	cagataccgg	ctttcctctg	420
ccggcagacg	gatctgatcg	tgcggcaagc	ctacaccggg	cgaatcgtca	atgtgaagaa	480
agggcagttc	tctcggcgaa	gccatggctt	tcgtggcacg	aaagtgcgtg	gacagcggca	540
cagccaagtg	attctgaccg	agcgtggcaa	taccttcggc	tacacggatt	ggtggtggac	600
taccggaata	ttccggcaat	gcgttcgctg	ggctttccgt	agtaatggac	gtgactcact	660
ccctccagca	acccaatcag	ggtagtgcgt	gacgggggga	aaacccgaac	tgatagagac	720
catcgcgaag	gctgcatagc	cgtaggtgcg	gacgggcttt	tcatcgaaac	gcatcccgat	780
cctgttcggc	caaaagcgat	ggagccaaca	tgctccgact	ggatttgctc	gaaggctgct	840
cacgaagctg	atgcgcatac	gggcagcgat	cagggattga	gctgcaagta	accgtcttat	900
cggccgatta	cacatattgt	aggaaggtcc	ttcaggaacc	gaaagaaata	tgatcgagga	960
ggaaacgagg	ctgattcgct	ctcttagaaa	tcccgacatt	atgtccccaa	ccggcgaact	1020
cctccttcct	aacaagagtc	gcagcatccc	tctcttggct	gtacataaat	aacttgtact	1080
ttgtgcaact	ataaaaaaga	atcaaatact	${\tt attccccttt}$	tatggaataa	aaaagactac	1140
acgtatcgaa	agccgatctt	atcggagaac	gcgagaaccc	ggccatattc	tatatggcgt	1200

- (2) INFORMATION FOR SEQ ID NO:911
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 557 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
    - (ix) FEATURE:
      - (A) NAME/KEY: misc_feature
      - (B) LOCATION 1...557
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:911

tgcgctatgt aatggagcag attctcttg agttgtgagc gcagttccct atttctcgg acgggatttg ctctattatt tcccaagcgg attcttcacc tgacggctga gaaaatccgt gccaagatgc cgttcataga acctctgctc tccggagaag cccaggtcgg aaggtgtacg cattggtga catgtctaca tgcagctctt cggcaaagaa gccgggccat acgggagcga acatcttcgc gagactactc catgcagata gctgactcca ttggcctcct gacagtgtg agtgcaaaga cactcatgga gaacttttcg ttcgagccg gtgcgttcgt cccatgtcga tgaactcctg ccagctgatg ccaagtctgc gagaaaatgt cccatgtaac gccccaaaaag ctcttcatcg aagtagtcat gcctgccggt acaggggtgt gaaccgtgta gagcgaggag acgttgagca ttcaanggca atatcgaaac tcaatccctt tggttcacat agtcnggccg acgttgagca ttgatca

60

120

180

240 4

300

360

420

480

540/ 557

- (2) INFORMATION FOR SEQ ID NO:912
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 881 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...881
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:912

caaagatacg	gtccatcgct	tggtgcatga	agaagaagat	ggccttcccg	ccttattata	60
gatgtatatg	gacatacggc	ctnatgcagg	cacacagcta	ggtatgccnc	cacgcacgan	120
cggatatagc	gaaggctctt	atagcgagac	tgcaggcttg	gtagatgccg	tttattacaa	180
gtcggacagt	actctacatt	caaagccgga	ctggaatcgg	ccgatggctt	cctgatcggt	240
tcagccaagc	cgaagcagag	tacgaaaacg	gacttctctt	cctgcccgac	tggacaaagg	300
acagaagacg	gggttcttta	tcgaccagcg	agagaacagg	gcctgctgga	ggagtatgcc	360
tccggacgta	aggtgctcaa	tatgttctgc	taagcggtgg	tttctccctg	tatgcaatga	420
gaggaggagc	atacaaggta	cctcggtgga	tagctcggcc	agagccgtgc	atctgttgga	480
gaaaaatatg	cactgaattt	tgccggagac	gatcgtcacg	aatcttatgc	cgccgatgct	540
tccatttcct	tgacgagatg	gctgtcggag	cttatgatct	gatcgtacgg	atccaccggc	600
ttttgccaaa	catcgcaaag	tgctgcgcaa	tgcgctgtag	gttaccgcaa	actgaatgcg	660
gtagcttttc	gcaagattgc	tccgggggcg	tgctcttcac	cttcagctgt	tcgcaagcgg	720
tcagtcggga	ggaatccgtt	tggcggtctt	taccgcagca	gcatcggccg	gcagaaaggt	780
gcgatactgc	atcagcttac	ccaacctggc	cgatcacccc	atcaacatct	atctccggaa	840
ggcgaatacc	tggaagggct	tggtctctac	gtagaatact	а		881

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 855 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...855
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:913

```
gggcaaaaac attcaataca atgacgatag aacaattcaa tttcgccgga agaaagcctt
                                                                        60
cgtgcgcgtc gatttcaacg ttcccctcga tgacaactta agatcaccga cgacacccgc
                                                                       120
atccgcgcag ccctccccac tctccgcaga tcatagccga cggcggtatg accatcatcg
                                                                       180
gctctcatct gggacgccca aaggcgtagc accggagttc tccctccggc atatcctgcc
                                                                       240
gcacgatccg aactgctcgg cgtggatgtc ctctttgccg atgactgcat cggaccgatg
                                                                       30b
ccatggacaa agcggccaag ctcaaagccg gccaagtgct gctctcgaaa àtctccgctt
                                                                       36,0
ctatgccgag gaggaaggta agccgcgcgg acctccgacg atgcttcgga cgaagaaaaa
                                                                       420
gccgcagcga agaaagccgt caggctgctc agaaagagtt tacgcaaaag ctggcttcca
                                                                       480
tggccgactg tacgtgaacg atgctttcgg cacagcgcat cgggcacatg cttccacaga
                                                                       540
ctgatcgctg actacttcga ccgagaccac aaaatgttcg gctatctgtg gagaaagaag
                                                                       600
taaaagccgt agaaagagtg ctgcacgaca tcaagcgccg ttcaccgcca tcatgggagg
                                                                       660
ctccaaggta tcgaccaaga tagaaacatc gagaacctac tcaacaaagt ggataacctg
                                                                       720
atcctgaccg gcggatgacc tatactttca ccaaagcggc aggcggtcgg ataggcctct
                                                                       780
ccatgtggaa gacgacaagc tggatttggc tcgcgacatc gtgaagaaag cagcgaaggg
                                                                       840
gcgtcaatct gatac
                                                                       855
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 280 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...280
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:914

		acctetatee	ttgaggetga	agtactccgg	aatagcaccg	60
ttgccgctat	gaaaggactg	gccccgccc		antctctttc	aggtcgataa	120
ataatatcga	ttgccacgaa	tagaatcacg	aaggagccat	gattitte	aggtcgataa	180
		++ ~+ ~ + ~ ~ ~ ~ ~ ~	atccatcgtt	LULEALLER	L L E L C L E C L L	
ggcccaaacc	ctooggtaat	totcacoatc	ttgacagtcg	caaaattaac	gtttttcgcc	240
aggttggaag	giccggcggc	cgccacgaco	tactaccaac			280
ctatcaaaga	taaccatcgg	cgaaaaaagg	tactgccggc			

- (2) INFORMATION FOR SEQ ID NO:915
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 623 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...623
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:915

aggcgttgca agcctatttg ccggaagatg gctggttata atcgacacgc gtatcgccgt	aaaaaggttt tccgcacatt atgggacgca	gaccggctgg aagcgtgaat gccggcatgt atcaactgtt ctttctgatc ctcagcggat tagcagtatt	aagaggaacc aacaagatcg atgccgaacg ggaactgctc gtgctgtcca cgtgacagcc ctgacagcac	aagagatggg tacggcgttc tttcatgccg tccggggccg tggttcagcc tgctcacgaa	ttttatcggc aacgccaagc tcagctggtc atcgtgttcg gctacatctc gatacagatc	60 120 180 240 300 360 420 480 540
gtatcgccgt cgtctatctc ctgatgctca ctggtactac	atgggacgca tggctgccgg	ctcagcggat tagcagtatt gcccagttgc tcctgatcgg	cgtgacagcc ctgacagcac aagacgtgaa	tgctcacgaa ctatatgccc	gctacatctc gatacagatc gattcgggaa accgactgtt	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 718 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...718
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:916

gtggaaggat atcagaagat tgtcaaatta tttctttgat gatcggaatg cgttctgtcc 60 gatattgcaa tcaagcaata tgaatttgca ggaccacgag cttacttcaa ttagcggatc 120 acagagcgag tgcaaaggaa gagtcaaatg catcccggat ccgattgctt tttcttatac 180 ctttcctgaa aagtggaaaa aagacctgtt caaaagctgg tagaaaagca ttggagagac 240 gaactctttt agtacgagca cccactggtg ctggaaaaac ggatgcagca ctctgtgggc 300 360 ttctcatcaa atcaaacaca gaaaagcaga ccgcttgatt attctatgcc cactcgtttt acaacaaatg cactagetet aagegtatet teaccettte ttetacagge etgtateatt 420 480 ccagtgcatg gacacagaat tcagtagcaa aatagacaac ggggaaatag ctttagagca ggcaagatac atcataacca agctcgctta ctacagaccc ctataacggt atgcaccatg 540 atcatctcct ctcttcattg actctttgtg acgaggaaca tcagaccata cttttgcact 600 660 ggcaaatgca tgtctcggta ttgatgaggc agatttcatg atcaatttac acaagctaat atattagtat tactagaggg tctaaatatg gaaagtgccg atattgctga tgagtgcc 718

- (2) INFORMATION FOR SEQ ID NO:917
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 541 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...541
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:917

aacggatcac ccggcgcagg	atcggggtcg	tattgagtgc	cggagcagcc	tctatctgct	60
gaacgnatgg atactgagco	tgccggtcgg	catagacctc	gggctgtctg	ctacctcctt	120
acactgagcg caggatttat	ctgtctgtga	tggccggctc	ctggatcagc	cgcctgttga	180

			canantan	agtttcatgc	aggaaacccg	240
agcacaacct	gatggagatg	tattcaatgt	ggagaatgaa	ageceaege	aggaaacccg	300
_		aataaatete	CCGACTCATL	LLLALLALLE	gaaaag c 66°	
tctgagacga	acgagiacic	66 6 6 6 6 6 6 6	+ 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	catatactca	gtacgccggg	360
oceaceette	gatcaatgtc	gtgaatccti	CCCECECEAE	cacecee	60000-000	420
	1 L C C C C	+categaraa	CICALLAGEL	aacanaccea	Auu666	
gccgggaaaa	LCCLACECEM	\ t t = = = = = = = = = = = = = = = =	accettecca	agatogotta	caaccatctt	480
gccatgtata	tttatgacta	taatteeeg	accenteces	agacegeeca	1	540
8	cagaagggg	tattgaagtg	cagcccgaan	gttttaccgt	aatcaacttc	
gcttcagaca	CRRTTER	500000000000000000000000000000000000000	0 0	~		541
σ						

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1429 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1429
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:918

```
aaatagtcac atatttcgcg gcctgtcatt ttgcantggt gcaaagaaat tctggtacgg
                                                                        60
aatagatggc ggaacatgtg gtacatatag atcggaatcg ccgggcaaat ccgtattgat
                                                                       120
ggagagagga gcttgcaaat gatatatcgc gccggacttc gctcagcatc acatgatgaa
                                                                       180
tcagatccat gaaagggacg ggccgaacag agcgtctgca gaacttattt cggtggaaga
                                                                       240
aacaccatag gctcgttcac aaaccggcga acggcagctt catcggagga gaaagcgcca
                                                                       300
taaaggctga atcgggagta agccgcgata tgtccgtcaa gccccttcca ctctttatg
                                                                       360
cagtaccttg teteetttge gagegagaet gategeaeat eggaeaettt gteeaaatga
                                                                       420
ttggccggat tcagtacgag acggagtcgg cttctgctcc tttcaccctc cggctgtact
                                                                       480
cctgatgatc tgtcccagca atagtacatc tatgcctgcc acttcacgag cgagagtcaa
                                                                       540
ccggcatctt cgagatagtt cgaattgtca ttctccctgc cggaatgcgt acgcatacaa
                                                                       600
caaaatcagg titttccttt tggatcacaa acggtaccag tacttggccg attcgattat
                                                                       660
atcgtcgaat cgcattcccg tccacaactt tgcggcagcc actcaggaat agctggagtt
                                                                       720
ataaagccca acagaccacc ctcagcccgt tccgatcgaa gaccttataa ggagcccaat
                                                                       780
atggttgccg gtctcggtgt cgatagcgtt cgccgccaag aaagggaagt cgcgccggct
                                                                       840
accoatttgt catagacggc atggccggtc tcgatgtcgt gatgcccggt atggcggcgt
                                                                       900
catagogcaa gtagttcato gcacgggaga aagatgagta coogtogtgt coatgtagtt
                                                                       960
ataatagtag gccgtaggat gccctgcaat acgtcgccac catcgaagag cagcaactcc
                                                                      1020
gatetgteca eegggeaget tteagaaagg aageeaageg egacatteea eeegaagtgg
                                                                      1080
tettaaaget ttgaaateag tggggaatae atteeegtga agateegagt gtggataata
                                                                      1140
cgaagcgaat gctcctgcct gcttgcacat ccaccgggag aaacgtcgcc agcggaagca
                                                                      1200
ggacggacag caaaccgaaa agtctttctt cataccgtgc aatctgtagt attcctaaaa
                                                                      1260
gtctatttca cctgctacct gcagcaactt cagccgccgg cataatgacc ctgagcgaac
                                                                       1320
categoatee tetgeegaaa gaateatgee eteggaeteg atacetttea getgegege
                                                                       1380
                                                                       1429
ggcaaattgg cgataaagca tacctgcttg cctaccagct ctccggagc
```

## (2) INFORMATION FOR SEQ ID NO:919

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 443 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...4\overline{43}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:919

gccaatcaga acaatcct	ta cttccgaccg	aatcgagagt	ttgcctttct	cgccatacaa	60
cggacgaaat acttcttg					120
tattcccgaa cacgccti					180
gatatgctct ccggagaa	ac agcatcggct	gtctcaccca	atacgccccc	tacccgctac	240
atcttcggcc tacggcta	atg ccctgcatcg	cttccgtccg	ctttagacgg	atcagccaat	300
tctcctatag ctctttca					360
catcctcgtt cttataaa					420
agttnttcca aaatctga					443

- (2) INFORMATION FOR SEQ ID NO:920
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 952 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...952
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:920

gettgggege	agtggacttt	acggtggcgc	tgcactacgt	attcgatacc	cctacgaccg	60
				tcctgaccgg		120
				cccctcgcct		180
				tccgcagcac		240
				ccgtcattgg		300
				gtcttcccga		360
gatcatcctc	aatgacaaca	acatgtccat	cgcaggaatg	tcggaggact	gaaccgctat	420
atggtggaca	tcctcactag	cagacgtata	atacgattcg	ttacgacctt	tataagggct	480
				ctcctgcgct		540
ttcaaggcac	tactggcacg	cgagagcaat	ttattcgaag	gåttcagctc	cgttatttcg	600

			++a	ctcaatcaga	traaggatat	660
gccccgtcga	tggcaataat	gtgctccgct	tggtggagta	Cicaaccaga	tcaaggatat	700
BCCCCBB	- 00	anat acaaca	atcaaaoota	agggctactc	tccggccgag	720
ggccgggcct	aagatcctgc	accigcaacg	accaaagge	-888	tccggccgag	780
	contragrat	acaccaaaca	aattegatat	LaaaLLEEE	gaacg caage	
aagcaggcta	Cgattggtat	8-8888-8	+	ttcaaacata	caccgtggag	840
aagggagaaC	aagcccgagc	cacccaagtt	tcaggargrg	LLEEBECALA	cacceree.	000
uu666-8		tateateaga	gtcaccccgg	cttecceaca	ggttgctcca	900
ctggcggaca	gagacgagcg	LELLELLERE	Bccccc			952
	gat gaagaaa	tacccgaata	ggcctatgac	gtgggtattg	CC	932
tgaccttcct	gargangana			-		

- (2) INFORMATION FOR SEQ ID NO:921
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 445 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
    - (ix) FEATURE:
      - (A) NAME/KEY: misc_feature
      - (B) LOCATION 1...445
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:921

		atattaaaa	atatroatto	gtccatggcc	ctgcttcaat	60
gacgggtata	aacttcgatg	ctcttcccga	atgicegere	Breeze BBs	ctgcttcaat	120
ggcagccaga	gogacttccc	atgctcccgt	catttcgggt	cggcgatctt	CCECCEECE	
55000ttt0t	24244444	accttttcgg	togggataag	catcttcttc	tcccggcgga	180
accagillat	agacggaaag		anconcacat	otogcaggcg	taccgatgcc	240
tatattctcg	caggataatg	necegacgae	ggccgcacgc	6-86-488-8	taccgatgcc	300
gcaacggcga	gggctttgcg	ggcttcttcg	tccgcaactt	cccgtccggc	ggtgtccatg	• • • •
50000000	aacataactt	cccetataaa	ggggctttgg	gcttgtttga	tngntccngn	360
genegacage	aacacggccc		pagactttcc	ttoccattcc	pogaaagctg	420
catttcgaaa	tccgaaaaca	tcgagccggg	negeeeeee	cegeeacco	gggaaagctg	445
tccacaacgg	gtttcttcct	tnttc				443

- (2) INFORMATION FOR SEQ ID NO:922
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1048 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1048

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:922

	atataccgag	atactggaca	aatgagacac	totecaacac	aatagacagt	60
cccctcgcgt	atataccgag	atactggaca	aacgagacac	201022222	otototgage	120
acaaaacaaa	aatatggcga	aatgacagcg	agcaaaaccc	t-ttestese	atacatotaa	180
	aaaatttata	octttgagac	gactaccaag	Latiguicae	atagataca	240
	+acaaactca	aaaaagagaa	gagagggtac	gcagaacaga	acccc55	
	actoactoat	affafagaca	aaccttattt	CECCALCECA	6446466646	300
	a++aa+aaac	atacaatata	tagatatate	Lactagggau	CCCAAAGGGG	360
attacttggt	gttctcaacg	ctcaatcatc	aacotoaaga	cattgaacgg	atgttggcag	420
tataatttga	gttctcaacg	cccaaccacc	tacastcata	attacggaac	tatatacgac	480
agcgacctta	tgagaaacga	Cgcccagaga	estatesta	ttttgcaat	agccaagcgg	540
agacgaggtg	gcgatatcca	caacatatet	cgatcttctc		atatanator	600
	+craacttat	aacagaggca	agacctattg	gagcaaacgc	acacagacga	660
	anacadacto	-ctgcttctca	tatcgaaaat	ggiglacage	66666666	720
	+ccatatgac	ortracecce.	tttacaactt	Latticegat	Cucuucucu	
	actracocts.	aaaoctacta	ttccaccaaa	Latguegaag	capc cam-op	780
CCagaaagaa	agccagggc	aagctactat	actettceee	aggctatgga	aaatttggtc	840
agtgttgata	aggcagcccc	aagecaecae	aacattataa	totoctasac	taaagcaagg	900
ttactcgtga	ccagctctat	Caatatacta	aacgccataa	tcaaacctcc	cagcatcact	960
tcggaatgtc	ctcatttctc	agcaagaatt	gatgaagtee		cagcatcact	1020
cgataagtta	tttgttggtg	tatgggacac	cctcttatca	CCTTALLCLL	ttgcaactga	1048
atcaataaaa	taaccctcta	atcaacgg				1040

## (2) INFORMATION FOR SEQ ID NO:923

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 396 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...396
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:923

tagctcgccc tctc ttaggagttt cttc aacggcgtgt tttg aagctaataa agca tatatccacc ggga	ggtttc ttttcggaca tattaa agttatttat tgcagg agctgctcta gtgcct tcttcgctgc catagc agcattatct cgatct gcaatcttag	atccgatgag ctacaacgtc ttcgccaagc cccagacgat cagcaacatc	tgcgctttta atattctcat aaccggtctt	cgcttacgag tgtagtcaac caagtacggg	60 120 180 240 300 360 396
attatctgta gtaa	gagagg cgatcgcgag	aggcgt			396

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 897 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...897
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:924

teenactate	tractictest	toggggcctg	ttcttggctt	ggttacttgc	ataggcgtac	60
Eccugerace	theastatt	cacctccatt	ccctcctggt	cttatttgcg	gtgccgaacg	120
tgctgattcg	tttcggtatt	CgCCCCgcc	cetectegg	taaggatgcc	ettcagcttc	180
ggcggagata	gagggtgtac	ccgtttattt	gctcctcgtg	Laaggacgcc	antattatta	240
+ - + - c c c c t a	+++atctcco	acceatciec	gctcataccc	LLCLELEAGA	aacgeeecca	300
+000+0000	gaacataccc	gagcaacgca	ctttgtcgai	Cilligates	cceae cee	
tacatactat	tttggttcaa	tccetttect	tgggctttga	agccgatatg	cagcgcaatt	360
Lgcalgcigu	teeggeteen	actatactcc	tcgaggcgtg	agcagacgcg	aatatcaata	420
tggagttttt	ggccgaccgg	gergegetee	accassoct c	tototagttc	ttacaatata	480
tgaattgttg	ggatttacgc	tgaggtcgcg	gccggacctc	thenestest	acaaccaasc	540
aacgacttaa	agaaagaatc	agaatgatga	acaaaacgaa	acceatings	8088008800	600
caggtatett	gtogcactco	cetteectec	ccttatgcii	CLEAGLEGEAG	4666666	• • •
caggaraata	crotatroga	agtccgggaa	gtagtagaac	cgttgcgagc	gatecegeee	660
gcgggcaacg	testectase	atctcctgca	gcaggacgag	gatcctgtgt	gttccgagct	720
ccttgtctga	Lgccccgac	accecegea	teeggardee	tacactttct	gagcaagaat	780
agatactcca	ccatcttccc	cgggggaarg	CCCgaaccga	terester	gagcaagaat	840
ttaagtatcc	ggaacaatct	gcaaagaaca	gcatccaagg	tcgagilgig	gtccgtttat	897
tgtcgaaaaa	gacggcagac	tgactaacat	acaagtggaa	aaagcgtagc	acccgaa	091

- (2) INFORMATION FOR SEQ ID NO:925
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 374 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
    - (ix) FEATURE:
      - (A) NAME/KEY: misc_feature
      - (B) LOCATION 1...374
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:925

tggctgaatt ccatg	tates assetcects	tcagatagcc	ggtgatgcgc	gcaagcgagc	60
tatccgatcg ctgcc	gcata caggarattt	otcotagaca	cacctttgaa	gccacagccc	120
tatecgateg eige	ggatg attaatcaac	catagecoat	pttttcatcc	ttcatcatct	180
ttacaggtat ccaca	taccg atacattctt	cttagcttcg	ccatccaact	ccacataagt	240
tgacaatttt gagga	gtaat agcatggaaa	agaactcac	acttgatctt	ttcactatac	300
aatatgccac cgccg	catcc acatggaaag	anttancata	ataatgcasa	atccettacc	360
ctatcgattc gcgaa	icatcc acatggaaag	aattgatgta	acaacgcaaa		374
ccggggataa tccc				`	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 626 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...626
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:926

	cotootooct	constastto	coottecate	cctgcacatt	tccttgtgtt	60
tattcatcca	gataataget	Legacaacca	attonacan	atoaoaroat	tctcgtaagc	120
cgggaacatt	ccctgattcg	tagtettegt	CLLCgacagg	atgagacgat	tttatatata	180
gaaattatgg	gttgccataa	ctgtttatgt	tttgtcaggg	ttagaaaatg	LLLLLLarg	
actacattca	ocaptgatca	togtogtatt	cgtcctgaga	gaggctgatg	Citicigual	240
getgeattea	esecttctc	coacataatt	ttcccaactg	tacaggcgta	cataccgttt	300
ctttgcatag	Cagciffic	cgacacaaca	ttanatooga	catocacaac	agcagttcgg	360
cccttattca	ccgaaaccac	aggcacggcc	LLaaallega	catgcacaac	ogtccgaacc	420
tcaattcaca	ggcacgattt	ccgtattcgc	ttccacgata	agaatggata	Cgcccgaacc	
cattttata	cogtaatece	agaggagtta	tttcgtttcc	tgcgatccat	tgagtgattt	480
CECCCACE.	********	ctcacatttt	++++gcgtct	aaagctcgga	gtgtgccgat	540
aatctttctt	ttccataatg	Cigacacccc	tetet	caaggettee	gaaaaaatac	600
tcgtttcgtg	ggctgttcaa	ggtggccgga	gggtatatgt	caaggcttcc	Baaaaaaa	626
gacttggaac	gaaagtggaa	atgtgg				020

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 497 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...497
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:927

		+ +	ggcggaaagg	acaaaaacat	ccagccccaa	120
caaagaggaa	gaagatagcc	atacgacgic	ggcggaaagg	acadadage	caanataaaa	180
		+~++0++++	LLLECGEEGE	FF-~P-D-DD	~~~00~	240
		a a a a c c a c c v	Latteatate	Eug C C P C C C C		
						300
cccatcgcat	atategacee	t-t-t-cota	conactttct	ccaagcagta	taggctatcg cgggataaaa	360
ataggaggaa	attcgcgcac	tatatttata	Leggetteet	occapcataa	coogataaaa	420
		aacatatauc	ILLECAPARO	u K K u K u w u u u u	-000	
aaccaaataa	ctactcagcg	tgaagcataa	ccagcaatat	ggctccgatc	agatggcacg	497
aacggagcaa	tttatac	<b>-</b>				497
ctcccaagag	LLLBLBL					

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 484 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...484
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:928

acttcatcgc		gactcctttc	cctcttcctc	gccactttta	tcttggcgaa	60
acttcatcgc	cgtagcalag	gacticette	ctccctccc	traccateat	gatggccagc	120
gacgaaagga	tcgtaggcat	agcgaaaggc	Cigggigaca		+000000	180
	caccatagat	acceaecete.	CTTTCCCCCC	CECCEE		240
	22+2+++000	CCEPALERIE	gaagutgutg	gccaugccou		
agggaagaat	aggerage	cttgcgcaga	acgtccggac	gaaatacgcg	gccgcatgcc	300
agggaagaac	aggicageae	ecceptor aca	casaantaca	aataagttga	tgacgaacac	360
gccaatgagg	aaaaagcacg	accaccigca	ceaee.ce	actrograto	taaggcataa	420
gtaccccaat	tcgtagttcg	ggcggtagaa	gcatcgatct	accccggacg	nggattgaat	480
ataccgggga	cacagggang	agaaaaagat	cgtaaggacn	atgggtcanc	aggattgaat	484
	200 0	-				404
gtca						

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 964 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...964

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:929

+-+	catctcacct	cgttagcgga	ectttatctt	ttggataaca	aatccgtaag	60
gggtctggaa	Cgcccaccc	cacatactta	acaacactaa	actatoggt	aaccaaatcc	120
ctggagggtc	tggaacgtct	cacgtcctta	gcaacgccga	attaccobbs	constaacca	180
gtaagctgga	gggtctggaa	cgtctcagtc	cttagcaacg	citgaactat	teteeses	240
aatccgtaaa	ctagaggtct	ggaacgtctc	acttcgttaa	caaagcttcg	tctaagaagt	
aaccaatcag	taaactagag	ggcctggata	gtctcacctc	gctaacaaaa	CLLLCCCC	300
crataaccaa	atcagtaagc	tagagggtct	ggaacgtctc	acccgttagc	ggagctttat	360
cgattacean	accapatrag	taaactagag	ggctggaacg	tctcacgtcc	ttagcaacgc	420
CLLLEgala	accuaaccag	accgtaagct	ogaggetetg	gaacgtctca	cgtccttagc	480
ttgaactatc	gggtaaccaa	accetaaget	554555555	atrtagaara	tctcacttct	540
aacgcttgaa	tatcgggtaa	Ccaaacccgc	aagctagagg	Perceptage	tctcacttct	600
taacaaagct	tcgtctaaga	agtaaccaaa	tcagtaagct	agagggccgg	aacgtctcac	660
oficitagea	acgcttgaac	tatcgggtaa	ccaaatcgta	agctggaggg	tttggaatgt	
ctcacgtcct	tagcaacgct	tgaacttcgg	gtaaccaaat	cagtaagcta	gagggtetgg	720
aacatctctc	ttcgtaacaa	agcttcgtct	aagaagtaac	cagatcagta	aactagaggg	780
aacgccccc	teaceteact	pacaaaactt	totototoce	ataaccaaat	cagaagctag	840
cctgaacgtc	ccaccicgec	tosttasses	anctttatct	ttogataacc	aaatccgtaa	900
agggtctgga	acgteteace	LUGLLAGUEG	agecerate	togtotage	antaccasa	960
gcctggaggg	cctggaacgg	tcttacctng	tacaaagctt	LUBLULAABA	agtacccaaa	964
tcag						<b>90</b> 4

### (2) INFORMATION FOR SEQ ID NO:930

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 136 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...1\overline{3}6$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:930

tgtgcagaca cttttaagat tccttaaaag gaggtcgggc ggagaccttt gaaaaa	aggtctgtaa gacttcgttt	ttgtctcaga ttattattct	gtatgaatcg gtccggtaaa	tcgcccgact cttgtcaaga	120 136
ggagacette gaaaaa					

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 484 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...484
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:931

cttatcaatc tcagtaaaaa cagtacatgt attgatgttt cttctttgta	tcagaccaaa taggtttgtg cttaccaatc ctttgattac aatagagtaa	gaatatattt atattcgtac cagctgctgc agaaatgata ggcatactga pcaaattctg	ttctacaaca tcagaagtcc tgtactggta tgatctccta	catctctgtt agatttatat acaagatgtg catttatagc cttatgtcac ttaatggcat	atctcatatg caccttttct atctctgcat tgccgcaata ttgcagtggt	60 120 180 240 300 360 420
atactttact	toattagtgg	gcaaattctg	tgatctccta	ttaatggcat	ttgcagtggt	420 480 484

- (2) INFORMATION FOR SEQ ID NO:932
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1058 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1058
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:932

taacettg attecatege atgggategt tggcaaaatg accgttatea t		69
cttcagcc ggtacgcct cggtacgtaa tatctcttat tgagctgagc	ttttccggaa 1	.20
tatcagge ctatttectg ategtaattt gtagecacat gegaagattg t	ccggcatac i	80
tccatgtc gaaacgccaa tgggtgaata ggctaaaatt gtcggtattc t	tgtcatctgc 2	40
ctaaagag catagccctc attatttcca cgattagcta cataaaaata t	tgcagagagc 3	00
tootottg tgatgtgata cocototoag catotoottg cogtaaacgt a	aatogatgga 3	60
tottgtca gatactgctg tttgtcccat tccaaggata cctgtcgcaa a	agccagccga 4	20
cagactca aagctcgctc ttcgtaaccg gagcagaatg tccctgcatg g	gcaatgccaa 4	80
agcattac atggctaaaa gaaaactttt tttcattgaa ggtgatattc c	cgaattatgg 5	540
tttttgct gtggtcgccc tatggggcat tgtagaattt gctgcattta c	caaaagtgtt	500
tgatgatg tagtattagg atcaggcaat ctgaatgaaa aagccggaat t	ttatattett	560
caatcotg coattitaa gagotgaacg gotgottocg tgcotttgtt	gccatgcttg	720
cccggcac gctctcggcc tgaagcattg tttccgtggt aaggactccg a	aaaatgactg	780
acaageeg teaatgttea actgggtgat teeetgtgtt acceettgge &	agaatagteg c	340
gtgggggg tgtcgcctct gactacacag ccgatagcga tcctgcatct a	acttcatgct c	900
6-888888 - 3 - 3 - 3 - 3 - 3 - 3 - 3 - 3		

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1666 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1666
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:933

```
60
tagggaatat ttattttttg aaggaaatta tgaatgtgta attaaaatga tcctcaactg
                                                                       120
gttgatttgc tatcaaaaac actcccccaa caaaacatgg gtatttgggc aacagcgaag
                                                                       180
gttgggttac actttacctt gaagaaagtc atgaatacaa atcattatta tatccgatat
                                                                       240:
ggatgtgcaa taactcgtat gataatcatg tatcagagag ggaaaggcta actccaaaag
aattggatto agcattgaaa aagoggttto otottttagg atccaagoco aggacotttt
                                                                       300
tccccaggat caaaggcccg tttctctttt gtcaaaagaa aagtggaaac acaaagaacg
                                                                       360
gaatatttct ctccccacat attgtcacga aaacatgcac gcccaaaaag tttggacaaa
                                                                       420
                                                                       480
agcatctaaa tttcttgaaa tgactattta ggcaaagaca atgaacgaga aggcttactc
                                                                       540
aaaaaagaca tgtgagcatg tctaatatcc cgatatccgg agaatadctg acttttggca
aaaagatact gggcgaggct ctgcaaaaat atctgttgaa gaacaaacta tggacttatt
                                                                       600
actacactaa cgcccttaaa gcctgcattg caagtcggaa agataatttt tgcatcattc
                                                                       660
ctgatatece acteaateaa atggteattt catagetete tttgacaaaa tgeaaateae
                                                                       720
                                                                       78Ó
tcatttatca ggagagcaat gttaggaaac atagataata aaggaattcc tcatcgtcca
                                                                       840
aaaactttcg agggaatttc cctaattcac ccaaaagtga cagaatggga gcattgcgtt
gttaggggct ataggagaat ttgccaagca tgcagaattt tcactcttgc tcaaaaggtg
                                                                       900
                                                                       960
ctagattcat tgaaaggatc aaccttgtat cgattacata cggcaatgca attccattta
cgtttcatca ttatataata atctagcaaa agaggggaaa ctacactcta tagtggatag
                                                                      1020
                                                                      1080
cttattttaa agtcggctct ataaaaaaga aaaaagagtt tatggggata ccgattatac
cgatttgact ttttcaccaa tcgttttta caatcattca ataaggcgct ttcgatgact
                                                                      1140
tttttagctc cagagtagaa tatccaaatc aaatcaaata ttatttcaaa tgttttttac
                                                                      1200
                                                                      1260
caaaatggag aaattaaaaa ctgacttatt gcatctgccc agatattggg ttagttgggc
tcaaccaagt tgcaattttg cagcaaaaga agaagccgat tcatgaatct ctccaggaaa
                                                                      1320
tattttgaag aaaaagctaa atttttagtg atgatggaga gcagtattta tgagcaaagc
                                                                      1380
                                                                      1440
gaggagatgo totoattgot caaatootoa ttttagcagg agattatoaa agaatgaago
                                                                      1500
tccaaaagag gcattgcttt tcatggagaa accattaccg gagaaataga tttgtctgtt
                                                                      1560
gcaaagaatc ttctaattga tacatgcgta ttctgcagag aatgagaaac aacgagattt
gaacagogta aaaaogatga ogoattacoa totgatataa acattgatga ottaacaaca
                                                                      1620
cataatactt catatatgga aacaaaaaaa ttgcaggagt tttggt
                                                                      1666
```

#### (2) INFORMATION FOR SEQ ID NO:934

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 510 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...510
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:934

gggttgcatc	gtaattacgg	gcacaagcat	ctcttcgagc	gatatgcctc	gtgctggaat	60
gtattgcgat	agtattgtac	gtagtagttg	tagttattgg	gtaggcgaag	aagtcatcct	120
ctttcgtgaa	gatgaatttg	tccgagagtt	gttatggggc	agccctacac	ttgcaggatc	180
tttgatctcg	aatactcttt	cgggttgtag	tcgaggttct	tacctatttt	gtatctgagg	240
ttggtttggt	acttctgtct	ccgatcactt	tgacgggatt	cttcacctga	atagaccatg	300
gtcagtggtc	aataccactt	tataacccat	ttcggcaatg	ctgggaagag	attgtaggta	360
gtcgaatgct	tgaaccagct	tcttcgtcag	cggcgatagg	ctgcttcgtt	ggatgccagc	420
tctcgaatca	tcttgctatc	agtacgagca	tgcgacatca	tgtccaccga	aagttcagga	480
		tgcgacagtg				510

- (2) INFORMATION FOR SEQ ID NO:935
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 549 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...549
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:935

noggoatosa	acaaatcaaa	ctacaggtcg	attctcggga	ctcacgtcca	ccggtgccat	60
acggcaccaa	acaaaccgag	caaaggcog	tacaaaaaca	ccaatatcaa	topcacgaaa	120
gattactctg	gaagatggga	caaagaccgc	tacaaaaaca	ccgccatagaa	ottotogato	180
getteteecg	geetgeteeg	acccacgaga	aagactatcc	agacacagaa	tattaacaaa	240
tccgataata	aaaaccatct	tagteegttt	cctctttgat	agaaagaggu	cattactgac	300
caacgaaaac	tatgaaccaa	acaacgaaaa	cactgtcgat	cattettate	ggtagetgae	360
cttccttgtc	ggggcaagcg	caaaactcaa	cgcccccct	tgtgggaccg	Lgctggagga	420
ggtacctttc	tcccgaagaa	atcaaccttt	tcgcagacaa	cgtcagccct	tcttcaaag	
cctatattga	attggcattc	accgaaggaa	accaaagcca	tgctcaccat	tccgaaatag	480
aagggatggg	gaccaaaacc	ggcagaatcg	aaagaaggaa	atcgactacc	gaatgcaacg	540

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1631 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION  $1...1\overline{6}31$
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:936

```
aaggacgaac cagatcacca aaccggaaga tttccgatca ctactggcgt atcggatgcc
                                                                        60
tatttctatc gaaagccttt ctgaagacta tcgggagcga acgaatcgat agcctccctc
                                                                       120
attcgcacct caggcagagg ataagctccg ggccactgta tcttagcagc tacctccacg
                                                                       180
gttttctct gaaaggatgg agtggagtta ttttattatt ctgcgtttta tcatcccttt
                                                                       240
tgtgtctttt gcccacgata ctaaagagtt atagattaga aataaaaaga cttagcttaa
                                                                       300
cgttgtaagt aagactatcg atctgggaga tggtcgttcc atcagatcga aaccggtaaa
                                                                       360
ttggccaagc aggccgatgg cgccgtgaca gtaccatggg caatacggta ttgctcgcta
                                                                       420
cagtttgtgc agccaaagac gtaaccccgg ctgcgacttc atgcctcttc aggtggaata
                                                                       480
caaagagaaa actccgccat cggacgcttc cccggaggat tcactcgccg cgaaggcaag
                                                                       540
cttcggatta cgagatcctg acctgccgcc ttgtggatcg tgcccttctc cgctattccc
                                                                       600
ggacaattat catgcagagg tattcgtcaa tgtgatctct tttcagccga tggcgaggat
                                                                       660
atgcccgacg ccttggccgg tctggcgctt cggcggctct tgccgtttcc gatataccgt
                                                                       720
tcaacggccc tatcacgaag tgcgcgtagc acgtgtggac ggccgctata tcgtcaatcc
                                                                       780
tacttcgagc agctcgaacg cgcagacatc gacttgatgg tcggagccac aatgacaaca
                                                                       840
                                                                       900
tcatgatggt cgaaggtgaa atggacgagg tacaggaatc cgaatgctcg aaggcatacg
cgtggcacac gaagccatca aggtacagtg caggcgcagc tcgaactatc cgaagctgta
                                                                       960
ggaaaacttc aaaagcgtga tacagccatg aagtaaacga tgaagacctg cgcaagaaag
                                                                      1020
tgcacgacga tgctatgctc gtgcctatga ggtggctacc agcggaaccg gcaaacacag
                                                                      1080
                                                                       1140
cgcggcgaag cttttgaaaa gatcgtggaa gagttcaaag ctcaataacg gaagaagaac
ttgccgagaa ggccgaaatg atagctcgct actacccgat gtggaaaaag aagcgatgcg
                                                                       1200
tegtgecate etegacgaag geaaageete gatgggegta agaccaegga gateegteeg
                                                                       1260
                                                                       1320
atatggatcg agacgactgc ctacceggcc cgcatggctc agctatattc actcgtggtg
agagcagtcg cttacgaccg ttacgcttgg tacgaagagc gacgaaaagc tctggacgat
                                                                       1380
gtactcaatt atacgaaaga gcgattcctg ctgcactaca attccctcct ttctctacag
                                                                       1440
gtgaagcccg tccccaacgc ggtgtaggcc ccgcgagatc ggtcatggca atttggcgca
                                                                       1500
                                                                       1560
 togogocoto aagogtatgt acogacggao taccootatg tggtacgtgt aatoagogao
 attetggate caatgggete gteettegat ggecaetggt etgegeeggt aettttgete
                                                                       1620
                                                                       1631
 tgcgccgatg c
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1191 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1191
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:937

	ttcagaaaaa	aagtgtcggc	ttcggaaaag	tcgggcaatc	acggcgtgtc	60
tcatgtccaa	tgtccgtgta	aabcaacatc	toctcataac	ttgtgctccg	ccgatgacaa	120
agatagattt	tgtccgtgta	ggncagcacc	ataccacttc	pppcgaagct	tgccccattc	180
aggcntctgc	ctctttcgcc	Caccagecca	tessesses	ttacatctat	toppcaaage	240
gggctcccgg	aaaatctgct	gcatcctgct	taggatgata	testatess	tototrattt	300
++	acasacaas	totocoocta	CCCatgataa	LECTRE	-6-6	360
+++	+++nagatco	occoocapat	gccagaggag	gictities	accepaces.	420
	actatagraa	caacgattga	aacatattee	alaggigugg	aaaaa - B	
L-L	aaacattcco	tagactgcta	caacgcccgc	aatgtgtggu	CBCBB4C040	480
	compagatett	cotatioggaa	gtcgaagaga	CCERACACCE	CC664555	540
accettegag	gcaacgctct	cooctcacga	ctcagttgta	gctgtaccgt	tcgaggtggt	600
accatteggg	atgggcgtcg	cccantatat	gtacgaacgc	ccegetttca	gccctgtgac	660
taagatagat	atgggcgccg	cccagcgcac	geacgazes	toaacegtat	gcccagaaaa	720
atgagcgatc	atttgtagca	ggagcgacac	targecacce	nt cag coaca	tagaactgca	780
gaatcggcac	tgcgcgatag	agttgcaggc	Cagceggee	actacattcc	acggratacg	840
+	catogaggga	gatgcatatc	ggcaagctgg	CCCacacccc	4666646	900
at a at a cacc	aactatccaa	ttcttcgcgc	agctggcgca	guuluuu	acceppeda	960
+ a + a a a a t c c	ccastagtcc	ggccaactgc	gcactggtag	CCatatatag	geceauace	1020
	tragrecatt	officaaatg	CETACECCAL	gilligeag	graargraag	
++0a+a+cac	tctgaggaac	caaagcagtt	cgtatataat	ggacticaag	CECAGCCEC	1080
cccgcgccac	aaaaaaatc	cctcttcaag	gtcaaagcac	atctgatgcc	gaatacgctg	1140
ggicgiaage	tacccgtgcg	atcttcttt	cetactcctc	gtcgaggatg	С	1191
atcgtacccg	Lactegrace	geeeeeee	06000000	5 5 66 6		

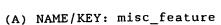
- (2) INFORMATION FOR SEQ ID NO:938
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 445 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...445
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:938

		acaaccataa	ccotactoga	cagccacgct	gtctgatttg	60
tatcggacat	cctcaatatc	acggccacgg	CCELACCEGA		nacatatatt	120
attcaggtat	aaatccgtac	aacaaataga	ggctgtttac	tgcagaaacg	agectetate	
+++ccc++ac	agctataaga	aagcctacgg	aagatgctaa	ggctaaaaag	caaagaggct	180
LLLCCCLEGG	age caseage	accetetta	tatttoooot	ttctatcttt	cggaaaagtt	240
gctccgcacg	atttgcgagc	agccccccg		anatttacto	agtagacatt	300
cccgaaagtc	gccttttatt	gtccttaaat	ccgatggact	gactttactc	ggcagacacc	
ctacccactt	gagtccgccg	gcggttctgc	cggcttccaa	gagggcaggt	tggcttccgt	360
Cigicogcic		tatcattcag	gracectact	teaceccacc	catagatact	420
cggaatgtag	atcacggici	tgttatttag	Percentage	-00	Ü	445
gaatgtattg	tgggcgtaaa	gcttg				7.75

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 537 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...537
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:939

actossasta	cttgccatga	eceeteaeea	cggaggaatc	aagagtctgt	caatctcaac	60
atestaces	tetetttgag	ctatgagtat	gacccctgga	ttacctgaaa	gcgcgcgaga	120
tactcaccge	acadcacaac	ccettattaa	gaaacccgtc	ggggaggatc	tgctgaatat	180
cgcccagcaa	attttcgcta	caaaggacgt	gttcactttg	ccataggtac	acccctaaga	240
gcagacaggc	gaggatggg	ocadatococ	cecatecce	gcagttcaca	gaggaggcaa	300
gaattgccga	gagcaceceg	atcatcacta	ccetctctat	ccggcaatta	tgtagcatgg	360
actgatcgat	gcagaaaccc	ccacaccaat	treattatag	caaggaggaa	aaagagacct	420
gatettetgg	acggatgtga	coatgoogge	antonagato	caggataagg	atgaagagga	480
ttgtaaacta	tetgteegea	taattggtaa	ageggagaeg	aagggcatat	atgaagagga tatgctg	537
attgaaacga	tggattctga	tcatgtatge	caacceggca	aagggcatat		

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 492 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:



(B) LOCATION  $1...4\overline{92}$ 

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:940

ggaagggtta	ttgtgtaacg	gtctaatgaa	aacgaaaaga	ttattgccgg	agagttgtgc	60
aacggaaaag	ccatgaatcc	gatagtcggg	attcatggtt	ttccgttaga	gtgagggaga	120
		cctttacatc				180
		cccattactt				240
gacggtgatt	atttcctgta	agatgggggt	cagttcctca	cgtgagagtt	gtttggtagg	300
taggcctcga	ttacctcggc	ttcggcaaag	ctcaggttcg	gccgttcggg	tctgccgttt	360
tctacaaaga	tggcagcact	ctcgcggcgc	tgttcaccat	cttttgcatg	atcttgaggg	420
ctgcatcttc	ngacagagtg	catcgctgcc	tttagctgtc	ttggcttcga	gaaattcttt	480
cttcactccg						492

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2202 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...2202
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:941

tgcgaaagga	agatcgagac	aatctttctg	catgaacgta	atccgattgc	caaattctcc	60
gaacgtgctt	tctgctcccc	tatcctcatc	atttccaaga	aagatcgaca	cccgtcacct	120
gcttgactga	agggatatgc	ctgcatattc	gatggctaaa	tcacccgttc	cggtagccac	180
atccagcact	gtatgtgagc	gaaaggctcg	atcatacgga	tagccttctg	ccgccataca	240
cgatcattcc	ccatgaaaag	aggtgattga	gacgatcgta	atgtccggcg	atatattgaa	300
catggcctct	acctgttcat	tcttggggca	ttcggtgtca	taggggttat	tctttcagga	360
ctttgcatgg	cacatgattg	ttcgacagtc	agcgactgct	aacgcagata	ctccgttatg	420
ttcttttcta	ttctttctgc	cgattgctca	ggtctgcctt	ttcgaagggc	ttacctacca	480
ctcgctcgta	aattctatgt	accgctccga	cacactgtcg	cagtatgctt	ccgtcatttc	540
ggtatttgct	ggccgggctt	gccctggaaa	ccgttctcga	tcagccacga	cgaacaaact	600
ccttggataa	ctgcttctgg	gcttcgcccc	gttcgaacgc	tcctgatagc	cctcggcata	660
gaagtagcga	gaagagtccg	gcgtattatc	tcgtcgatca	ggtagatctt	accgtccttc	720
ttgccgaatt	cgtattggta	tccaccaaaa	taagcccctt	ttcagcagcc	atttgagtac	780
cgcgtcgaaa	agtgcgtaag	tatagcgttc	tatctgctcg	tagtcctctt	tcgcaccagt	840
ccctgagcaa	tgatttcctg	acgagagata	ttctcatcgt	gacctcatcg	gccttggtcg	900
taggggtgat	aatgggatgt	tcgaaacgct	gttttcgcgc	atgccctcgg	gaagaggcag	960
accgcaaagc	actcgctcgc	ggcagcatag	gcacgccatg	cacttcctgt	gatgtagccg	1020
cggatgacct	ctcgaccttg	aacggttcgc	aacggtgtcc	gatagtaacc	atcgggtcgg	1080
cgtagctatc	ttccagttcg	gaactatatc	gcgagtggca	tcgaggtgtg	tgccgctatc	1140
tgattgagta	cctgaccctt	gtaagggata	ccggccgaag	gactacgtcg	aaagccgata	1200
				gtgtatacgt		1260
gccgtgatat	acggtttctg	tcccggcagt	ctgaagtcgg	tacgagctaa	tgtttctttc	1320
				tégectgatt		1380

gcgcaacgac agctgcggctatcaccaca cgctgtacgacctatccctc tcgttccttgtgggaagacg gtctgcgtaagtcaggaaca ttttcatctgcatcgttgag cgtacgtcctgatgtactct tttagcttcaagtaggaat cgacttatctccggcagga cgtgagagaaagactgatgg ctacgagggttggcctcgaa agcctccacatcccgttcca tgcaggataggaactgcaggaact tccaggaact tccaggaact tccaggaact tccaggaact tccaggaact tccaggaact tccaggaact	gcggatggcg aggatattca tgtcgccggt caactcggtc ctcatatagg cggcgggatc ttcatctcac tgatacggcg cttgcccgtt agtttctgcg atgtttaggg tcgggcagga	actatatcag gagcctgacg gacgatcatc gtattctgag ccaatgtgct atctcctca cgggcagaaa cacctgcttg ccggcagggc attatcacct acatcgtcag ggttgtactc	cgcgttggaa cagaccggag ttggcattgg cttcgtcaga atctggatga gcgcatcata tcccagcttc cttttcaagg gatggcaaaa ctggcaatga cgggcagctt acggcaatac	tgcaatatag tgcacacctc caccaagcgg atgaccacgg tgttgtttc cagaggctgc tcgccggctt ccggacagcc acgaggtcat tgctcttgcc ggcaccctgt	1440 1500 1560 1620 1680 1740 1800 1960 1920 1980 2040 2100 2160 2202
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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 784 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...784
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:942

gcaaaccgat	aatagaaata	gatatgcgag	catattacga	actgaagcgc	gtcgagacgc	60
atgcgataag	gaagcagaac	gataccagaa	ggacatcttc	gctgtttgga	tcatgtacgc	120
aacaattatg	gcgacatgat	tttcgaaaag	ttgagaccca	tctgatctat	cctggcagcc	180
		tcctcatcgg				240
		tctccatctg				300
		ggctttgtta				360
		gtcttttcgg				420
		ctgaaacaat				480
		gtaacctttt				540
		ccaacacaca				600
		ggtggggtga				660
		tatctccgaa				720
		cgtatgcatg				780
agnt		0 0 0	9 9 9	_		784

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1029 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular